

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 12.4614 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688
Sequence: 1 QVQLVQSGAEAKKRGSSVKV.....EPREDALDINGGTMVSS 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:1
2: PIR1:
3: PIR2:
4: PIR3:
5: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	74.9	128	2 PH0952	Ig heavy chain V r
2	509.5	74.1	133	2 C33548	Ig heavy chain V-1
3	509.5	74.1	627	2 S14683	Ig mu chain precu
4	502.5	73.0	135	2 PH0953	Ig heavy chain V r
5	501	72.8	116	2 PH0959	Ig heavy chain V r
6	498	72.4	120	2 PH0962	Ig heavy chain V r
7	498	72.4	122	2 PH0958	Ig heavy chain V r
8	498	72.4	132	2 S46394	Ig heavy chain V r
9	497.5	72.3	119	2 PH0961	Ig heavy chain V r
10	496	72.1	132	2 PH0954	Ig heavy chain V r
11	495	72.1	136	2 PH0960	Ig heavy chain V r
12	494.5	71.9	129	2 A33548	Ig heavy chain V-1
13	490.5	71.3	125	2 PH0957	Ig heavy chain V r
14	488.5	71.0	127	2 PH0955	Ig heavy chain V-1
15	486	70.6	126	2 B33548	Ig heavy chain V-1
16	481	69.9	135	2 B32274	Ig heavy chain pre
17	456.5	66.4	113	2 PH1663	Ig heavy chain V r
18	452.5	65.8	121	2 A49590	Ig heavy chain V r
19	451	65.7	108	2 PH1664	Ig heavy chain V r
20	451	65.6	98	2 S26915	Ig heavy chain V r
21	451	65.6	116	2 S31698	Ig heavy chain pre
22	451	65.6	116	2 S36261	Ig heavy chain V r
23	451	65.6	123	2 S44108	Ig heavy chain V-D
24	450	65.4	124	2 S19655	Ig heavy chain V r
25	450	65.4	136	2 S31600	Ig heavy chain V r
26	447.5	65.0	122	2 B49590	Ig heavy chain V r
27	447	65.0	98	2 S24680	Ig heavy chain V-1
28	447	65.0	119	2 S44106	Ig heavy chain V-D
29	446.5	64.9	142	2 A32483	Ig heavy chain V r

30	446	64.8	118	2 S36265	Ig heavy chain V r
31	442.5	64.3	122	2 C49590	Ig heavy chain V r
32	442	64.2	171	2 S23623	Ig heavy chain V r
33	437.5	63.6	160	2 PLO105	anti-PR2 erythrocy
34	436.5	63.4	109	2 PH1671	Ig heavy chain V r
35	435.5	63.3	129	2 S36260	Ig heavy chain V r
36	435	63.2	135	2 S49530	Ig heavy chain V r
37	434	63.1	98	2 S46463	anti-Sm antibody V
38	430.5	62.6	127	2 S34014	Ig heavy chain V-1
39	428.5	62.3	129	2 S46393	Ig heavy chain V r
40	428	62.2	98	2 A30523	Ig heavy chain V-1
41	426	61.9	97	2 PH0870	Ig heavy chain V r
42	422.5	61.4	122	2 S36271	Ig heavy chain V r
43	420.5	61.1	117	2 G1H8U	Ig heavy chain V-1
44	420.5	61.1	121	2 S20783	Ig heavy chain V r
45	417	60.6	116	2 S31667	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH0952
Ig heavy chain V region (G6+ CIL-SMI) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0952
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; PMID:92202880; PMID:1552291
A/Accession: PH0952
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-128 <MAR>
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-50/Region: framework 2
F/51-67/Region: complementarity-determining 2
F/68-98/Region: framework 3
F/99-116/Region: complementarity-determining 3

Query Match 74.9%; Score 515; DB 2; Length 128;
Best Local Similarity 79.2%; Pred. No. 1,46-39;
Matches 103; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEAKKRGSSVKVSCRASGDTFNSPISWVROAPGQGLBWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEAKKRGSSVKVSCRASGDTFNSPISWVROAPGQGLBWMGGIIPFGSTKY 60
QY 61 AOKFQGRVITADKSTAYMEIINLSRSDPTAIYCCARQNGGNYEGPPLLEPRDALDIW 120
DB 61 AOKFQGRVITADKSTAYMEIINLSRSDPTAIYCCARQNGGNYEGPPLLEPRDALDIW 118

QY 121 GGGTMVSS 130
DB 119 GGGTMVSS 128

RESULT 2
C33548
Ig heavy chain V-1 region (783) - human
C/Species: Homo sapiens (man)
C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C/Accession: C33548
R/Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr.
A/Reference number: A33548; PMID:89345575; PMID:2503826
A/Accession: C33548

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tree
 A/Molecule type: DNA
 A/Residues: 1-133 <KIP>
 A/Experimental source: the sequence was determined from the differentiated gene
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMV>

Query Match 74.1%; Score 509.5; DB 2; Length 133;
 Best Local Similarity 72.7%; Pred. No. 4,76-39;
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVQLVSGAEAKKPGSSVSKVSCKASGDTFNSPFIWVROAPGQGLEMMGGIIPFGSTKY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGDTFSSVVAISWVROAPGQGLEMMGGIIPFGTANY 60
 QY 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCAR-----QONGWYEGPLLEPRPD 115
 DB 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCAR-----QONGWYEGPLLEPRPD 114
 QY 116 ----ALDIWGQGTMTVTVSS 130
 DB 115 YYYGMDVWGQGTMTVTVSS 133

RESULT 3

1g mu chain precursor, membrane-bound (clone 201) - human
 S14683
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
 C/Accession: S14683; S08047
 R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
 Nucleic Acids Res. 18, 4278, 1990
 A/Title: Complete nucleotide sequence of the membrane form of the human 1g mu heavy chain.
 A/Reference number: S14683; MUID:90332450; PMID:2115996
 A/Accession: S14683
 A/Molecule type: mRNA
 A/Residues: 1-627 <PRI>
 A/Cross-references: EMBL:X17115; NID:933450; PID:CA34971.1; PID:933451
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: immunoglobulin; membrane protein
 F/1-15/Domain: signal sequence; status predicted <SIG>
 F/16-627/Product: 1g mu chain #status predicted <MAT>
 F/1-17/Domain: immunoglobulin homology <IMV>

Query Match 74.1%; Score 509.5; DB 2; Length 627;
 Best Local Similarity 72.7%; Pred. No. 2,56-38;
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVQLVSGAEAKKPGSSVSKVSCKASGDTFNSPFIWVROAPGQGLEMMGGIIPFGSTKY 60
 DB 20 QVQLVSGAEVKKPGSSVKVSCKASGDTFSSVVAISWVROAPGQGLEMMGGIIPFGTANY 79
 QY 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCAR-----QONGWYEGPLLEPRPD 115
 DB 80 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCAR-----QONGWYEGPLLEPRPD 133
 QY 116 ----ALDIWGQGTMTVTVSS 130
 DB 134 YYYGMDVWGQGTMTVTVSS 152

RESULT 4

PH0953
 1g heavy chain V region (G6+ CTL-SIC) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0953
 R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0953; MUID:92202880; PMID:1552291
 A/Accession: PH0953

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA
 A/Residues: 1-135 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-30/Region: framework 1
 F/15-98/Domain: immunoglobulin homology <IMV>
 F/31-35/Region: complementarity-determining 1
 F/36-50/Region: framework 2
 F/51-67/Region: complementarity-determining 2
 F/68-98/Region: framework 3
 F/99-123/Region: complementarity-determining 3

Query Match 73.0%; Score 502.5; DB 2; Length 135;
 Best Local Similarity 75.2%; Pred. No. 26-38;
 Matches 103; Conservative 8; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVSKVSCKASGDTFNSPFIWVROAPGQGLEMMGGIIPFGSTKY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGDTFSSVVAISWVROAPGQGLEMMGGIIPFGTANY 60
 QY 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCARQONG-----GWYEGPLLEPR 113
 DB 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCAR--NGYCGDCYSKELLRFDPFS 118
 QY 114 PDALDIWGQGTMTVTVSS 130
 DB 119 EDAPDIWGQGTMTVTVSS 135

RESULT 5

PH0959
 1g heavy chain V region (G6+ T-L26) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0959
 R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0959
 A/Status: nucleic acid sequence not shown

A/Molecule type: DNA
 A/Residues: 1-116 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-30/Region: framework 1
 F/15-98/Domain: immunoglobulin homology <IMV>
 F/31-35/Region: complementarity-determining 1
 F/36-50/Region: framework 2
 F/51-67/Region: complementarity-determining 2
 F/68-98/Region: framework 3
 F/99-104/Region: complementarity-determining 3

Query Match 72.8%; Score 501; DB 2; Length 116;
 Best Local Similarity 76.2%; Pred. No. 2,46-38;
 Matches 99; Conservative 8; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVSKVSCKASGDTFNSPFIWVROAPGQGLEMMGGIIPFGSTKY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGDTFSSVVAISWVROAPGQGLEMMGGIIPFGTANY 60
 QY 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCARQONGWYEGPLLEPRDALDIW 120
 DB 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIVYCARQNG--WF-----Dpw 106
 QY 121 GQGTMTVTVSS 130
 DB 107 GQGTMTVTVSS 116

RESULT 6

PH0962

Ig heavy chain V region (G6+ T-142) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C/Accession: PH0962

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J:Exp. Med. 175, 983-991, 1992

A>Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0962

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-120 <MAR>

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

Query Match 72.4%; Score 498; DB 2; Length 120;

Best Local Similarity 77.7%; Pred. No. 4.6e-38;

Matches 101; Conservative 8; Mismatches 11; Indels 10; Gaps 3;

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPQGGLMMGGIIPFGSTKY 60

Db 61 AOKFQGRVTITADGSTSTAYMELNSLRSEDTAYYCARVFN-----PLF--FAVGMQV 112

Qy 121 GGGTMTVSS 130

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

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Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 61 AOKFQGRVTITADGSTSTAYMELNSLRSEDTAYYCARVFN-----PLF--FAVGMQV 112

Qy 121 GGGTMTVSS 130

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

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Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 113 GGGTMTVSS 122

Qy 113 GGGTMTVSS 122

Db 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGTANY 60
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPRDALDI 120
 Db 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPRDALDI 120
 QY 121 GGGTMTVSS 130
 Db 110 GGGTMTVSS 119

RESULT 10

PH0954
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0954
 R/Martin, T.J.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; PMID:92202880; PMID:1552291
 A/Accession: PH0954
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-132 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-30/Region: framework 1
 F/15-98/Domain: immunoglobulin homology <IMM>
 F/31-35/Region: complementarity-determining 1
 F/36-50/Region: complementarity-determining 2
 F/51-67/Region: complementarity-determining 3
 F/68-98/Region: framework 3
 F/99-120/Region: complementarity-determining 3

Query Match 72.1%; Score 496; DB 2; Length 132;
 Best Local Similarity 71.4%; Pred. No. 7.7e-38;
 Matches 100; Conservative 10; Mismatches 12; Indels 18; Gaps 3;
 QY 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGSTKY 60
 Db 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGTANY 60
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPR 114
 Db 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPR 114
 QY 115 D----ALDINGGGTMTVSS 130
 Db 113 NYTYGMDVMGGTMTVSS 132

RESULT 11

PH0960
 Ig heavy chain V region (G6+ T-L30) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0960
 R/Martin, T.J.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; PMID:92202880; PMID:1552291
 A/Accession: PH0960
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-136 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-30/Region: framework 1
 F/15-98/Domain: immunoglobulin homology <IMM>
 F/31-35/Region: complementarity-determining 1
 F/36-50/Region: complementarity-determining 2
 F/51-67/Region: complementarity-determining 3

F/68-98/Region: framework 3
 F/99-124/Region: complementarity-determining 3

Query Match 72.1%; Score 496; DB 2; Length 136;
 Best Local Similarity 67.8%; Pred. No. 7.9e-38;
 Matches 99; Conservative 10; Mismatches 11; Indels 26; Gaps 2;
 QY 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGTANY 60
 Db 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGTANY 60
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPR 104
 Db 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPR 104
 QY 105 YEGPLLEPRDALDINGGGTMTVSS 130
 Db 121 Y-----GMDVMGGTMTVSS 136

RESULT 12

A33548
 Ig heavy chain V-1 region (NE1) - human
 C/Species: Homo sapiens (man)
 C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 C/Accession: A33548; PH0956
 R/Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene ex
 A/Reference number: A33548; PMID:89345575; PMID:2503826
 A/Accession: A33548
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-129 <KIP>
 R/Martin, T.J.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; PMID:92202880; PMID:1552291
 A/Accession: PH0956
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-129 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-30/Region: framework 1
 F/15-98/Domain: immunoglobulin homology <IMM>
 F/31-35/Region: complementarity-determining 1
 F/36-50/Region: complementarity-determining 2
 F/51-67/Region: complementarity-determining 3
 F/68-98/Region: framework 3
 F/99-117/Region: complementarity-determining 3

Query Match 71.9%; Score 494.5; DB 2; Length 129;
 Best Local Similarity 73.4%; Pred. No. 1e-37;
 Matches 102; Conservative 8; Mismatches 10; Indels 19; Gaps 4;

QY 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGSTKY 60
 Db 1 QVOLVOSGAEVKKRGGSSVKVSCKASGDTFSSVAISVROAPGQGLEWGGIIPFGTANY 60
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPR 111
 Db 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGEGPLLEPR 111
 QY 112 PRPDALDINGGGTMTVSS 130
 Db 116 -----FDYMGGLTMTVSS 129

RESULT 13

PH0957
 Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
 C/Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0957
R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A>Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0957
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-125 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-113/Region: complementarity-determining 3

Query Match 71.3%; Score 490.5; DB 2; Length 125;
Best Local Similarity 71.5%; Pred. No. 2.3e-37;
Matches 98; Conservative 10; Mismatches 10; Indels 19; Gaps 3;

QY 1 QVQLVQSGAEAKKPGSSVSKVSCKASGDTFNSPISWVROAPGQGLEWMGIIPIFGSTKY 60
DB 1 QVQLVQSGAEVKKPSSSVSKVSCKASGDTFSSVAIMVWROAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFGRTVTMTADGSTSTAYMELNSLRSEDTAIYYCARO-----WYEGPLLEPR 113
DB 61 AOKFGRTVTITADESTTAYMELSLRSEDTAVYYCARDCGSGCYFWGPF----- 112

QY 114 PDALDIWGQGTMTVSS 130
DB 113 ----DPMWGKGTITVSS 125

RESULT 14
PH0955
Ig heavy chain V region (G6+ CLU-AND) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0955
R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A>Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0955
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-127 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-115/Region: complementarity-determining 3

Query Match 71.0%; Score 488.5; DB 2; Length 127;
Best Local Similarity 71.0%; Pred. No. 3.5e-37;
Matches 98; Conservative 10; Mismatches 11; Indels 19; Gaps 2;

QY 1 QVQLVQSGAEAKKPGSSVSKVSCKASGDTFNSPISWVROAPGQGLEWMGIIPIFGSTKY 60
DB 1 QVQLVQSGAEVKKPSSSVSKVSCKASGDTFSSVAIMVWROAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFGRTVTMTADGSTSTAYMELNSLRSEDTAIYYCAROONG-----WYEGPLLEPR 112
DB 61 AOKFGRTVTITADESTTAYMELSLRSEDTAVYYCARVSIFGVQHYHYHY----- 113

QY 113 RPDALDIWGQGTMTVSS 130
DB 114 ----MDVWGKGTITVSS 127

RESULT 15
B33548
Ig heavy chain V-1 region (AND) - human
C/Species: Homo sapiens (man)
C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C/Accession: B33548
R/Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A>Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A/Reference number: A33548; MUID:89345575; PMID:2503826
A/Accession: B33548
A/Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: DNA
A/Residues: 1-126 <KIP>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 486; DB 2; Length 126;
Best Local Similarity 71.5%; Pred. No. 5.8e-37;
Matches 98; Conservative 9; Mismatches 12; Indels 18; Gaps 2;

QY 1 QVQLVQSGAEAKKPGSSVSKVSCKASGDTFNSPISWVROAPGQGLEWMGIIPIFGSTKY 60
DB 1 QVQLVQSGAEVKKPSSSVSKVSCKASGDTFSSVAIMVWROAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFGRTVTMTADGSTSTAYMELNSLRSEDTAIYYCAROONG-----WYEGPLLEPR 113
DB 61 AOKFGRTVTITADESTTAYMELSLRSEDTAVYYCARVSIFGVQHYHYHY----- 112

QY 114 PDALDIWGQGTMTVSS 130
DB 113 --MDVWGKGTITVSS 126

Search completed: December 30, 2003, 11:03:13
Job time : 13.4614 secs

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Db      1 QVQLVDSGAEVKKPGSSVKVSCAKGCGTFFSSALISWVQAQPGQLIEWNGGIIPFTGANY 60
Qy      61 AOKFQGRVMTADGSGTSTAYMELNSLRSEDTAIYYCAQONQGWYEGPLLEPPDALDIW 120
Db      61 AOKFQGRVITTADESTIAYMELSLRSRSDTAIVYCAARGY--YYG-----MDVW 109
Qy      121 GGGTWTVSS 130
Db      110 GGGTIVTVSS 119

RESULT 10
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_rev1510 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0954
R:Martin, T.; Duffey, S.F.; Carson, D.A.; Kipps, T.J.
J: Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; PMID:92202880; PMID:1552291
A:Accession: PH0954
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-132 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-120/Region: complementarity-determining 3

Query Match      72.1%; Score 496; DB 2; Length 132;
Best Local Similarity 71.4%; Pred. No. 7, 7e-38;
Matches 100; Conservative 10; Mismatches 12; Indels 18; Gaps 3

Qy      1 QVQLVDSGAEVKKPGSSVKVSCAKSGDTFNSFPISMVQAQPGGLEWNGGIIPFGSTKY 60
Db      1 QVQLVDSGAEVKKPGSSVKVSCAKSGDTFSSALISWVQAQPGGLEWNGGIIPFGTANY 60
Qy      61 AOKFQGRVMTADGSGTSTAYMELNSLRSEDTAIYYCAQON-----GQWYEGPLLEPP 114
Db      61 AOKFQGRVITTADESTIAYMELSLRSRSDTAIVYCAAPHASIDDFMGYY-----P 112
Qy      115 D---AIDWGSGTWTVSS 130
Db      113 NYYYGMDVWGQGTIVTVSS 132

RESULT 11
PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_rev1510 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0960
R:Martin, T.; Duffey, S.F.; Carson, D.A.; Kipps, T.J.
J: Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; PMID:92202880; PMID:1552291
A:Accession: PH0960
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-136 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-120/Region: complementarity-determining 3

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F:68-98/Region: framework 3
F:99-124/Region: complementarity-determining 3

Query Match      72.1%; Score 496; DB 2; Length 136;
Best Local Similarity 67.8%; Pred. No. 7.9e-38;
Matches 99; Conservative 10; Mismatches 11; Indels 26; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWTRQAPGQGLFEMWGIIPIFGSTRY 60
   1 QVQLVSGAEYKVRGSSVKVSCKASGDTFSSYALSWTRQAPGQGLFEMWGIIPIFGTANY 60
Db 1 QVQLVSGAEYKVRGSSVKVSCKASGDTFSSYALSWTRQAPGQGLFEMWGIIPIFGTANY 60

QY 61 AOKFQGRVTMTADSGTSTAYWELNSLRSEDTAIIYCARQON-----GGW 104
   61 AOKFQGRVTITADKSTSTAYWELNSLRSEDTAIVYCARGRTRVSSTLYDSSGYDFSGY 120
Db 61 AOKFQGRVTITADKSTSTAYWELNSLRSEDTAIVYCARGRTRVSSTLYDSSGYDFSGY 120

QY 105 YEGPLEPRPDALDIWQGTMTVYSS 130
   121 Y-----GMDVWGQGITVTVSS 136
Db 121 Y-----GMDVWGQGITVTVSS 136

RESULT 12
A33548
Ig heavy chain V-1 region (NEI) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: A33548; PH0956
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: A33548
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-129 <KIP>
R:Martin, T.; Duffly, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic deletion of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0956
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-129 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-117/Region: complementarity-determining 3

Query Match      71.9%; Score 494.5; DB 2; Length 129;
Best Local Similarity 73.4%; Pred. No. 1e-37;
Matches 102; Conservative 8; Mismatches 10; Indels 19; Gaps 4;

QY 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWTRQAPGQGLFEMWGIIPIFGSTRY 60
   1 QVQLVSGAEYKVRGSSVKVSCKASGDTFSSYALSWTRQAPGQGLFEMWGIIPIFGTANY 60
Db 1 QVQLVSGAEYKVRGSSVKVSCKASGDTFSSYALSWTRQAPGQGLFEMWGIIPIFGTANY 60

QY 61 AOKFQGRVTMTADSGTSTAYWELNSLRSEDTAIIYCARQON-----WYEGPLLE 111
   61 AOKFQGRVTITADKSTSTAYWELNSLRSEDTAIVYCAR---GPRLADVLWF--GEISE 115
Db 61 AOKFQGRVTITADKSTSTAYWELNSLRSEDTAIVYCAR---GPRLADVLWF--GEISE 115

QY 112 PRPDALDIWQGTMTVYSS 130
   116 -----FDYWGQGITVTVSS 129
Db 116 -----FDYWGQGITVTVSS 129

RESULT 13
PH0957
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C:Species: Homo sapiens (man)

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Db      61  AAKFQGRITIIADESTSTAINMELSLRSEDTAVYICARVPN-----PLF--FAVGMDDVM 112
QY      121  GCGTMTVTSS 130
          ||| |||
          ||| |||
Db      113  GCGTIVTVSS 122

RESULT 8
S46394
I9 heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C/Accession: S46394
R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A/Reference number: S46390; MUID:94254092; PMID:8196048
A/Accession: S46394
A/Status: preliminary
A/Status: preliminary
A/Molecule type: DNA
A/Accession: S46394
A/Status: preliminary
A/Molecule type: DNA
A/Accession: S46394
A/Status: preliminary
A/Molecule type: DNA

```

Query Match	72.4%	Score 498	DB 2	Length 132
Best Local Similarity	75.9%	Pred. No. 5.1e-18		
Matches 101	Conservative 11	Mismatches 17	Indels 4	Gaps 2

QY	1	QVQLVQSGAEAEKRRGSSSVKRYSCAKSGDTFSPISWVRAPQGLEWGGIIPIFGSTKY	60
Db	1	QVQLVQSGAEAEKRRGSSSVKRYSCAKSGDTFSSVYISWVRAPQGLEWGGIIPIFGTANH	60
QY	61	AKRGRVYTKTADGSGTSTAYVMEINSRSEDITAYYCARGOONGWYEGPPLLEPRPD--AL	117

```

RESULT 9
PH0961
lig heavy chain V region (G6+ T-133) - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C.Accession: PH0961
R.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
Article: Evidence for somatic selection of natural autocabibodies.
A.Reference number: PH0952; MUID:9202880; PMID:1525291
A.Accession: PH0961
A.Status: nucleic acid sequence not shown
A.Molecule type: DNA
A.Residues: 1-119 <MAR>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F.1-30/Region: framework 1
F.31-35/Region: complement-binding site
F.31-35/Domain: immunoglobulin homology <IMM>

```

```

199-107/Region: complementarity-determining 3
Query Match      72.3%; Score 497.5; DB 2; Length 119;
Best Local Similarity 76.2%; Pred. No. 5e-38;
Matches 99; Conservative 9; Mismatches 11; Indels 11; Gaps 2
1 QVQLVDSGAEAKPGSSVYKSCASDPTNSPISMTQAQPGCELEWCGITIPFGSTKY 60

```

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A/Molecule type: DNA
 A/Residues: 1-133 <RIP>
 C/Experimental source: the sequence was determined from the differentiated gene
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 509.5; DB 2; Length 133;
 Best Local Similarity 72.7%; Pred. No. 4.7e-39;
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSFPISWROAPGQGLEMMGIIPIFGSTKY 60
 |||||
 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 60
 |||||
 DB 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCAR-----QONGWYEGPLLEPRPD 115
 |||||
 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCAKTGILGPYSSGMY-----PNSD 114
 |||||
 QY 116 ----ALDIWGQGTMTVTVSS 130
 :|||
 DB 115 YYYGMDVMWGQGTMTVTVSS 133

RESULT 3

Ig mu chain precursor, membrane-bound (clone 201) - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999

C/Accession: S14683; S08047

R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 19, 4278, 1990

A/Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A/Reference number: S14683; MUID:90332450; PMID:2115996

A/Accession: S14683

A/Molecule type: mRNA

A/Residues: 1-627 <PRT>

C/Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin; membrane protein

F/1-15/Domain: signal sequence #status predicted <SIG>

F/16-627/Product: Ig mu chain #status predicted <MAT>

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 509.5; DB 2; Length 627;
 Best Local Similarity 72.7%; Pred. No. 2.5e-38;
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSFPISWROAPGQGLEMMGIIPIFGSTKY 60
 |||||
 20 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 79
 |||||
 QY 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCAR-----QONGWYEGPLLEPRPD 115
 |||||
 60 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCAKTGILGPYSSGMY-----PNSD 133
 |||||
 QY 116 ----ALDIWGQGTMTVTVSS 130
 :|||
 DB 134 YYYGMDVMWGQGTMTVTVSS 152

RESULT 4

Ig heavy chain V region (G6+ CTL-SIC) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C/Accession: PH0953

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0953

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-135 <MAR>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology <IMM>

F/11-35/Region: complementarity-determining 1

F/16-50/Region: framework 2

F/51-67/Region: complementarity-determining 2

F/68-98/Region: framework 3

F/99-123/Region: complementarity-determining 3

Query Match 73.0%; Score 502.5; DB 2; Length 135;
 Best Local Similarity 75.2%; Pred. No. 2e-38;
 Matches 103; Conservative 8; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSFPISWROAPGQGLEMMGIIPIFGSTKY 60
 |||||
 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 60
 |||||
 DB 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCARQONG-----GWYEGPLLEPR 113
 |||||
 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCAKNGYCGDCYSRWELLRFDFS 118
 |||||
 QY 114 PDALDIWGQGTMTVTVSS 130
 :|||
 DB 119 EDAPDIMGPGTMTVTVSS 135

RESULT 5

Ig heavy chain V region (G6+ T-L26) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C/Accession: PH0959

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0959

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/36-50/Region: framework 2

F/51-67/Region: complementarity-determining 2

F/68-98/Region: framework 3

F/99-104/Region: complementarity-determining 3

Query Match 72.8%; Score 501; DB 2; Length 116;
 Best Local Similarity 76.2%; Pred. No. 2.4e-38;
 Matches 99; Conservative 8; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSFPISWROAPGQGLEMMGIIPIFGSTKY 60
 |||||
 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 60
 |||||
 DB 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCARQONGWYEGPLLEPRPDALDIW 120
 |||||
 61 AOKFGGRVTITADGSTSTAYMELNSLRSEDTAYYCARQNGWYEGPLLEPRPDALDIW 120
 |||||
 QY 121 GQGTMTVTVSS 130
 :|||
 DB 107 GQGTMTVTVSS 116

RESULT 6

PH0962

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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:09 : Search time 12.4614 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688

Sequence: 1 QVOLVSGAEKKRGGSSVKV.....EPRPDALDIMGQIMTVSS 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	74.9	128	2	PH0952 Ig heavy chain V r
2	509.5	74.1	133	2	C33548 Ig heavy chain V-1
3	509.5	74.1	627	2	S14683 Ig mu chain precu
4	502.5	73.0	135	2	PH0953 Ig heavy chain V r
5	501	72.8	116	2	PH0959 Ig heavy chain V r
6	498	72.4	120	2	PH0962 Ig heavy chain V r
7	498	72.4	122	2	PH0958 Ig heavy chain V r
8	498	72.4	132	2	S46394 Ig heavy chain V r
9	497.5	72.3	119	2	PH0961 Ig heavy chain V r
10	496	72.1	132	2	PH0954 Ig heavy chain V r
11	496	72.1	136	2	PH0960 Ig heavy chain V r
12	494.5	71.9	129	2	A33548 Ig heavy chain V-1
13	490.5	71.3	125	2	PH0957 Ig heavy chain V r
14	488.5	71.0	127	2	PH0955 Ig heavy chain V r
15	486	70.6	126	2	B33548 Ig heavy chain V-1
16	481	69.9	135	2	B32274 Ig heavy chain pre
17	456.5	66.4	113	2	PH1663 Ig heavy chain V r
18	452.5	65.8	121	2	A49590 Ig heavy chain V r
19	452	65.7	108	2	PH1664 Ig heavy chain V r
20	451	65.6	98	2	S26915 Ig heavy chain V r
21	451	65.6	116	2	S31698 Ig heavy chain pre
22	451	65.6	116	2	S36261 Ig heavy chain V r
23	451	65.6	123	2	S44108 Ig heavy chain V-D
24	450	65.4	124	2	S19665 Ig heavy chain V r
25	450	65.4	136	2	S31600 Ig heavy chain V r
26	447.5	65.0	122	2	B49590 Ig heavy chain V r
27	447	65.0	98	2	S24680 Ig heavy chain V1
28	447	65.0	119	2	S44106 Ig heavy chain V-D
29	446.5	64.9	142	2	A32483 Ig heavy chain V r

30	446	64.8	118	2	S36265 Ig heavy chain V r
31	442.5	64.3	122	2	C49590 Ig heavy chain V r
32	442	64.2	171	2	S23623 Ig heavy chain V r
33	437.5	63.6	160	2	PL0105 anti-PR2 erythrocy
34	436.5	63.4	109	2	PH1671 Ig heavy chain V r
35	435.5	63.3	129	2	S36260 Ig heavy chain V r
36	435	63.2	135	2	S49530 anti-5m antibody V
37	434	63.1	98	2	S46463 Ig heavy chain V1
38	430.5	62.6	127	2	S34014 Ig heavy chain V r
39	428.5	62.3	129	2	S46393 Ig heavy chain V r
40	428	62.2	98	2	A30523 Ig heavy chain V-1
41	426	61.9	97	2	PH0870 Ig heavy chain V r
42	422.5	61.4	122	2	S36271 Ig heavy chain V r
43	420.5	61.1	117	1	G1HUB3 Ig heavy chain V-1
44	420.5	61.1	121	2	S20783 Ig heavy chain V r
45	417	60.6	116	2	S31667 Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
PH0952
Ig heavy chain V region (G6+ CTL-SWI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0952
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0952
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-128 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-116/Region: complementarity-determining 3

Query Match          74.9%; Score 515; DB 2; Length 128;
Best Local Similarity 79.2%; Pred. No. 1.4e-39;
Matches 103; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY      1 QVOLVSGAEKKRGGSSVKVSCKASGDTFNSFPISWRQAFQGLBWMGIIPIFGSTKY 60
DB      1 QVOLVSGAEKKRGGSSVKVSCKASGDTFSSYAIISWRQAFQGLBWMGIIPIFGTANY 60
QY      61 AOKQGRVTMTADGSTTAAYWELNSLRSEDTAIIYYCARQOQGWVEGLLEPRPDALDIW 120
DB      61 AOKQGRVTITADKSTSTAYWELNSLRSEDTAIIYYCARQGWYDIWGSYRS-NDAPDIW 118
QY      121 GQGTMTVSS 130
DB      119 GQGTMTVSS 128

RESULT 2
C33548
Ig heavy chain V-1 region (783) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: C33548
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```
US-09-880-748-1190
; Sequence 1190, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1190
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1190

Query Match      73.9%; Score 525.5; DB 11; Length 255;
Best Local Similarity 78.0%; Pred. No. 2,4e-42;
Matches 103; Conservative 8; Mismatches 18; Indels 3; Gaps 2;

QY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVQAPGQGLMMGMISYSGNTDY 60
DB 1 OVQLVQSGAEVKKPKGASVSKVSCASGYTTTSTGISMVWQAPGQGLMMGMISYNGNTNY 60
QY 61 AOKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVVYCCARDGGGAYEDVWSGEYPEYYAM 120
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCCARD--PEPYDILTYGFLPY--MD 117
QY 121 VWGQGTIVTVSS 132
DB 118 VWGKGTLTVSS 129

RESULT 3
US-10-041-860-31
; Sequence 31, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-31

Query Match      73.8%; Score 524.5; DB 12; Length 127;
Best Local Similarity 78.9%; Pred. No. 1,4e-42;
Matches 105; Conservative 6; Mismatches 15; Indels 7; Gaps 3;
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QY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVQAPGQGLMMGMISYSGNTDY 60
DB 1 OVQLVQSGAEVKKPKGASVSKVSCASGYTTTSTGISMVWQAPGQGLMMGMISYNGNTNY 60
QY 61 AOKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVVYCCARDGGGAYEDVWSGEY--PEYYAM 119
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCCARD---HYYD--SSDYLYYYGL 114
QY 120 DVWGQGTIVTVSS 132
DB 115 DVWGQGTIVTVSS 127

RESULT 4
US-10-041-860-243
; Sequence 243, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 243
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-243

Query Match      73.8%; Score 524.5; DB 12; Length 127;
Best Local Similarity 78.9%; Pred. No. 1,4e-42;
Matches 105; Conservative 6; Mismatches 15; Indels 7; Gaps 3;

QY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVQAPGQGLMMGMISYSGNTDY 60
DB 1 OVQLVQSGAEVKKPKGASVSKVSCASGYTTTSTGISMVWQAPGQGLMMGMISYNGNTNY 60
QY 61 AOKFQGRVTMTTDTSRRTAYMELRSLRSDDTAVVYCCARDGGGAYEDVWSGEY--PEYYAM 119
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCCARD---HYYD--SSDYLYYYGL 114
QY 120 DVWGQGTIVTVSS 132
DB 115 DVWGQGTIVTVSS 127

RESULT 5
US-10-041-860-325
; Sequence 325, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 28.3087 Seconds
(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 1 QVQLQSGATVEKKGASMKV.....YPEYVMDWGQGTITVSS 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530.5	74.6	125	15	US-10-269-805-45
2	525.5	73.9	255	11	US-09-880-748-1190
3	524.5	73.8	127	12	US-10-041-860-31
4	524.5	73.8	127	12	US-10-041-860-243
5	524.5	73.8	127	12	US-10-041-860-325
6	524	73.7	252	11	US-09-880-748-1674
7	523	73.6	251	11	US-09-880-748-1921
8	521.5	73.3	259	11	US-09-880-748-973
9	520	73.1	253	11	US-09-880-748-1777
10	514.5	72.4	248	11	US-09-880-748-1778
11	514.5	72.4	257	11	US-09-880-748-1610
12	513	72.2	249	11	US-09-880-748-1425
13	512.5	72.1	257	11	US-09-880-748-1575
14	510.5	71.8	251	11	US-09-880-748-1562
15	510.5	71.8	259	11	US-09-880-748-1452

16	508.5	71.5	125	12	US-10-041-860-42	Sequence 42, App1
17	508.5	71.5	125	12	US-10-041-860-207	Sequence 207, App
18	508.5	71.5	257	11	US-09-880-748-1354	Sequence 1354, App
19	508	71.4	126	12	US-10-041-860-354	Sequence 354, App
20	508	71.4	254	11	US-09-880-748-1405	Sequence 1405, App
21	507	71.3	250	11	US-09-880-748-1595	Sequence 1595, App
22	506.5	71.2	125	12	US-10-041-860-48	Sequence 48, App1
23	506.5	71.2	125	12	US-10-041-860-200	Sequence 200, App
24	506.5	71.2	125	12	US-10-041-860-237	Sequence 237, App
25	506.5	71.2	125	12	US-10-041-860-372	Sequence 372, App
26	506.5	71.2	257	11	US-09-880-748-1579	Sequence 1579, App
27	505	71.0	247	11	US-09-880-748-1873	Sequence 1873, App
28	504.5	71.0	123	15	US-10-269-805-51	Sequence 51, App1
29	504.5	71.0	248	11	US-09-880-748-1472	Sequence 1472, App
30	504	70.9	247	11	US-09-880-748-1116	Sequence 1116, App
31	504	70.9	250	11	US-09-880-748-1560	Sequence 1560, App
32	503.5	70.8	123	12	US-10-330-613-21	Sequence 21, App1
33	503.5	70.8	123	12	US-10-330-530-21	Sequence 21, App1
34	503.5	70.8	248	11	US-09-880-748-1446	Sequence 1446, App
35	500.5	70.4	251	11	US-09-880-748-1586	Sequence 1586, App
36	500.5	70.4	251	11	US-09-880-748-1872	Sequence 1872, App
37	500	70.3	126	12	US-10-041-860-19	Sequence 19, App1
38	500	70.3	126	12	US-10-041-860-201	Sequence 201, App
39	500	70.3	126	12	US-10-041-860-288	Sequence 288, App
40	499.5	70.3	253	11	US-09-880-748-1636	Sequence 1636, App
41	498.5	70.1	259	11	US-09-880-748-1356	Sequence 1356, App
42	498	70.0	125	11	US-09-880-748-1315	Sequence 1315, App
43	497.5	70.0	125	12	US-10-041-860-38	Sequence 38, App1
44	497.5	70.0	125	12	US-10-041-860-203	Sequence 203, App
45	497.5	70.0	125	12	US-10-041-860-240	Sequence 240, App

ALIGNMENTS

RESULT 1

US-10-269-805-45

Sequence 45, Application US/10269805

Publicatation No. US20030124129A1

GENERAL INFORMATION:

APPLICANT: OLINER, JONATHAN D.

TITLE OR INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269, 805

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328, 604

PRIOR FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 45

LENGTH: 125

TYPE: PRT

ORGANISM: Homo sapiens

US-10-269-805-45

Query Match 74.6%; Score 530.5; DB 15; Length 125;
Best Local Similarity 77.8%; Pred. No. 3.7e-43;
Matches 105; Conservative 4; Mismatches 13; Indels 13; Gaps 2;

QY 1 QVQLQSGATVEKKGASMKVSCMAAGPFTSYDSWVRQAPGGLLEWGMCHSTISGUTDY 60

DB 1 QVQLVDSAGVKKRGASVSKSCASGTFSTYGSWVRQAPGGLLEWGMCHSTISGUTDY 60

QY 61 AOKKQGVMTTPTDTSRTAYMELRLSDPTAVYYCARDGCG---GCAVEDWSGEPEY 117

DB 61 AOKKQGVMTTPTDTSRTAYMELRLSDPTAVYYCARDGCIARSAY-----Y 110

QY 118 AMDWGQGTITVSS 132

DB 111 GMDVWGQGTITVSS 125

RESULT 2

CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and anti-ADs activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP413990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX
XX
SQ Sequence 257 AA;

Query Match 71.5%; Score 508.5; DB 23; Length 257;
Best Local Similarity 73.7%; Pred. No.2.1e-39;
Matches 98; Conservative 13; Mismatches 13; Indels 3; Gaps 2

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
PS
XX
XX Claim 1; Page 2079-2080; 314bpb; English.
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiids activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4722 represent
CC the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
XX Sequence 254 AA;

CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 251 AA;
Query Match 71.8%; Score 510.5; DB 23; Length 251;
Best Local Similarity 76.5%; Pred. No. 1.3e-39;
Matches 101; Conservative 7; Mismatches 17; Indels 7; Gaps 2;
QY 1 QVQLQSGATPEVKKPKGASMKVSCNAGSYPTSYDISWVRQAPGQGLEMMGMSISYSGNTDY 60
DB 1 QVQLVSGAEVKKPKGASVKVSCASGYTFTSYISWVRQAPGQGLEMMGMSISYSGNTDY 60
QY 61 AOKFQGRVTMTTDSRTAYMELRSRSDDTAVYCARPGCGGAYEDVWSGEY--PEYYA 120
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSRSDDTAVYCAR-----MEYDILGYGGYF--D 113
QY 121 WVGQGTIVTVSS 132
DB 114 WVGQGTIVTVSS 125
RESULT 13
ID ABP45441 standard; Protein; 259 AA.
XX
AC ABP45441;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1452.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN MO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1; Page 2135-2136; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 259 AA;
Query Match 71.8%; Score 510.5; DB 23; Length 259;
Best Local Similarity 73.9%; Pred. No. 1.4e-39;
Matches 99; Conservative 12; Mismatches 20; Indels 3; Gaps 2;
QY 1 QVQLQSGATPEVKKPKGASMKVSCNAGSYPTSYDISWVRQAPGQGLEMMGMSISYSGNTDY 60
DB 1 QVQLVSGAEVKKPKGASVKVSCASGYTFTSYISWVRQAPGQGLEMMGMSISYSGNTDY 60
QY 61 AOKFQGRVTMTTDSRTAYMELRSRSDDTAVYCARPGCGGAYEDVWSGEY--PEYYA 118
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSRSDDTAVYCARPGCGGAYEDVWSGEY--PEYYA 119
QY 119 MDVWQGTIVTVSS 132
DB 120 FDIWGRGTIVTVSS 133
RESULT 14
ID ABP45343 standard; Protein; 257 AA.
XX
AC ABP45343;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1354.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN MO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1; Page 2018-2019; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to

Db 61 AOKLGRVTMTDTSTSTAYMELRSLRSDPTAVVYCAR---CGNV-DILTG---YYIGA 112
 QY 119 MDVWGQGTIVTVSS 132
 Db 113 FDIWGQGLTVTVSS 126
 RESULT 11
 ABP45565 standard; Protein; 257 AA.
 ID ABP45565 standard; Protein; 257 AA.
 AC ABP45565;
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 1576.
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX MO200202641-A1.
 XX 10-JAN-2002.
 PD 15-JUN-2001; 2001MO-US19110.
 XX 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PT WPI; 2002-114799/15.
 DR 2002-114799/15.
 XX Claim 1; Page 2283-2284; 3148pp; English.
 PS This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic, and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 SQ Sequence 257 AA;
 Query Match 72.1%; Score 512.5; DB 23; Length 257;
 Best Local Similarity 75.9%; Pred. No. 9e-40;

Matches 101; Conservative 8; Mismatches 21; Indels 3; Gaps 2;
 QY 1 QVQLQSATEVKKPKGASMKVSGASGYPSTYSIDISWVRAPQCGLEMGWISITSGNDY 60
 Db 1 QVQLVSGAEVKKRQASVSVCSASGYTFTSISGVNKAPOGGLMMGWSITNGNTRY 60
 QY 61 AOKFQGRVTMTDTSTSRRIAYMELRSLRSDPTAVVYCARGGGGAAYEDVWSGEP- EYAM 119
 Db 61 PQQLQGRVTMTDTSTSTAYMELRSLRSDPTAVVYCAR--GRLSYDILTGTYADYGM 118
 QY 120 DVWGQGTIVTVSS 132
 Db 119 DDMGRGTMVTVSS 131
 RESULT 12
 ABP45551
 ID ABP45551 standard; Protein; 251 AA.
 AC ABP45551;
 DT 19-AUG-2002 (first entry)
 DE Human Blys binding scFv SEQ ID 1562.
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX MO200202641-A1.
 XX 10-JAN-2002.
 PD 15-JUN-2001; 2001MO-US19110.
 XX 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PT WPI; 2002-114799/15.
 DR 2002-114799/15.
 XX Claim 1; Page 2267-2268; 3148pp; English.
 PS This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic, and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

XX 10-JAN-2002.
PD
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PS the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1; Page 2522-2523; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 253 AA;
Query Match 73.1%; Score 520; DB 23; Length 253;
Best Local Similarity 75.8%; Pred. No. 1.8e-40;
Matches 100; Conservative 12; Mismatches 18; Indels 2; Gaps 2;
QY 1 OVQLQSGATEYKRGKSGAMKVSCKASGYPTFSYDISWRAPGQGLEWMGMSISYSGNTDY 60
DB 1 EVQLVQSGAEVKKRQASVKSVCKASGYFTSYGITWRAPGQGLEWMGMSISYNGDTNY 60
QY 61 AOKFQGRVTMTTDSRTATYMEI RSLRSDTAYYYCARDDGGAYEDWVGEPETAYND 120
DB 61 AOELOGRVMTTDTSTSTAYMEI RSLRSDTAYYYCAR-GDFDY-DILTGYPYVYGMND 118
QY 121 VMGQGTIVTVSS 132
DB 119 VMGQGTIVTVSS 130
RESULT 8
ABP45767
ID ABP45767 standard; Protein; 248 AA.
XX
XX ABP45767;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1778.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX

KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1; Page 2524-2525; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 248 AA;
Query Match 72.4%; Score 514.5; DB 23; Length 248;
Best Local Similarity 75.8%; Pred. No. 5.6e-40;
Matches 100; Conservative 9; Mismatches 16; Indels 7; Gaps 2;
QY 1 OVQLQSGATEYKRGKSGAMKVSCKASGYPTFSYDISWRAPGQGLEWMGMSISYSGNTDY 60
DB 1 OVQLQSGAEVKKRQASVKSVCKASGYFTSYGITWRAPGQGLEWMGMSISYNGDTNY 60
QY 61 AOKFQGRVTMTTDSRTATYMEI RSLRSDTAYYYCARDDGGAYEDWVGEPETAYND 120
DB 61 AOKLQGRVTMTTDTSTSTAYMEI RSLRSDTAYYYCAR-----SYDILTGYP--FGMD 113
QY 121 VMGQGTIVTVSS 132
DB 114 VMGQGTIVTVSS 125
RESULT 9
ABP45599
ID ABP45599 standard; Protein; 257 AA.
XX
XX ABP45599;
XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI: 2002-114799/15.
DR

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX

PS Claim 1; Page 2693-2694; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX Sequence 251 AA:

Query Match 73.6%; Score 523; DB 23; Length 251;
Best Local Similarity 74.6%; Pred. No. 9.3e-41;
Matches 103; Conservative 5; Mismatches 14; Indels 16; Gaps 2;

QY 1 QVQLQSATEVKKPKKASMKVSCASGYPTSTDISWVQAPOGGLMMGMISISGNTDY 60
DB 1 QVQLVSGAEVMPKPKASVSKASGYPTSTISWVQAPOGGLMMGMISAINGNTNY 60

QY 61 AOKFGQRYMTTDTSRRTAYMELRLSRDDTAIVYCAR-----DGGGAYEDVMSGEYP 114
DB 61 AOKLQGRVTMTTDTSTRTAYMELRLSRDDTAIVYCARVTSLSYSSSGGY----- 111

QY 115 EYYAMDVWGQGTITVTVSS 132
DB 112 -YYGMDVWGRTVTVSS 128

RESULT 6

ABP44962
ID ABP44962 standard; Protein; 259 AA.

XX ABP44962;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 973.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX MO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001MO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI: 2002-114799/15.

CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX Sequence 259 AA:

Query Match 73.3%; Score 521.5; DB 23; Length 259;
Best Local Similarity 74.5%; Pred. No. 1.3e-40;
Matches 102; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

QY 1 QVQLQSATEVKKPKKASMKVSCASGYPTSTDISWVQAPOGGLMMGMISISGNTDY 60
DB 1 QVQLVSGAEVMPKPKASVSKASGYPTSTISWVQAPOGGLMMGMISAINGNTNY 60

QY 61 AOKFGQRYMTTDTSRRTAYMELRLSRDDTAIVYCARDDGGGAYEDVMSGEYPY--- 117
DB 61 AOKLQGRVTMTTDTSTRTAYMELRLSRDDTAIVYCARDDGGGAYEDVMSGEYPY--- 116

QY 118 --AMDVWGQGTITVTVSS 132

DB 117 SDAFDIWGQGTITVTVSS 133

RESULT 7

ABP45766
ID ABP45766 standard; Protein; 253 AA.

XX ABP45766;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1777.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX MO200202641-A1.

CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

CC Sequence 255 AA;

Query Match 73.9%; Score 525.5; DB 23; Length 255;
 Best Local Similarity 78.0%; Pred. No. 5.5e-41;
 Matches 103; Conservative 8; Mismatches 16; Indels 3; Gaps 2;

QY 1 QVOLLQSATEVKKPKGASMKVSCMASGYPTSTDISWROAPGGLGEMGMSISGNTDY 60
 DB 1 QVQLVQSGAEVKKPKQASVSKVSCKASGYTFTSYGISWVROAPGGLGEMGMSISGNTNY 60
 QY 61 AOKFGGRVTMTTDTTSRRTAYMELRSLSRSDTAIVYVCARDGGGAYEDVWSGEPEYYAMD 120
 DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDTAIVYCAR--PSPYYDILTGTFPEY--MD 117
 QY 121 VMGQGTITVYSS 132
 DB 118 VMGKGLTVYSS 129

RESULT 4
 ABP45663
 ID ABP45663 standard; Protein; 252 AA.

AC ABP45663;
 XX
 DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1674.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

XX 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX

PS Claim 1; Page 2400-2401; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 252 AA;

Query Match 73.7%; Score 524; DB 23; Length 252;
 Best Local Similarity 78.0%; Pred. No. 7.5e-41;
 Matches 103; Conservative 7; Mismatches 16; Indels 6; Gaps 2;

QY 1 QVOLLQSATEVKKPKGASMKVSCMASGYPTSTDISWROAPGGLGEMGMSISGNTDY 60
 DB 1 QVQLVQSGAEVKKPKQASVSKVSCKASGYTFTSYGISWVROAPGGLGEMGMSISGNTNY 60
 QY 61 AOKFGGRVTMTTDTTSRRTAYMELRSLSRSDTAIVYVCARDGGGAYEDVWSGEPEYYAMD 120
 DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDTAIVYCAR----GAYDILTGTFPEY--YGMD 114
 QY 121 VMGQGTITVYSS 132
 DB 115 VMGQGLTVYSS 126

RESULT 5
 ABP45910
 ID ABP45910 standard; Protein; 251 AA.

AC ABP45910;

XX 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1921.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

XX 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Example 4; Fig 4B; 61pp; English.
 XX
 CC This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specifically which has
 CC hemostatic activity. (I) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents the human
 CC anti-factor VIII antibody VH IT-2 protein which is used in the method
 CC of the invention.
 XX
 SQ Sequence 132 AA;
 XX
 Query Match 100.0%; Score 711; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1,6e-58;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLQSATEVKKPGASKMKVSCMASGYPPTSVDISWVROAPQGLEMMGMSISGNTDY 60
 DB 1 QVQLQSATEVKKPGASKMKVSCMASGYPPTSVDISWVROAPQGLEMMGMSISGNTDY 60
 QY 61 AOKFGGRVMTTDTSRRTAYMELRSLRSDDTAVYVCARDGGGAYEDVWSGEYPEYYAMD 120
 DB 61 AOKFGGRVMTTDTSRRTAYMELRSLRSDDTAVYVCARDGGGAYEDVWSGEYPEYYAMD 120
 QY 121 VMGGGTTVTSS 132
 DB 121 VMGGGTTVTSS 132
 XX
 Db 121 VMGGGTTVTSS 132
 XX
 RESULT 2
 AAY50950
 ID AAY50950 standard; Protein; 132 AA.
 XX
 AC AAY50950;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human anti-factor VIII antibody VH clone IT-2 encoded protein.
 XX
 KW Human; heavy chain; antibody; factor VIII; hemostatic;
 KM hemophilia A; VH gene.
 XX
 OS Homo sapiens.
 XX
 PN M0958680-A2.
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99MO-NL00285.
 XX
 PR 08-MAY-1998; 98EP-0201543.
 XX
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
 XX
 PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
 XX
 DR WPI; 2000-053102/04.
 XX
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for
 PT treatment of hemophilia A patients with these antibodies -
 XX
 PS Example 4; Fig 4A; 61pp; English.
 XX
 CC This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specifically which has
 CC hemostatic activity. (I) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents the human
 CC anti-factor VIII antibody clone IT-2 protein which is used in the method
 CC of the invention.
 XX
 SQ Sequence 132 AA;
 XX
 Query Match 98.2%; Score 702; DB 21; Length 132;
 Best Local Similarity 99.2%; Pred. No. 1,1e-57;
 Matches 131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QVQLQSATEVKKPGASKMKVSCMASGYPPTSVDISWVROAPQGLEMMGMSISGNTDY 60
 DB 1 QVQLQSATEVKKPGASKMKVSCMASGYPPTSVDISWVROAPQGLEMMGMSISGNTDY 60
 QY 61 AOKFGGRVMTTDTSRRTAYMELRSLRSDDTAVYVCARDGGGAYEDVWSGEYPEYYAMD 120
 DB 61 AOKFGGRVMTTDTSRRTAYMELRSLRSDDTAVYVCARDGGGAYEDVWSGEYPEYYAMD 120
 QY 121 VMGGGTTVTSS 132
 DB 121 VMGGGTTVTSS 132
 XX
 Db 121 VMGGGTTVTSS 132
 XX
 RESULT 3
 ABP45179
 ID ABP45179 standard; Protein; 255 AA.
 XX
 AC ABP45179;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1190.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumor necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antineutrotic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-273799P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 DR Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 PT WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 1822-1823; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumor necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory.

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 42.463 Seconds

(Without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 1 QVQLQSLATPEVKKPGASMKV.....YPERYAMDVGQTTVTASS 132

Sequence: 1 QVQLQSLATPEVKKPGASMKV.....YPERYAMDVGQTTVTASS 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seque, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	132	21	AAV50953
2	702	98.7	132	21	AAV50950
3	525.5	73.9	255	23	ABP45179
4	524	73.7	252	23	ABP45663
5	523	73.6	251	23	ABP45910
6	521.5	73.3	259	23	ABP44962
7	520	73.1	253	23	ABP45766
8	514.5	72.4	248	23	ABP45767
9	514.5	72.4	257	23	ABP45599

10	513	72.2	249	23	ABP45414	Human Blys binding
11	512.5	72.1	257	23	ABP45565	Human Blys binding
12	510.5	71.8	251	23	ABP45551	Human Blys binding
13	510.5	71.8	259	23	ABP45441	Human Blys binding
14	508.5	71.5	257	23	ABP45343	Human Blys binding
15	508	71.4	254	23	ABP45394	Human Blys binding
16	507.5	71.4	121	22	AAU02549	Anti-adipocyte mon
17	507	71.3	250	23	ABP45584	Human Blys binding
18	506.5	71.2	257	23	ABP45568	Human Blys binding
19	505	71.0	247	23	ABP4562	Human Blys binding
20	504.5	71.0	248	23	ABP45461	Human Blys binding
21	504	70.9	247	23	ABP45105	Human Blys binding
22	504	70.9	250	23	ABP45549	Human Blys binding
23	503.5	70.8	248	23	ABP45435	Human Blys binding
24	500.5	70.4	251	23	ABP45575	Human Blys binding
25	500.5	70.4	251	23	ABP45861	Human Blys binding
26	499.5	70.3	253	23	ABP45625	Human Blys binding
27	498.5	70.1	259	23	ABP45345	Human Blys binding
28	498	70.0	251	23	ABP45304	Human Blys binding
29	497.5	70.0	251	23	ABP45867	Human Blys binding
30	496.5	69.8	248	23	ABP45860	Human Blys binding
31	496.5	69.8	251	23	ABP45859	Human Blys binding
32	495.5	69.7	251	23	ABP45544	Human Blys binding
33	494.5	69.5	251	23	ABP45725	Human Blys binding
34	494.5	69.5	251	23	ABP45858	Human Blys binding
35	494	69.5	250	23	ABP45550	Human Blys binding
36	494	69.5	250	23	ABP45582	Human Blys binding
37	492.5	69.3	248	23	ABP45866	Human Blys binding
38	492.5	69.3	251	23	ABP45727	Human Blys binding
39	492.5	69.3	252	23	ABP45484	Human Blys binding
40	492	69.2	254	23	ABP45769	Human Blys binding
41	490.5	69.0	253	23	ABP45164	Human Blys binding
42	489.5	68.8	251	23	ABP44919	Human Blys binding
43	489.5	68.8	253	23	ABP45600	Human Blys binding
44	489.5	68.8	253	23	ABP45953	Human Blys binding
45	489	68.8	98	21	AAV50954	Human anti-factor

ALIGNMENTS

RESULT 1
AAV50953
ID AAV50953 standard; Protein; 132 AA.
XX
AC AAV50953;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH protein VH IT-2.
XX
KW Human; heavy chain; antibody; factor VIII; hemostatic;
KW hemophilia A; VH protein.
XX
OS Homo sapiens.
XX
PN MO9958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99MO-NI00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SANO-) STICHTING SANGUIN BLOEDVOORZIENING.
XX Voorberg JJ, Van Den Brink EN, Turehout EM;
XX WPI; 2000-053102/04.
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -

```

QY      1  OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMWISYSGNTDY 60
      3  OVKLQOSPEVVRPFSVSVKISCKSGYFTDYSHMHWLGMNHAQSLWIGIISTYDGNITNY 62
QY      61  AOKFGQRTVMTTDSRTATAYMELRSLRSDPTAVVYCARDDGGGAYEDVWSGEYREYAMD 120
      63  NOKFKGKATLVVDSSSTATAYMELARLTSDSAIYYCAR-----YGSFYFFD 111
QY      121  VMGQGTIVTVSS 132
      112  YWGQGTIVTVSS 123

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RESULT 14

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O9QXE9  PRELIMINARY; PRT; 117 AA.
AC  O9QXE9
DT  01-MAY-2000 (TREMblrel. 13, Created)
DT  01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  Immunoglobulin heavy chain V-D-J region (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL  Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ225174; CAB65237.1; -
DR  HSSP; P01810; 2FBJ.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER 1
FT  NON_TER 117
SQ  SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

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Query Match 53.0%; Score 376.5; DB 11; Length 117;
 Best Local Similarity 55.3%; Pred. No. 8.2e-31;
 Matches 73; Conservative 18; Mismatches 26; Indels 15; Gaps 1;

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QY      1  OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMWISYSGNTDY 60
      1  EVQLQOSPELVKPGASVSKVSCKASGYFTDYMKWKVQSHGKSLWIGIDINPNNGTISY 60
QY      61  AOKFGQRTVMTTDSRTATAYMELRSLRSDPTAVVYCARDDGGGAYEDVWSGEYREYAMD 120
      61  NOKFKGKATLVVDSSSTATAYMELARLTSDSAIYYCAR-----RYAMD 105
QY      121  VMGQGTIVTVSS 132
      106  YWGQGTIVTVSS 117

```

RESULT 15

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ID  O92401  PRELIMINARY; PRT; 142 AA.
AC  O92401
DT  01-DEC-2001 (TREMblrel. 19, Created)
DT  01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  V23-D-J-C mu protein (Fragment).
DE  V23-D-J-C MU.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON  NCBI_TaxId=10090;
RN  [1]

```

```

RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6.
RA  Kozono Y., Kozono H., Azuma T.;
RT  "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT  Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT  Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL  Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB069913; BAB63929.1; -
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER 1
FT  NON_TER 142
SQ  SEQUENCE 142 AA; 15622 MW; 24A265CEAE4A318B CRC64;

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Query Match 52.8%; Score 375.5; DB 11; Length 142;
 Best Local Similarity 56.8%; Pred. No. 1.3e-30;
 Matches 75; Conservative 17; Mismatches 25; Indels 15; Gaps 2;

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QY      1  OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMWISYSGNTDY 60
      1  OVQLQOSPELVKPGASVSKVSCKASGYFTSYMHWVQRPQGLEWIGINIPNSGNTNY 60
QY      61  AOKFGQRTVMTTDSRTATAYMELRSLRSDPTAVVYCARDDGGGAYEDVWSGEYREYAMD 120
      61  NEKFKGKATLVVDSSSTATAYMELARLTSDSAIYYCARG-----WE-----AMD 105
QY      121  VMGQGTIVTVSS 132
      106  YWGQGTIVTVSS 117

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 Job time : 32.169 secs

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QY 61 AOKFOGRVTMTTDSRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWGSGEYREYAMD 120
DB 63 NEKFKGATLISVDSSSTAYMELTRLTSEDSAYVFCAR-----GDYRRY-FD 109
QY 121 VMGGGTTVTYSS 132
DB 110 VMGGGTTVTYSS 121

RESULT 11
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID 091WT1
AC 091WT1
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 54.9%; Score 390.5; DB 11; Length 481;
Best Local Similarity 57.6%; Pred. No. 1.7e-31;
Matches 76; Conservative 14; Mismatches 27; Indels 15; Gaps 1;

QY 1 OVOLLGSATVKKPKGASMKVSCMASGYPTFSYDISWVRQAPGCGLEMMGWTISYSGNTDY 60
DB 20 OVOLLGSQPELVKKGASVKISCKASGYTFTSYIHWVQKRGQGLVWIGWYPCDGNITKY 79
QY 61 AOKFOGRVTMTTDSRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWGSGEYREYAMD 120
DB 80 NEKFKGATLISVDSSSTAYMELTRLTSEDSAYVFCAR-----WAFD 124
QY 121 VMGGGTTVTYSS 132
DB 125 VMGGGTTVTYSS 136

RESULT 12
Q9Y298 PRELIMINARY; PRT; 150 AA.
ID 09Y298
AC 09Y298
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE 1G6 VH protein precursor (Fragment).
GN 1G6 VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G.; Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT 1G64 monoclonal antibody derived from a hemophilia A patient with
```

```
RT inhibitor.";
RL Blood 92:496-506 (1998).
DR EMBL; AJ224083; CAA11629.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Signal.
FT SIGNAL.
FT NON_TER. 1 19 POTENTIAL.
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 53.8%; Score 382.5; DB 4; Length 150;
Best Local Similarity 59.1%; Pred. No. 2.7e-31;
Matches 78; Conservative 10; Mismatches 29; Indels 15; Gaps 1;

QY 1 OVOLLGSATVKKPKGASMKVSCMASGYPTFSYDISWVRQAPGCGLEMMGWTISYSGNTDY 60
DB 20 OVOLLGSQPELVKKGASVKISCKASGYTFTSYIHWVQKRGQGLVWIGWYPCDGNITKY 79
QY 61 AOKFOGRVTMTTDSRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWGSGEYREYAMD 120
DB 80 AREFQGSVTMTADTSDIAYMELSLRSDDTAVYYCA-----VPPDPAFD 124
QY 121 VMGGGTTVTYSS 132
DB 125 VMGGGTTVTYSS 136

RESULT 13
Q925S2 PRELIMINARY; PRT; 170 AA.
ID 0925S2
AC 0925S2
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717 (2000).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).
DR EMBL; AF240167; AAK43732.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 53.1%; Score 377.5; DB 11; Length 170;
Best Local Similarity 56.1%; Pred. No. 1e-30;
Matches 74; Conservative 14; Mismatches 33; Indels 11; Gaps 2;
```

OY 121 VMGCGTTVSS 132
 DB 108 YMGCGTTVSS 119

RESULT 8

OBWY24 PRELIMINARY; PRT: 497 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE SNC66 protein.
 OS Homo sapiens (Human).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;

RP SEQUENCE FROM N.A.

RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong O.
 RT "Identification and characterization of SNC66, a Ig-like gene which is
 down-regulated in colorectal cancer."

RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF283666; AAL36987.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; 1.
 SQ SEQUENCE 497 AA; 5365 MW; F24D08DFA5A63E5 CRC64;

Query Match 56.8%; Score 403.5; DB 4; Length 497;
 Best Local Similarity 59.0%; Pred. No. 8.6e-33;
 Matches 79; Conservative 16; Mismatches 28; Indels 11; Gaps 2;

OY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLMMGMISYSGNTDY 60
 DB 20 QOQLSSGAEVTKPKASVSKASGYTITAIIDINWROAPGQGLMMGMNPOTNTTF 79
 OY 61 AAKFGQRTVTDTTSRRATYMEIRSLRSDDTAVYVCARDG--GGGAYEDVMSGEYPEYVA 118
 DB 80 AAKFGQLTFSRDTSINTAYMTLSLSTEDSAITFCARGLRGGRFGYVNM----- 130
 OY 119 MDVWGCTTVSS 132
 DB 131 FDPWGHGLTVSS 144

RESULT 9

Q9UL89 PRELIMINARY; PRT: 116 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035025; AAD56261.1; -.
 DR HSSP; P01810; 2FBU.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1 16
 FT TER 1 16

SQ SEQUENCE 116 AA; 12605 MW; C6F9131DE13EA898 CRC64;

Query Match 55.3%; Score 393; DB 4; Length 116;
 Best Local Similarity 62.5%; Pred. No. 1.7e-32;
 Matches 80; Conservative 11; Mismatches 25; Indels 12; Gaps 1;

OY 5 LOSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLMMGMISYSGNTDYAOKF 64
 DB 1 VQSGAEVKKPKSSVSKVSCKASGTFSSAIVSWVROAPGQGLMMGRITPIIGIANVYAKF 60
 OY 65 QGRVTMTDTTSRRATYMEIRSLRSDDTAVYVCARDGGGAYEDVMSGEYPEYVANDVWQ 124
 DB 61 QGRVTITADKSTAYVELSLRSEDTAVYCA-----SSNMGPYWFDDLWGR 108

OY 125 GTTVTVSS 132
 DB 109 GLTVTVSS 116

RESULT 10

Q925S3 PRELIMINARY; PRT: 147 AA.

DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE MRP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=BAUB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after irradiation in mice."
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BAUB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain."
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240165; AAK34371.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 55.1%; Score 391.5; DB 11; Length 147;
 Best Local Similarity 59.1%; Pred. No. 3.2e-32;
 Matches 78; Conservative 15; Mismatches 26; Indels 13; Gaps 2;

OY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLMMGMISYSGNTDY 60
 DB 3 QVXLHSGPEVVKPKASVSKASGYITSTIDWVROTPGQGLMMGMIFPGSGSTFY 62

Qy 118 AMDVWGQTTVTSS 132
 |||||
 Db 135 GMDVWGQTTVTSS 149

RESULT 5

Q96GAG PRELIMINARY; PRT; 614 AA.
 ID 096GAG; AC 096GAG; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009851; AAH09851.1; -
 DR InterPro; IPR000005; HTHATAC.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 59.6%; Score 423.5; DB 4; Length 614;
 Best Local Similarity 62.9%; Pred. No. 1e-34;
 Matches 83; Conservative 13; Mismatches 25; Indels 11; Gaps 2;

Qy 1 QVOLLQSTAEVKKPKGASMKVSCMASGYPTSYDLSWVRQAPGQGLEMMGIMISYSGNTDY 60
 |||||
 Db 20 QMVLVSGAEVRKKKGSVSKVSCAKSGYTFYRYLHWVRQAPGQALEMMGIMTFPNTY 79
 |||||
 Qy 61 AOKFGQVRVTMTDTSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120
 |||||
 Db 80 AOKFGQVRVTMTDTSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120
 |||||
 Qy 121 VMGQGTIVTVSS 132
 |||||
 Db 129 VMGQGTIVTVSS 140

RESULT 6

Q9UL92 PRELIMINARY; PRT; 124 AA.
 ID 09UL92; AC 09UL92; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berner S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

DR EMBL; AF035022; AA056258.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 124
 SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 59.5%; Score 423; DB 4; Length 124;
 Best Local Similarity 65.9%; Pred. No. 1.6e-35;
 Matches 87; Conservative 11; Mismatches 26; Indels 8; Gaps 2;

Qy 1 QVOLLQSTAEVKKPKGASMKVSCMASGYPTSYDLSWVRQAPGQGLEMMGIMISYSGNTDY 60
 |||||
 Db 1 EVOLVSGAEVRKKKGSVSKVSCAKSGYTFSSYVMHWVRQAPGQGLEMMGIMISYSGNTDY 60
 |||||
 Qy 61 AOKFGQVRVTMTDTSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120
 |||||
 Db 61 AOKFGQVRVTMTDTSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120
 |||||
 Qy 121 VMGQGTIVTVSS 132
 |||||
 Db 113 VMGQGTIVTVSS 124

RESULT 7

Q9GYZ2 PRELIMINARY; PRT; 119 AA.
 ID 09GYZ2; AC 09GYZ2; DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
 DE (Fragment).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 NCBI_TaxID=6182;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Song X.T., Peng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282622; AAG01452.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13567 MW; BA893873PD5FA6AB CRC64;

Query Match 58.7%; Score 417.5; DB 5; Length 119;
 Best Local Similarity 61.4%; Pred. No. 5.5e-35;
 Matches 81; Conservative 17; Mismatches 21; Indels 13; Gaps 1;

Qy 1 QVOLLQSTAEVKKPKGASMKVSCMASGYPTSYDLSWVRQAPGQGLEMMGIMISYSGNTDY 60
 |||||
 Db 1 QVOLLQSTAEVKKPKGASMKVSCMASGYPTSYDLSWVRQAPGQGLEMMGIMISYSGNTDY 60
 |||||
 Qy 61 AOKFGQVRVTMTDTSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120
 |||||
 Db 61 AOKFGQVRVTMTDTSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120
 |||||

Db 1 EVOLVESGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60
 QY 61 AOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 120
 Db 61 AOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 113
 QY 121 VMGQGTIVTVSS 132
 Db 114 VMGQGTIVTVSS 125

RESULT 2

Q9BRV0 PRELIMINARY; PRT; 500 AA.
 AC Q9BRV0; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005951; AAH05951.1; -.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 62.8%; Score 447; DB 4; Length 500;
 Best Local Similarity 68.2%; Pred. No. 3, 1e-37;
 Matches 90; Conservative 10; Mismatches 28; Indels 4; Gaps 2;

QY 1 QVQLQSATEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60
 Db 20 QVHLVSGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 79
 QY 61 AOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 120
 Db 80 AKKFGGRVMTTDTSTRTAYMELRLSRSDPTAVYYCAR--RCSYSYCONDY--YYMD 135
 QY 121 VMGQGTIVTVSS 132
 Db 136 VMGQGTIVTVSS 147

RESULT 3

Q9UL94 PRELIMINARY; PRT; 119 AA.
 AC Q9UL94; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035020; AAD56256.1; -.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 119
 FT NON_TER 1 119
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345FAA16E CRC64;

Query Match 62.8%; Score 446.5; DB 4; Length 119;
 Best Local Similarity 67.4%; Pred. No. 6e-38;
 Matches 89; Conservative 9; Mismatches 21; Indels 13; Gaps 2;

QY 1 QVQLQSATEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60
 Db 1 EVOLVESGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60
 QY 61 AOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 120
 Db 61 AOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 107
 QY 121 VMGQGTIVTVSS 132
 Db 108 VMGQGTIVTVSS 119

RESULT 4

Q96QSO PRELIMINARY; PRT; 159 AA.
 AC Q96QSO; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative matrix cell adhesion molecule-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Tjelson M.D.;
 RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
 RT mRNA (Matrix Cell Adhesion Molecule-3, Mac-CAM 3).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY039025; AAK82649.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 62.0%; Score 441; DB 4; Length 159;
 Best Local Similarity 67.4%; Pred. No. 3, 1e-37;
 Matches 91; Conservative 13; Mismatches 23; Indels 8; Gaps 3;

QY 1 QVQLQSATEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60
 Db 20 QVHLVSGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 79
 QY 61 AOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 117
 Db 80 SOKFQGRVMTTDTSTRTAYMELRLSRSDPTAVYYCARDDGGGAVEDVMSGEYFEYAMD 134

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	452.5		63.6	125	4	Q9UL95	Q9UL95 homo sapien
	2	444.7		62.9	500	4	Q9BRV0	Q9BRV0 homo sapien
	3	446.5		62.8	119	4	Q9UL94	Q9UL94 homo sapien
	4	441.1		62.0	159	4	Q9GOS0	Q9GOS0 homo sapien
	5	423.5		59.6	614	4	Q9GAG6	Q9GAG6 homo sapien
	6	423		59.5	124	4	Q9UL92	Q9UL92 homo sapien
	7	417.5		58.7	119	5	Q9GXY2	Q9GXY2 schistosoma
	8	403.5		56.8	497	4	Q8MY24	Q8MY24 homo sapien
	9	393		55.3	116	4	Q9UL89	Q9UL89 homo sapien
	10	391.5		55.1	147	11	Q9Z553	Q9Z553 mus musculus
	11	390.5		54.9	481	11	Q91W11	Q91W11 mus musculus
	12	382.5		53.8	150	4	Q9Y298	Q9Y298 homo sapien
	13	377.5		53.1	170	11	Q9Z562	Q9Z562 mus musculus
	14	376.5		53.0	117	11	Q9QX89	Q9QX89 mus musculus
	15	375.5		52.8	142	11	Q9Z401	Q9Z401 mus musculus
	16	372		52.3	109	11	Q9JL75	Q9JL75 mus musculus

17	371	52.2	145	11	Q924R1	Q924T1	mus	musculus
18	371	52.2	613	11	Q8VCX7	Q8VCX7	mus	musculus
19	370	52.0	145	11	Q924Q6	Q924Q6	mus	musculus
20	369	51.9	145	11	Q924R4	Q924R4	mus	musculus
21	368.5	51.8	484	11	Q991A6	Q991A6	mus	musculus
22	368	51.8	143	11	Q924R0	Q924R0	mus	musculus
23	368	51.8	482	11	Q8K172	Q8K172	mus	musculus
24	367.5	51.7	480	11	Q8K0Z4	Q8K0Z4	mus	musculus
25	367	51.6	145	11	Q924Q9	Q924Q9	mus	musculus
26	367	51.6	145	11	Q924P7	Q924P7	mus	musculus
27	366.5	51.5	157	4	Q95978	Q95978	homo	sapien
28	364.5	51.3	473	11	Q9DBL4	Q9DBL4	mus	musculus
29	364	51.2	145	11	Q924R3	Q924R3	mus	musculus
30	364	51.2	241	11	Q921A6	Q921A6	mus	musculus
31	364	51.2	463	11	Q991C4	Q991C4	mus	musculus
32	364	51.2	488	11	Q8K0F2	Q8K0F2	mus	musculus
33	363.5	51.1	123	11	Q8V1J1	Q8V1J1	mus	musculus
34	363.5	51.1	168	11	Q8VDC9	Q8VDC9	mus	musculus
35	361.5	50.8	146	11	Q924Q3	Q924Q3	mus	musculus
36	360	50.6	143	11	Q924P9	Q924P9	mus	musculus
37	359.5	50.6	117	11	Q90XFP	Q90XFP	mus	musculus
38	358.5	50.4	120	11	Q920E8	Q920E8	mus	musculus
39	358	50.4	118	11	Q921C2	Q921C2	mus	musculus
40	357.5	50.3	142	11	Q924Q4	Q924Q4	mus	musculus
41	357	50.2	143	11	Q924Q5	Q924Q5	mus	musculus
42	357	50.2	143	11	Q924R7	Q924R7	mus	musculus
43	356.5	50.1	144	11	Q924P5	Q924P5	mus	musculus
44	356.5	50.1	146	11	Q924R8	Q924R8	mus	musculus
45	356	50.1	143	11	Q924Q0	Q924Q0	mus	musculus

ALIGNMENTS

RESULT 1

ID	Q9UL95;	PRELIMINARY;	PRT;	125 AA.
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAY-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Myosin-Ia, active immunoglobulin heavy chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RT	Young D.C.;			
RT	"Myosin-Ia: reactive autoantibodies in rheumatic carditis and normal fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035019; AAD56255.1; .			
DR	HSSP; P01810; 2FbJ.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER	1	125	
FT	NON_TER	1	125	
SQ	SEQUENCE	125 AA;	13516 MW;	0D3CD5C23248BEAC CRC64;

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Query Match          63.6%   Score 452.5;   DB 4, Length 125;
Best local Similarity 68.2%   Pred. No. 1.6e-38;
Matches    90; Conservative 11; Mismatches 24; Indels 7; Gaps 2
QY      1 OVQLDSATVEKKGCAAMKVSCMAAGVPPFSYDISWVRAPGCGELWMGMISIVSGNDY 60
       :|::||| |::||| ||| | | | | | | | | | | | | | | | | | | | |
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Tue Dec 30 11:48:58 2003

us-09-674-752-25.rsp

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Job time : 7.07717 secs

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ID HV16 MOUSE STANDARD; PRT; 136 AA.
AC P01753;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adeyupo K., Milestein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
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DR EMBL; J00522; AAD15290.1; -
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
DR KIMMUNOGLOBULIN V region; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 1
FT DOMAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT NON TER 136 Y -> W (IN REF. 2).
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 47.5%; Score 338; DB 1; Length 136;
Best Local Similarity 50.4%; Pred. No. 1.5e-28;
Matches 66; Conservative 23; Mismatches 30; Indels 12; Gaps 3;

2 VOLLOSGATEVKKRGKSGAMKVSQMASGYPFTSYDLSWTRQAPGCGLEMGWISISGNTDYA 61
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
18 VOLVESGGGLVQVGRSKLSQASGFTFSFGHWRQAPKGLGVAVYISGSSSTLHYA 77
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

62 AQFGQGVMTTDSRTATMELSLRSDTAVYCCARDGGAGAYEDVWSGEYPEYVAMD 121
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
78 DTVKGFITSRDNPKNITLFLQMTSLRSEDTATYTCAR-----N-GNTP-TYANDY 125
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

122 WGGGTIVTVSS 132
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
126 WGGGTIVTVSS 136
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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RESULT 15
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA8172.1; -
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
DR KIMMUNOGLOBULIN V region; Signal.
FT SIGNAL 1
FT CHAIN 1
FT DOMAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match 47.4%; Score 337; DB 1; Length 137;
Best Local Similarity 53.8%; Pred. No. 1.9e-28;
Matches 71; Conservative 13; Mismatches 34; Indels 14; Gaps 3;

1 QVQLQSGATEVKKRGKSGAMKVSQMASGYPFTSYDLSWTRQAPGCGLEMGWISISGNTDY 60
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
20 QVQLQSGATEVKKRGKSGAMKVSQMASGYPFTSYDLSWTRQAPGCGLEMGWISISGNTDY 79
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

61 AQFGQGVMTTDSRTATMELSLRSDTAVYCCARDGGAGAYEDVWSGEYPEYVAMD 120
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
80 NEHRSKATLTLPKPSSTAYMQSLTSSEDSAVYYCAR-----YR---LGR-----FD 125
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

121 WGGGTIVTVSS 132
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
126 WGGGTIVTVSS 137
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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```

RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.B.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Biochemistry 9:3168-3196(1970).
CC MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90563; GIHUEU.
DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_v.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PSS0835; IG_Like; 1.
DR Immunoglobulin V region; Pyroliidone carboxylic acid.
KW DOMAIN 1 112
FT MOD_RES 1 112
FT DISULFID 1 112
FT NON_TER 117 96
FT SEQUENCE 117 AA; 12472 MW; 99D60ADABED52818 CRC64;

Query Match
Beet Local Similarity 50.4%; Score 358.5; DB 1; Length 117;
Matches 80; Conservative 8; Mismatches 29; Indels 15; Gaps 3;

QY 1 OVQLLOSATEVKKKGASMKVSCMASGVPFTSYDTSWTRQAPGGLGEMWGISYSGNTDY 60
DB 1 OVQLVQSAPAEVKKKSSVKKVSCKASGGTFRSALITWRQAPGGLGEMWGISVPEFGPNY 60
QY 61 AOKFQGRVTMTDTSRRTAYMELRSDDPAVYCCARPGGAYEDVSGEYPEYAMD 120
DB 61 AOKFQGRVTITADSTWYAVELSLRSDDPAVYCCARPGGAYEDVSGEYPEYAMD 120
QY 61 AOKFQGRVTITADSTWYAVELSLRSDDPAVYCCARPGGAYEDVSGEYPEYAMD 120
DB 61 AOKFQGRVTITADSTWYAVELSLRSDDPAVYCCARPGGAYEDVSGEYPEYAMD 120
QY 121 VMGCGTTVTVSS 132
DB 109 ---NGGLTVTVSS 117

RESULT 10
HV51 MOUSE STANDARD; PRT; 118 AA.
ID P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R.; Boyens J.; Stekevitz M.; Beyreuther K.; Rajewsky K.;
RT "A region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes.";
DR EMBL U.3:517-523(1984).
DR PIR; A02040; MMS38.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_v.1.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PSS0835; IG_Like; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.

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FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match
Beet Local Similarity 50.4%; Score 358; DB 1; Length 118;
Matches 71; Conservative 17; Mismatches 30; Indels 14; Gaps 1;

QY 1 OVQLLOSATEVKKKGASMKVSCMASGVPFTSYDTSWTRQAPGGLGEMWGISYSGNTDY 60
DB 1 EVQLQSGPELVKPGASVKISCASTGFTDYMMNWVKOSHGLEIMGINPNNCGTSY 60
QY 61 AOKFQGRVTMTDTSRRTAYMELRSDDPAVYCCARPGGAYEDVSGEYPEYAMD 120
DB 61 NOKFKGATLVTKSSATYMEELSLTSDDSAVYCCARPGGAYEDVSGEYPEYAMD 120
QY 121 VMGCGTTVTVSS 132
DB 107 VMGCGTTVTVSS 118

RESULT 11
HV07 MOUSE STANDARD; PRT; 139 AA.
ID P01751;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M.; Paekind M.; Reith M.; Imanishi-Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL; J00529; AAA38170.1; -
DR PIR; A90809; MMS18.
DR PDB; 1A6W; 27-MAY-98.
DR PDB; 1A6W; 15-JUL-98.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_v.1.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PSS0835; IG_Like; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

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OY      121 VMGCGTTVTSS 132
DB      109 VMGCGTTVTSS 120

RESULT 7
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 9367 precursor.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sime J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00493; AAA8128.1; -
DR PIR; A94264; HVMG7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 50.7%; Score 360.5; DB 1; Length 140;
Best Local Similarity 53.0%; Pred. No. 6,8e-31;
Matches 70; Conservative 22; Mismatches 29; Indels 11; Gaps 1;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kenty W.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447841 CRC64;

Query Match 50.6%; Score 359.5; DB 1; Length 117;
Best Local Similarity 54.5%; Pred. No. 7.1e-31;
Matches 72; Conservative 18; Mismatches 27; Indels 15; Gaps 2;

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OY      1 OVOLLOSAATEVKKPKASMKVSCMASGYPFTSYDISWVRQAPQGLMWMGMSISVSGNTDY 60
DB      20 EVOLQOSGAEIVLRASGVKSKASGYFTSYGINWVKRPOGKLEWIGYINPGMGYNY 79
OY      61 AOKFOGRVMTTDTSRRTAYMELRSLSRSDDTAVYYCARDGGGAGAYEDVWSGEYPEYVAMD 120
DB      80 NKKPKKATLTVDKSSSTAYMQLRSLTSDSAVYFCAR-----SHYGGSGYDFD 128
OY      121 VMGCGTTVTSS 132
DB      129 VMGCGTPTVTSS 140

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RESULT 9
HV1A_HUMAN
ID HV1A_HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-1 region EU.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Maxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8131846; Pubmed=6186498;
 RA Stekevitz M., Gefter M.L., Brodeur P., Riblet R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenate
 idotype response of the strain A mouse."
 RT Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 CC SEGMENT. JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Hybridoma.
 KM DOMAIN 1 111
 FT NON_TER 120 120
 FT IG-LIKE.
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match
 Best Local Similarity 51.7%; Score 367.5; DB 1; Length 120;
 Matches 72; Conservative 20; Mismatches 28; Indels 11; Gaps 1;

OY 2 VOLQSGATEVKKPGASMKVSCMASGYPTTSYDISWVRAPGQGLEMGWISISYSGNTDY 61
 DB 1 VOLQSGAEIVRAGSVSMSCASGYTTFTSYGNVKKRPGQGLEMGWISYSGNTDY 60
 OY 62 OKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGCGGAYEDVWSGEYPEYVAMD 121
 DB 61 EKFKKATLTVDKSSSTAYMQLSRSLTSDESAVYCAR-----SYVYGGSYTFDY 109
 OY 122 WGGGTTTVSS 132
 DB 110 WGGGTTTVSS 120

RESULT 5

HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; Pubmed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments."
 RL Nature 283:35-40(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DB InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 116
 FT DISULFID 22 96
 FT NON_TER 117 117
 FT BY SIMILARITY.
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match
 Best Local Similarity 51.1%; Score 363.5; DB 1; Length 117;
 Matches 71; Conservative 18; Mismatches 28; Indels 15; Gaps 1;

OY 1 OVQLQSGATEVKKPGASMKVSCMASGYPTTSYDISWVRAPGQGLEMGWISISYSGNTDY 60
 DB 1 EVQLQSGPELVKPGASVKSCASGYTFIDYVMKWVKQSHGKSLKLEIGININNGTST 60
 OY 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGCGGAYEDVWSGEYPEYVAMD 120
 DB 61 NOKFKGATLTVDKSSSTAYMQLSLTSDESAVYCAR-----RYWYFD 105
 OY 121 WGGGTTTVSS 132
 DB 106 WGGGTTTVSS 117

RESULT 6
 HV50_MOUSE STANDARD; PRT; 120 AA.
 ID HV50_MOUSE
 AC P06329;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1998 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region AC38 15.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=84182519; Pubmed=6201362;
 RA Dildrop R., Bovens L., Stekevitz M., Beyreuther K., Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes."
 RL EMBO J. 3:517-523(1984).
 DR PIR: A02037; MEMS15.
 DR HSSP: P01810; 2PRJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; IGV_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 98
 FT DISULFID 99 105
 FT DOMAIN 106 120
 FT DISULFID 22 96
 FT NON_TER 120 120
 FT BY SIMILARITY.
 SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09814 CRC64;

Query Match
 Best Local Similarity 50.8%; Score 361; DB 1; Length 120;
 Matches 71; Conservative 18; Mismatches 31; Indels 12; Gaps 2;

OY 1 OVQLQSGATEVKKPGASMKVSCMASGYPTTSYDISWVRAPGQGLEMGWISISYSGNTDY 60
 DB 1 OVQLQSGTELVKPGASVSMSCASGYTTFTSYGNVKKRPGQGLEMGWISYSGNTDY 60
 OY 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGCGGAYEDVWSGEYPEYVAMD 120
 DB 61 NEKFKGATLTVDKSSSTAYMQLSLTSDESAVYCAR-----WDYEDRIF--D 108

```

QY 1 QVOLLQATVEVKPKGASMKVSCMASGYPTSYDISVWRQAPQGLQEMMGWISYSGNTDY 60
DB 20 QVOLLQVQSGAEVKKPGASVAVSCASGYTFIDSYIMIMQAGHGLEWGMINPNSGNTY 79
QY 61 AOKFGQAVTMTTDSRTTAYMELRLSRDSDTAIVYCARQGGGAYEDVSGEYP-EY-YA 118
DB 80 AFRFGQAVTMTTDRDAFSTRAYMDRLRLSRDSDSAVFYCAKAS-----DPFWSDYNYFDYSYT 133
QY 119 MDVWQGGTTVTVSS 132
DB 134 LDVWQGGTTVTVSS 147

```

RESULT 2

```

ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region H3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxId=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

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CC EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUNG.
DR HSSP; P01772; ZPB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H3.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

```

```

Query Match 54.3%; Score 386; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 1.2e-33;
Matches 75; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

```

```

QY 1 QVOLLQATVEVKPKGASMKVSCMASGYPTSYDISVWRQAPQGLQEMMGWISYSGNTDY 60
DB 20 QVOLLQVQSGAEVKKPGASVAVSCASGYTFIDSYIMIMQAGHGLEWGMINPNSGNTY 79
QY 61 AOKFGQAVTMTTDSRTTAYMELRLSRDSDTAIVYCAR 98
DB 80 AOKFGQAVTMTTDSRTTAYMELRLSRDSDTAIVYCAR 117

```

```

RESULT 3
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxId=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus.";
RL EMBO J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVHJ35.
DR HSSP; P01772; ZPB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE6ICE63F8CE97BD CRC64;

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Query Match 53.7%; Score 382; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 3.1e-33;
Matches 75; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

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```

QY 1 QVOLLQATVEVKPKGASMKVSCMASGYPTSYDISVWRQAPQGLQEMMGWISYSGNTDY 60
DB 20 QVOLLQVQSGAEVKKPGASVAVSCASGYTFIDSYIMIMQAGHGLEWGMINPNSGNTY 79
QY 61 AOKFGQAVTMTTDSRTTAYMELRLSRDSDTAIVYCAR 98
DB 80 AOKFGQAVTMTTDSRTTAYMELRLSRDSDTAIVYCAR 117

```

RESULT 4

```

ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 7.07717 Seconds

(Without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711
Sequence: 1 QVQLLOSATEVKKPGASMKV.....YPEYVMDVWGQGTITVSS 132Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	427	60.1	147	1	P01744 homo sapien
2	386	54.3	117	1	HV1B_HUMAN
3	382	53.7	117	1	HV1G_HUMAN
4	367.5	51.7	120	1	HV03_MOUSE
5	363.5	51.1	117	1	HV13_MOUSE
6	361	50.8	120	1	HV50_MOUSE
7	360.5	50.7	140	1	HV02_MOUSE
8	359.5	50.6	117	1	HV12_MOUSE
9	358.5	50.4	117	1	HV1A_HUMAN
10	358	50.4	118	1	HV51_MOUSE
11	354	49.8	139	1	HV07_MOUSE
12	341	48.0	114	1	HV00_MOUSE
13	339.5	47.7	136	1	HV15_MOUSE
14	338	47.5	136	1	HV16_MOUSE
15	337	47.4	137	1	HV11_MOUSE
16	335	47.1	117	1	HV52_MOUSE
17	335	47.1	120	1	HV1H_HUMAN
18	325.5	45.8	121	1	HV3J_HUMAN
19	323.5	45.5	121	1	HV01_MOUSE
20	323.5	45.5	125	1	HV1F_HUMAN
21	323.5	45.5	125	1	HV1E_HUMAN
22	319	44.9	122	1	HV3G_HUMAN
23	318	44.7	117	1	HV09_MOUSE
24	318	44.7	117	1	HV14_MOUSE
25	316	44.4	117	1	HV04_MOUSE
26	313	44.0	126	1	HV3K_HUMAN
27	309	43.5	117	1	HV06_MOUSE
28	306	43.0	122	1	HV3H_HUMAN
29	306	43.0	146	1	HV2I_HUMAN
30	303	42.6	119	1	HV3B_MOUSE
31	302.5	42.5	115	1	HV3D_HUMAN
32	301	42.3	124	1	HV1E_HUMAN
33	300	42.2	116	1	HV3T_HUMAN

34	299	42.1	117	1	HV05_MOUSE	P01749 mus musculu
35	299	42.1	124	1	HV1D_HUMAN	P01760 homo sapien
36	298.5	42.0	119	1	HV3I_HUMAN	P01770 homo sapien
37	297.5	41.8	117	1	HV02_CANFA	P01785 canis fam1
38	297.5	41.8	144	1	HV43_MOUSE	P01819 mus musculu
39	296.5	41.7	117	1	HV42_MOUSE	P01812 mus musculu
40	296	41.6	117	1	HV10_MOUSE	P01784 mus musculu
41	296	41.6	117	1	HV45_MOUSE	P06328 mus musculu
42	295	41.5	122	1	HV3A_HUMAN	P01762 homo sapien
43	292	41.1	120	1	HV3U_HUMAN	P01782 homo sapien
44	290.5	40.9	123	1	HV24_MOUSE	P01793 mus musculu
45	290	40.8	114	1	HV01_CANFA	P01784 canis fam1

ALIGNMENTS

RESULT 1

HV1C_HUMAN STANDARD; PRT; 147 AA.

AC P01744; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE IG heavy chain V-I region ND precursor (Fragments).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

RA Bell L.O., Gould H.J.;

RT "Cloning and sequence determination of the gene for the human

RT immunoglobulin epsilon chain expressed in a myeloma cell line.;"

RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RN [2]

RP SEQUENCE OF 20-147.

RA Bemmich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;

RL (In) Bach M.K. (eds.);

RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).

CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

CC PROTEIN.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSP: P01789; 1MCP.

DR GO: GO:000576; C:extracellular; NAS.

DR GO: GO:0003623; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

34	299	42.1	117	1	HV05_MOUSE	P01749 mus musculu
35	299	42.1	124	1	HV1D_HUMAN	P01760 homo sapien
36	298.5	42.0	119	1	HV3I_HUMAN	P01770 homo sapien
37	297.5	41.8	117	1	HV02_CANFA	P01785 canis fam1
38	297.5	41.8	144	1	HV43_MOUSE	P01819 mus musculu
39	296.5	41.7	117	1	HV42_MOUSE	P01812 mus musculu
40	296	41.6	117	1	HV10_MOUSE	P01784 mus musculu
41	296	41.6	117	1	HV45_MOUSE	P06328 mus musculu
42	295	41.5	122	1	HV3A_HUMAN	P01762 homo sapien
43	292	41.1	120	1	HV3U_HUMAN	P01782 homo sapien
44	290.5	40.9	123	1	HV24_MOUSE	P01793 mus musculu
45	290	40.8	114	1	HV01_CANFA	P01784 canis fam1

ALIGNMENTS

RESULT 1

HV1C_HUMAN STANDARD; PRT; 147 AA.

AC P01744; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE IG heavy chain V-I region ND precursor (Fragments).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

RA Bell L.O., Gould H.J.;

RT "Cloning and sequence determination of the gene for the human

RT immunoglobulin epsilon chain expressed in a myeloma cell line.;"

RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RN [2]

RP SEQUENCE OF 20-147.

RA Bemmich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;

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RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).

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DR HSP: P01789; 1MCP.

DR GO: GO:000576; C:extracellular; NAS.

DR GO: GO:0003623; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

34	299	42.1	117	1	HV05_MOUSE	P01749 mus musculu
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37	297.5	41.8	117	1	HV02_CANFA	P01785 canis fam1
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40	296	41.6	117	1	HV10_MOUSE	P01784 mus musculu
41	296	41.6	117	1	HV45_MOUSE	P06328 mus musculu
42	295	41.5	122	1	HV3A_HUMAN	P01762 homo sapien
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44	290.5	40.9	123	1	HV24_MOUSE	P01793 mus musculu
45	290	40.8	114	1	HV01_CANFA	P01784 canis fam1

ALIGNMENTS

RESULT 1

HV1C_HUMAN STANDARD; PRT; 147 AA.

AC P01744; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE IG heavy chain V-I region ND precursor (Fragments).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

RA Bell L.O., Gould H.J.;

RT "Cloning and sequence determination of the gene for the human

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RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RN [2]

RP SEQUENCE OF 20-147.

RA Bemmich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;

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CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSP: P01789; 1MCP.

DR GO: GO:000576; C:extracellular; NAS.

DR GO: GO:0003623; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

34	299	42.1	117	1	HV05_MOUSE	P01749 mus musculu
35	299	42.1	124	1	HV1D_HUMAN	P01760 homo sapien
36	298.5	42.0	119	1	HV3I_HUMAN	P01770 homo sapien
37	297.5	41.8	117	1	HV02_CANFA	P01785 canis fam1
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41	296	41.6	117	1	HV45_MOUSE	P06328 mus musculu
42	295	41.5	122	1	HV3A_HUMAN	P01762 homo sapien
43	292	41.1	120	1	HV3U_HUMAN	P01782 homo sapien
44	290.5	40.9	123	1	HV24_MOUSE	P01793 mus musculu
45	290	40.8	114	1	HV01_CANFA	P01784 canis fam1

ALIGNMENTS

RESULT 1

HV1C_HUMAN STANDARD; PRT; 147 AA.

AC P01744; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE IG heavy chain V-I region ND precursor (Fragments).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

RA Bell L.O., Gould H.J.;

RT "Cloning and sequence determination of the gene for the human

RT immunoglobulin epsilon chain expressed in a myeloma cell line.;"

RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RN [2]

RP SEQUENCE OF 20-147.

RA Bemmich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;

RL (In) Bach M.K. (eds.);

RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).

CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

CC PROTEIN.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSP: P01789; 1MCP.

DR GO: GO:000576; C:extracellular; NAS.

DR GO: GO:0003623; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

P01749	mus	musculu
P01760	homo	sapien
P01770	homo	sapien
P01785	canis	famill
P01819	mus	musculu
P01812	mus	musculu
P01754	mus	musculu
P06328	mus	musculu
P01762	homo	sapien
P01782	homo	sapien
P01793	mus	musculu
P01784	canis	famill

C/Accession: S26792
 R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
 Eur. J. Immunol. 22, 241-245, 1992
 A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family
 A/Reference number: S26786; MUID:92111632; PMID:1730251
 A/Accession: S26792
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-131 <MOR>
 A/Cross-references: EMBL:X61012; NID:932804; PIDN:CAA43346.1; PID:g1335131
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterodimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 66.7%; Score 474.5; DB 2; Length 131;
 Matches 89; Conservative 17; Mismatches 25; Indels 1; Gaps 1;
 QY 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 Db 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 120
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 120
 QY 121 VMGCGTTVTYVSS 132
 Db 120 VMGCGTTVTYVSS 131

RESULT 7

PH0954
 Ig heavy chain V region (G6+ CUL-HEN) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0954
 R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 U. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0954
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-132 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterodimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: complementarity-determining 2
 F:51-67/Region: complementarity-determining 3
 F:68-98/Region: framework 3
 F:99-120/Region: complementarity-determining 3

Query Match
 Best Local Similarity 56.5%; Score 473; DB 2; Length 132;
 Matches 95; Conservative 9; Mismatches 26; Indels 4; Gaps 2;
 QY 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 Db 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 118
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 118
 QY 119 MDVWGCGTTVTYVSS 132
 Db 119 MDVWGCGTTVTYVSS 132

RESULT 8

S34014
 Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C/Accession: S34014; S30535
 R/Mariette, X.; Teaple, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A/Reference number: S34001; MUID:93209281; PMID:7681398
 A/Accession: S34014
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-127 <MAR>
 A/Cross-references: EMBL:218321
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterodimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 65.2%; Score 463.5; DB 2; Length 127;
 Matches 94; Conservative 12; Mismatches 21; Indels 5; Gaps 2;
 QY 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 Db 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 120
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 120
 QY 121 VMGCGTTVTYVSS 132
 Db 116 VMGCGTTVTYVSS 127

RESULT 9

C33548
 Ig heavy chain V-1 region (783) - human
 C/Species: Homo sapiens (man)
 C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 C/Accession: C33548
 R/Kipps, T.J.; Tomhave, E.; Prater, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene
 A/Reference number: A33548; MUID:89345575; PMID:2503826
 A/Accession: C33548
 A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A/Molecule type: DNA
 A/Residues: 1-133 <KIP>
 A/Experimental source: the sequence was determined from the differentiated gene
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterodimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 65.0%; Score 462.5; DB 2; Length 133;
 Matches 94; Conservative 8; Mismatches 27; Indels 7; Gaps 2;
 QY 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 Db 1 QVOLLQSATEVKKPGASMKVSCMASGYFTSYDLSWVROAPGCGLEWGMISTISGNTDY 60
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 116
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAAYVYCARDDGGGAYEDVWSGEYPEYAMD 116
 QY 117 YAMDVWGCGTTVTYVSS 132
 Db 118 YAMDVWGCGTTVTYVSS 133

RESULT 10

S14683

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 12.6531 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711
Sequence: 1 QVQLQSGAEVKKPKASMKV.....YPEYVMDVWGCGTIVTSS 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520.5	73.2	129	2 S36260	Ig heavy chain V r
2	507.5	71.4	122	2 S36271	Ig heavy chain V r
3	486	68.4	124	2 S19665	Ig heavy chain V r
4	481.5	67.7	160	2 PL0105	anti-PR2 erythrocy
5	478.5	67.3	129	2 S46393	Ig heavy chain V r
6	474.5	66.7	131	2 S26792	Ig heavy chain V r
7	473	66.5	132	2 PH0954	Ig heavy chain V r
8	463.5	65.2	127	2 S34014	Ig heavy chain V r
9	462.5	65.0	133	2 C33548	Ig heavy chain V-1
10	462.5	65.0	627	2 S14683	Ig mu chain precur
11	460	64.7	136	2 S31600	Ig heavy chain V r
12	454	63.9	114	2 PH1667	Ig heavy chain V r
13	453	63.7	118	2 PH1666	Ig heavy chain V r
14	452.5	63.6	125	2 S68170	Ig heavy chain V r
15	451	63.4	118	2 S36265	Ig heavy chain V r
16	450	63.3	98	2 S26919	Ig heavy chain V r
17	450	63.3	128	2 PH0952	Ig heavy chain V r
18	449.5	63.2	123	2 D33548	Ig heavy chain V-1
19	446	62.7	110	2 PH1670	Ig heavy chain V r
20	445	62.6	131	2 S21924	Ig heavy chain V r
21	443	62.3	135	2 S49530	anti-Sm antibody V
22	443	62.3	116	2 PH0961	Ig heavy chain V r
23	442.5	62.2	119	2 PH0951	Ig heavy chain V r
24	438.5	61.7	127	2 PH0955	Ig heavy chain V r
25	434	61.0	135	2 B32274	Ig heavy chain pre
26	433	60.9	126	2 B33548	Ig heavy chain V-1
27	433	60.7	126	2 S23623	Ig heavy chain V r
28	431.5	60.7	125	2 PH0957	Ig heavy chain V r
29	429.5	60.4	129	2 A33548	Ig heavy chain V-1

30	427	60.1	132	2 S31596	Ig heavy chain V r
31	427	60.1	143	1 E1HUND	Ig heavy chain pre
32	426	59.9	122	2 PH0958	Ig heavy chain V r
33	426	59.9	132	2 S46394	Ig heavy chain V r
34	425.5	59.8	135	2 PH0953	Ig heavy chain V r
35	419.5	59.0	142	2 A32483	Ig heavy chain V r
36	419	58.9	110	2 PH1669	Ig heavy chain V r
37	419	58.9	120	2 PH0962	Ig heavy chain V r
38	418.5	58.9	148	2 S29257	Ig heavy chain V r
39	417.5	58.7	126	2 I44151	Ig heavy chain V r
40	416	58.5	120	2 S31999	Ig heavy chain V r
41	414	58.2	111	2 S21925	Ig heavy chain V r
42	413	58.1	98	2 S26918	Ig heavy chain V r
43	412	57.9	116	2 PH0959	Ig heavy chain V r
44	411.5	57.9	109	2 PH1668	Ig heavy chain V r
45	407.5	57.3	122	2 B49590	Ig heavy chain V r

ALIGNMENTS

RESULT 1

Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36260
R:Gciffilth, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; WUID:93178448; PMID:7679990
A:Accession: S36260
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-129 <GRI>
A:Cross-references: EMBL:Z18851; NID:G33124; PIDN:CAA79303.1; PID:G939903
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 520.5; DB 2; Length 129;
Best Local Similarity 79.5%; Pred. No. 5.6e-41;
Matches 105; Conservative 4; Mismatches 20; Indels 3; Gaps 2;

QY 1 QVQLQSGAEVKKPKASMKVSCVAGYPTFSYDLSWVROAPGGGLEMGWISYSGNTDY 60
DB 1 QVQLQSGAEVKKPKASVKSCASGTFSTYGISVROAPGGGLEMGWISVNGNTNY 60
QY 61 AGRFQGRVTMTTDSRTTAVMELRLSRDPTAVYCCARDGGGAYEDVMSGEYPEYVAMD 120
DB 61 AQLQGRVTMTTDTSTSTAVMELRLSRDPTAVYCCARDGFG--YCSSTSCPY-YYVYMD 117
QY 121 VMGCGTTTVSS 132
DB 118 VMGKGTTTVSS 129

RESULT 2

Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36271
R:Gciffilth, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; WUID:93178448; PMID:7679990
A:Accession: S36271
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <GRI>
A:Cross-references: EMBL:Z18832; NID:G33115; PIDN:CAA79284.1; PID:G939895
C:Superfamily: immunoglobulin V region; immunoglobulin homology

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2400
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_1
US-08-964-690-22

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Query Match 68.5%; Score 471; DB 3; Length 128;

Best Local Similarity 72.6%; Pred. No. 2e-41; Matches 98; Conservative 6; Mismatches 19; Indels 12; Gaps 3;

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QY 1 QVQLVSGAEAKKPKGSSVKVSCKASGDTFNSPISWRQAPGQGLEWMGIIPI-FGSTK 59
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Db 1 QVQLVSGAEVKKPKGSSVKVSCKASGYTFTSTAIISWRQAPGQGLEMMGIMIPYNGDNT 60
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QY 60 YAKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ---ONGGWYEGPILPRPD 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 YAKFGGRVTITADTSTSTAYMELSLRSEDTAVYYCARAPGYSGGCGYRG-----D 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 116 ALDIMGQGTMTVSS 130
   |||||:|||||
Db 114 YFDYWGQGTTLTVSS 128
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RESULT 15

US-08-217-918-4
; Sequence 4, Application US/08217918
; Patent No. 5506132

GENERAL INFORMATION:

APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-918-4

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Query Match 68.5%; Score 471; DB 1; Length 147;

Best Local Similarity 70.7%; Pred. No. 2.4e-41; Matches 94; Conservative 13; Mismatches 18; Indels 8; Gaps 2;

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QY 1 QVQLVSGAEAKKPKGSSVKVSCKASGDTFNSPISWRQAPGQGLEWMGIIPIPGSTKY 60
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Db 20 QVQLVSGAEVKKPKGSSVKVSCKASGDTFNSPISWRQAPGQGLEMMGIMIPFVTSY 79
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QY 61 AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGGWYEGPILPRPD---DAL 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 AOKFGGRVTISADASTSTAYMELSLRSDDTAVYYCARD---ITAPGAPPTPLNFGM 134
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QY 118 DIMGQGTMTVSS 130
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Db 135 DVMGQGTTLTVSS 147
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Search completed: December 30, 2003, 11:05:31
Job time: 14.284 secs

Query Match	68.5%	Score 471;	DB 1;	Length 128;
Best Local Similarity	72.6%;	Pred. No. 2e-41;		
Matches	98;	Conservative	6;	Mismatches 19;
				Indels 13;
				Cross

QY QVQLVSGAELAKKPPGSSVYVSCFKAGDTFPNFPSPISMTVQALPGCLEWVGIGPI-FCSTK 59
Db QVQLVSGAEVKKPKASVAVYSCFKAGDTFTFTSYALTSWRAQAGGLEWVGWVNPVGNDDTN 60
QY YAAKFGGRITMTADGSTSTAYWELNSLRSEDTAYTCARQ-----QNGAWYEGPLLEPRD 115
Db YAAKFGGRITMTADGSTSTAYWELNSLRSEDTAYTCARAVGYGGGGCGVRG-----D 113
QY 116 ALDIWGGGTMTVSS 130
Db 114 YFDYWGQGLTVTVSS 128

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-8

```

```

Query Match      69.7%; Score 479.5; DB 2; Length 123;
Best Local Similarity 70.1%; Pred. No. 2,6e-42;
Matches 94; Conservative 13; Mismatches 12; Indels 15; Gaps 2;

```

```

QY 1 QVQLVSGAEAKKPGSSVYKSCASGDTFNSPISWVROAPQGLEMMGIIPIFGSTKY 60
DB 1 QVQLVSGAEVKKPGSSVYKSCASGDTFNSPISWVROAPQGLEMMGIIPIFGSTKY 60
QY 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 116
DB 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 116
QY 117 LDWVGQGTWTVSS 130
DB 110 MDWVGQGTWTVSS 123

```

```

RESULT 11
US-08-652-816A-1
; Sequence 1, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Oxbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-1

```

```

Query Match      69.0%; Score 474.5; DB 2; Length 123;
Best Local Similarity 72.5%; Pred. No. 8,5e-42;
Matches 95; Conservative 11; Mismatches 16; Indels 9; Gaps 2;

```

```

QY 1 QVQLVSGAEAKKPGSSVYKSCASGDTFNSPISWVROAPQGLEMMGIIPIFGSTKY 60
DB 1 QVQLVSGAEVKKPGSSVYKSCASGDTFNSPISWVROAPQGLEMMGIIPIFGSTKY 60
QY 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 119
DB 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 119
QY 120 WCGGTWTVSS 130
DB 113 WCGGTWTVSS 123

```

```

RESULT 12
US-08-652-816A-9
; Sequence 9, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Oxbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991

```



```

/ FILING DATE: 29-OCT-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Howell, Stacy L.
/ REGISTRATION NUMBER: 34,842
/ REFERENCE/DOCKET NUMBER: FD-2630
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 455-5100
/ TELEFAX: (619) 455-5110
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ CLONE: KAS
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..120
/ US-08-428-197-13

```

```

Query Match      69.8%; Score 480.5; DB 2; Length 120;
Best Local Similarity 73.6%; Pred. No. 2e-42;
Matches 95; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

```

```

QY 2 VOLVSGAEAKKPGSSVSKVSCKASGDTFNSFPISWROAPGQGLEWGGIIPFGSTKYA 61
   |||||
Db 1 VHLVSGAEVKKPGSSVSKVSCKASGDTFSSVAISWROAPGQGLEWGGIIPFGQANYA 60
   |||||
QY 62 QKFGQVMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 121
   |||||
Db 61 QKFGQVMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 111
   |||||
QY 122 QGTWTVSS 130
   |||||
Db 112 QGTWTVSS 120

```

```

RESULT 9
PCT-US93-10555-13
/ Sequence 13, Application PC/TUS9310555
/ GENERAL INFORMATION:
/ APPLICANT: SILVERMAN, GREGG J.
/ TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
/ TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
/ TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Spensley Horn Juba & Lubitz
/ STREET: 1880 Century Park East - Suite 500
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90067
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/10555
/ FILING DATE: 29-OCT-1993
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Howell, Stacy L.
/ REGISTRATION NUMBER: 34,842
/ REFERENCE/DOCKET NUMBER: FD-2630
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 455-5100
/ TELEFAX: (619) 455-5110
/ INFORMATION FOR SEQ ID NO: 13:

```

```

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ CLONE: KAS
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 1..120
/ PCT-US93-10555-13

```

```

Query Match      69.8%; Score 480.5; DB 5; Length 120;
Best Local Similarity 73.6%; Pred. No. 2e-42;
Matches 95; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

```

```

QY 2 VOLVSGAEAKKPGSSVSKVSCKASGDTFNSFPISWROAPGQGLEWGGIIPFGSTKYA 61
   |||||
Db 1 VHLVSGAEVKKPGSSVSKVSCKASGDTFSSVAISWROAPGQGLEWGGIIPFGQANYA 60
   |||||
QY 62 QKFGQVMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 121
   |||||
Db 61 QKFGQVMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 111
   |||||
QY 122 QGTWTVSS 130
   |||||
Db 112 QGTWTVSS 120

```

```

RESULT 10
US-08-652-816A-8
/ Sequence 8, Application US/08652816A
/ Patent No. 5872215
/ GENERAL INFORMATION:
/ APPLICANT: Oshourn, JK
/ APPLICANT: Allen, DJ
/ TITLE OF INVENTION: Specific binding members, materials and
/ TITLE OF INVENTION: methods.
/ NUMBER OF SEQUENCES: 53
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/652,816A
/ FILING DATE: 23-MAY-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9125579.4
/ FILING DATE: 02-DEC-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9125579.8
/ FILING DATE: 02-DEC-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9206318.9
/ FILING DATE: 24-MAR-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9206372.6
/ FILING DATE: 23-SEP-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9525004.9
/ FILING DATE: 07-DEC-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9610824.6
/ FILING DATE: 23-MAY-1996

```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-232-081B-41

Query Match 70.1%; Score 482.5; DB 2; Length 121;
Best Local Similarity 73.1%; Pred. No. 1.2e-42;
Matches 95; Conservative 11; Mismatches 15; Indels 9; Gaps 2;

QY 1 QVQVQSGAEAKKPGSSVYKVCCKASGDTFNSFPISWVROAPQGLMMGGIIPFGSTKY 60
DB 1 EVHLVQSGAEVYKPGSSVYKVCCKASGDTFNSFPISWVROAPQGLMMGGIIPFGSTKY 60
QY 61 AOKQGRVTMTADGSTATYMEIINLSRSEDYAIYCARQONGWYEGPDLLEPRDALDIW 120
DB 61 AOKQGRVTMTADGSTATYMEIINLSRSEDYAIYCARQONGWYEGPDLLEPRDALDIW 120
QY 121 GQGTMTVYSS 130
DB 112 GQGTMTVYSS 121

RESULT 7
US-08-983-607-50
Sequence 50, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: XIAOHONG CAI
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: Bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Mary M. Kinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fuses
CLONE: 2-71
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-50

Query Match 70.0%; Score 481.5; DB 3; Length 119;
Best Local Similarity 77.2%; Pred. No. 1.5e-42;
Matches 95; Conservative 7; Mismatches 10; Indels 11; Gaps 2;

QY 8 GAEAKKPGSSVYKVCCKASGDTFNSFPISWVROAPQGLMMGGIIPFGSTYAKPGGR 67
DB 8 GAEAKKPGSSVYKVCCKASGDTFNSFPISWVROAPQGLMMGGIIPFGSTYAKPGGR 67
QY 68 VMTADGSTATYMEIINLSRSEDYAIYCARQONGWYEGPDLLEPRDALDIWGGTMT 127
DB 68 VMTADGSTATYMEIINLSRSEDYAIYCARQONGWYEGPDLLEPRDALDIWGGTMT 127
QY 128 VSS 130
DB 117 VSS 119

RESULT 8
US-08-428-197-13
Sequence 13, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Juba & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555

APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: BOR
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
US-08-428-197-12

Query Match 70.4%; Score 484.5; DB 2; Length 120;
Best Local Similarity 75.2%; Pred. No. 7.7e-43;
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

QY 2 VOLVSGAEAKKPGSSVYKVCCKASGDTFNSPISWVROAPGQLEWNGIIPFGSTKYA 61
DB 1 VOLVSGAEVKKPGSSVYKVCCKASGDTFSSAISWVROAPGQLEWNGIIPFGTPNYA 60

QY 62 OKFOGRVTMTADGSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDING 121
DB 61 OKFOGRVTITDSESTAYMEVSSLRSEDTALYYCAR-----EGRRMAINP--FDYWG 111

QY 122 OCTMTVYSS 130
DB 112 OCTLVTVSS 120

RESULT 5
PCT-US93-10555-12
Sequence 12, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: BOR
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
PCT-US93-10555-12

Query Match 70.4%; Score 484.5; DB 5; Length 120;
Best Local Similarity 75.2%; Pred. No. 7.7e-43;
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

QY 2 VOLVSGAEAKKPGSSVYKVCCKASGDTFNSPISWVROAPGQLEWNGIIPFGSTKYA 61
DB 1 VOLVSGAEVKKPGSSVYKVCCKASGDTFSSAISWVROAPGQLEWNGIIPFGTPNYA 60

QY 62 OKFOGRVTMTADGSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDING 121
DB 61 OKFOGRVTITDSESTAYMEVSSLRSEDTALYYCAR-----EGRRMAINP--FDYWG 111

QY 122 OCTMTVYSS 130
DB 112 OCTLVTVSS 120

RESULT 6
US-08-232-081B-41
Sequence 41, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:

QY 1 QVQLVSGAEAKKPKSSVKVSCKASGDTFNSFPISWVROAPGQGLEWMGIIPIFGSTKY 60
Db 1 QVQLVSGAEVKKPKSSVKVSCKASGDTFSSVYALSWVROAPGQGLEWMGIIPIFGTANY 60
QY 61 AAKFGQAVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGVYEGPPLLEPRPDALDIW 120
Db 61 AAKFGQAVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGVYEGPPLLEPRPDALDIW 120
QY 121 GGGTMTVSS 130
Db 111 GGGTMTVSS 120
RESULT 2
US-09-025-7698-57
Sequence 57, Application US/090257698
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-57
Query Match 74.4%; Score 512; DB 4; Length 120;
Best Local Similarity 76.9%; Pred. No. 1,le-45;
Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

Db 111 GGGTMTVSS 120
RESULT 3
US-09-025-7698-21
Sequence 21, Application US/090257698
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-21
Query Match 72.2%; Score 496.5; DB 4; Length 119;
Best Local Similarity 76.2%; Pred. No. 4.4e-44;
Matches 99; Conservative 8; Mismatches 12; Indels 11; Gaps 2;
QY 1 QVQLVSGAEAKKPKSSVKVSCKASGDTFNSFPISWVROAPGQGLEWMGIIPIFGSTKY 60
Db 1 QVQLVSGAEVKKPKSSVKVSCKASGDTFSSVYALSWVROAPGQGLEWMGIIPIFGTANY 60
QY 61 AAKFGQAVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGVYEGPPLLEPRPDALDIW 120
Db 61 AAKFGQAVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGVYEGPPLLEPRPDALDIW 120
QY 121 GGGTMTVSS 130
Db 110 GGGTMTVSS 119
RESULT 4
US-08-428-197-12
Sequence 12, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 (Search time 13.2007 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-23

Sequence: 1 QVQLVSGAARAKKFGSSVKY.....EPPRALDIWGQMTVTSS 130

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:.*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:.*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	74.4	120	4	US-09-025-769B-35
2	512	74.4	120	4	US-09-025-769B-57
3	496.5	72.2	119	4	US-09-025-769B-21
4	484.5	70.4	120	2	US-08-428-197-12
5	484.5	70.4	120	5	PCT-US93-10555-12
6	482.5	70.1	121	2	US-08-232-081B-41
7	481.5	70.0	119	3	US-08-983-607-50
8	480.5	69.8	120	2	US-08-428-197-13
9	479.5	69.7	120	5	PCT-US93-10555-13
10	479.5	69.7	123	2	US-08-652-816A-8
11	474.5	69.0	123	2	US-08-652-816A-1
12	471.5	68.5	128	1	US-08-202-047-22
13	471	68.5	128	1	US-08-964-690-22
14	471	68.5	147	1	US-08-217-918-4
15	471	68.5	129	2	US-08-652-816A-6
16	469.5	67.7	129	2	US-08-561-521-45
17	465.5	67.7	129	4	US-08-525-539A-77
18	465.5	67.7	129	5	PCT-US95-01219-45
19	463.5	67.4	120	4	US-08-378-939-10
20	463.5	67.4	120	4	US-09-025-769B-36
21	463	67.3	120	4	US-09-025-769B-59
22	463	67.3	123	1	US-08-482-862-53
23	462.5	67.2	123	1	US-08-482-862-53
24	462.5	67.2	123	2	US-08-487-113D-53
25	462.5	67.2	123	2	US-08-473-503-53
26	462.5	67.2	123	2	US-08-483-389-53
27	462.5	67.2	123	2	US-08-483-932-53

28	462.5	67.2	123	2	US-08-720-420A-53	Sequence 53, Appl
29	462.5	67.2	123	3	US-08-714-017-53	Sequence 53, Appl
30	462.5	67.2	123	3	US-08-475-680-53	Sequence 53, Appl
31	461.5	67.1	123	2	US-08-652-816A-7	Sequence 7, Appl
32	461.5	67.1	125	3	US-09-199-149-3	Sequence 3, Appl
33	459	66.6	139	4	US-09-355-925-7	Sequence 7, Appl
34	456.5	66.6	117	4	US-09-025-769B-22	Sequence 22, Appl
35	454	66.0	139	4	US-09-355-925-8	Sequence 8, Appl
36	447.5	65.0	121	3	US-08-579-378A-8	Sequence 12, Appl
37	447.5	65.0	140	3	US-08-579-378A-12	Sequence 12, Appl
38	447.5	65.0	140	5	PCT-US93-11612-12	Sequence 12, Appl
39	446	64.8	139	1	US-08-253-877C-19	Sequence 19, Appl
40	446	64.8	139	2	US-08-452-164A-19	Sequence 19, Appl
41	446	64.8	139	3	US-08-603-024-18	Sequence 18, Appl
42	446	64.8	139	4	US-08-450-809-14	Sequence 14, Appl
43	443.5	64.5	122	5	PCT-US95-00067-2	Sequence 2, Appl
44	437.5	63.6	140	3	US-08-836-561-63	Sequence 63, Appl
45	437.5	63.6	140	4	US-09-434-122-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-35
Sequence 35, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Motoney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-35
Query Match 74.4%, Score 512, DB 4, Length 120;
Best Local Similarity 76.9%, Pred. No. 1,1e-45;
Matches 100, Conservative 9, Mismatches 11, Indels 10, Gaps 1,


```
Query Match          74.4%; Score 512; DB 15; Length 120;
Best Local Similarity 76.9%; Pred. No. 9.8e-40;
Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQOQ-----NGWYEGPLP 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQCGDY-----ANDYW 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 GQGTMTVSS 130
   |||||:|||||
Db 111 GQGTMTVSS 120
   |||||:|||||

RESULT 10
US-09-880-748-1509
; Sequence 1509, Application US/09880748
; Publication No. US2003005937A1
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 253
; ORGANISM: Homo sapiens
US-09-880-748-1509

Query Match          74.3%; Score 511; DB 11; Length 253;
Best Local Similarity 72.1%; Pred. No. 2.7e-39;
Matches 101; Conservative 9; Mismatches 8; Indels 22; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQOQ-----NGWYEGPLP 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQCGDY-----NGWYEGPLP 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 111 EPPDALDINGQGTMTVSS 130
   |||||:|||||
Db 116 -----DPMGKGTMTVSS 128
   |||||:|||||

RESULT 11
US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US20020168367A1
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 253
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match          74.1%; Score 509.5; DB 14; Length 627;
Best Local Similarity 72.7%; Pred. No. 9.9e-39;
Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQOQ-----QONGWYEGPLP 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQCGDY-----PNSD 133
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 ----ALDINGQGTMTVSS 130
   |||||:|||||
Db 134 YYYGMDVWGQGTMTVSS 152
   |||||:|||||

RESULT 12
US-09-880-748-1880
; Sequence 1880, Application US/09880748
; Publication No. US2003005937A1
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 253
; ORGANISM: Homo sapiens
US-09-880-748-1880

Query Match          73.9%; Score 508.5; DB 11; Length 253;
Best Local Similarity 74.6%; Pred. No. 4.6e-39;
Matches 100; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQOQ-----CGWYEGPLP 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQCGDY-----S 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 LDIWGQGTMTVSS 130
   |||||:|||||
Db 114 FDIWGQGTMTVSS 127
   |||||:|||||
```

```
Query Match          74.1%; Score 509.5; DB 14; Length 627;
Best Local Similarity 72.7%; Pred. No. 9.9e-39;
Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQOQ-----QONGWYEGPLP 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQCGDY-----PNSD 133
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 ----ALDINGQGTMTVSS 130
   |||||:|||||
Db 134 YYYGMDVWGQGTMTVSS 152
   |||||:|||||

RESULT 12
US-09-880-748-1880
; Sequence 1880, Application US/09880748
; Publication No. US2003005937A1
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 253
; ORGANISM: Homo sapiens
US-09-880-748-1880

Query Match          73.9%; Score 508.5; DB 11; Length 253;
Best Local Similarity 74.6%; Pred. No. 4.6e-39;
Matches 100; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQOQ-----CGWYEGPLP 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQCGDY-----S 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 LDIWGQGTMTVSS 130
   |||||:|||||
Db 114 FDIWGQGTMTVSS 127
   |||||:|||||
```

Db 61 AOKFOGRVTITADESTSTAYMELSLRSEDPTAVYVCAREDTSGMYH-----YV 108

QY 121 GCGTMTVSS 130

Db 109 GCGTMTVSS 118

RESULT 6

US-09-880-748-1881

Sequence 1881, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1881

LENGTH: 244

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1881

Query Match 74.8%; Score 514.5; DB 11; Length 244;

Best Local Similarity 76.9%; Pred. No. 1.2e-39; Matches 100; Conservative 9; Mismatches 12; Indels 9; Gaps 1;

QY 1 QVQLVDSGAEAKKPKGSSVSKVSCAKASGDTFNSPISWYRQAPGQGLEWMGIIPIFGSTKY 60

Db 1 QVQLVDSGAEVKKRQSSVKVSCAKASGDTFSSYALSWRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFOGRVTITADGISTAYMELSLRSEDPTAVYVCARQONGWYEGPPLLEPRPDALDIW 120

Db 61 AOKFOGRVTITADGISTAYMELSLRSDPTAVYVCARDGSGYY-----DAFDIW 111

QY 121 GCGTMTVSS 130

Db 112 GCGTMTVSS 121

RESULT 7

US-10-269-805-25

Sequence 25, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:

APPLICANT: OLINER, JONATHAN D.

TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

FILE REFERENCE: A-722

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/328,604

PRIOR FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGTH: 124

TYPE: PRT

ORGANISM: Homo sapiens

US-10-269-805-25

Query Match 74.6%; Score 513; DB 15; Length 124;

Best Local Similarity 79.2%; Pred. No. 8.2e-40; Matches 103; Conservative 9; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVQLVDSGAEAKKPKGSSVSKVSCAKASGDTFNSPISWYRQAPGQGLEWMGIIPIFGSTKY 60

Db 1 QVQLVDSGAEVKKRQSSVKVSCAKASGDTFSSYALSWRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFOGRVTITADGISTAYMELSLRSEDPTAVYVCARQONGWYEGPPLLEPRPDALDIW 120

Db 61 AOKFOGRVTITADESTSTAYMELSLRSEDPTAVYVCARGYD--FWSGYSL---DAFDIW 114

QY 121 GCGTMTVSS 130

Db 115 GCGTMTVSS 124

RESULT 8

US-10-025-687-1

Sequence 1, Application US/10025687

Publication No. US2002014225A1

GENERAL INFORMATION:

APPLICANT: Luo, Peter

TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY

FILE REFERENCE: 26050-705

CURRENT APPLICATION NUMBER: US/10/025,687

CURRENT FILING DATE: 2002-04-17

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 120

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human consensus antibody heavy chain variable region

US-10-025-687-1

Query Match 74.4%; Score 512; DB 14; Length 120;

Best Local Similarity 76.9%; Pred. No. 9.8e-40; Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVDSGAEAKKPKGSSVSKVSCAKASGDTFNSPISWYRQAPGQGLEWMGIIPIFGSTKY 60

Db 1 QVQLVDSGAEVKKRQSSVKVSCAKASGDTFSSYALSWRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFOGRVTITADGISTAYMELSLRSEDPTAVYVCARQONGWYEGPPLLEPRPDALDIW 120

Db 61 AOKFOGRVTITADESTSTAYMELSLRSEDPTAVYVCARGGDSGFY-----AMDYV 110

QY 121 GCGTMTVSS 130

Db 111 GCGTMTVSS 120

RESULT 9

US-10-125-687-1

Sequence 1, Application US/10125687

Publication No. US20030054407A1

GENERAL INFORMATION:

APPLICANT: Luo, Peter

TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY

FILE REFERENCE: 26050-705

CURRENT APPLICATION NUMBER: US/10/125,687

CURRENT FILING DATE: 2002-04-17

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 120

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human consensus antibody heavy chain variable region

US-10-125-687-1


```
US-10-300-675-14
; Sequence 14, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
US-10-300-675-14
```

```
Query Match
Best Local Similarity 75.9%; Score 522; DB 12; Length 118;
Matches 100; Conservative 8; Mismatches 10; Indels 12; Gaps 1;
```

```
OY 1 QVQLVQSGAEAKKPKSSVYKVCCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKVCCKASGGTFSSYAISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYTITADESTSTAYMELSLRSDEDAVYVCAREDSGMYH-----YW 108
OY 121 GQGTMVTYSS 130
DB 109 GQGTLVTYSS 118
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```
RESULT 3
US-10-300-675-6
; Sequence 6, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-675-6
```

```
Query Match
Best Local Similarity 75.1%; Score 517; DB 12; Length 118;
Matches 99; Conservative 9; Mismatches 10; Indels 12; Gaps 1;
```

```
OY 1 QVQLVQSGAEAKKPKSSVYKVCCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKVCCKASGGTFSSYAISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYTITADESTSTAYMELSLRSDEDAVYVCAREDSGMYH-----YW 108
OY 121 GQGTMVTYSS 130
DB 109 GQGTLVTYSS 118
```

```
RESULT 4
US-10-300-675-10
; Sequence 10, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
US-10-300-675-10
```

```
Query Match
Best Local Similarity 75.0%; Score 516; DB 12; Length 118;
Matches 99; Conservative 8; Mismatches 11; Indels 12; Gaps 1;
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OY 1 QVQLVQSGAEAKKPKSSVYKVCCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKVCCKASGGTFSSYAISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYTITADESTSTAYMELSLRSDEDAVYVCAREDSGMYH-----YW 108
OY 121 GQGTMVTYSS 130
DB 109 GQGTLVTYSS 118
```

```
RESULT 5
US-10-300-675-12
; Sequence 12, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
US-10-300-675-12
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Query Match
Best Local Similarity 75.0%; Score 516; DB 12; Length 118;
Matches 99; Conservative 8; Mismatches 11; Indels 12; Gaps 1;
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OY 1 QVQLVQSGAEAKKPKSSVYKVCCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKVCCKASGGTFSSYAISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYTITADESTSTAYMELSLRSDEDAVYVCAREDSGMYH-----YW 108
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 27.8798 Seconds
(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688
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Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA: *
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3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	76.2	121	15	US-10-269-805-19
2	522	75.9	118	12	US-10-300-675-14
3	517	75.1	118	12	US-10-300-675-6
4	516	75.0	118	12	US-10-300-675-10
5	516	75.0	118	12	US-10-300-675-12
6	514.5	74.8	124	11	US-09-880-748-1881
7	513	74.6	124	11	US-10-269-805-25
8	512	74.4	120	15	US-10-125-687-1
9	512	74.4	120	15	US-10-125-687-1
10	511	74.3	123	14	US-09-880-748-1509
11	509.5	73.9	123	11	US-09-880-748-47
12	508.5	73.8	124	11	US-09-880-748-1880
13	508	73.8	124	11	US-09-880-748-1866
14	507.5	73.8	125	15	US-10-269-805-35
15	506.5	73.6	121	15	US-10-269-805-9

16	504	73.3	270	9	US-09-976-118-2	Sequence 2, Appl1
17	502.5	73.0	248	11	US-09-880-748-1733	Sequence 1733, Ap
18	502.5	73.0	248	11	US-09-880-748-1734	Sequence 1734, Ap
19	501.5	72.9	245	15	US-10-151-882-15	Sequence 15, Appl
20	501.5	72.9	248	11	US-09-880-748-1718	Sequence 1718, Ap
21	501.5	72.9	248	11	US-09-880-748-1718	Sequence 1879, Ap
22	500	72.7	257	11	US-09-880-748-1553	Sequence 1553, Ap
23	498.5	72.5	248	11	US-09-880-748-1732	Sequence 1732, Ap
24	498.5	72.5	248	11	US-09-880-748-1732	Sequence 1732, Ap
25	498.5	72.5	248	11	US-09-880-748-1732	Sequence 1732, Ap
26	497.5	72.3	248	11	US-10-308-817-191	Sequence 1737, Ap
27	497.5	72.3	248	11	US-09-880-748-1741	Sequence 1741, Ap
28	497.5	72.3	250	11	US-09-880-748-2066	Sequence 1741, Ap
29	497	72.2	254	11	US-09-880-748-1450	Sequence 1741, Ap
30	495.5	72.0	248	11	US-09-880-748-1727	Sequence 1727, Ap
31	495.5	72.0	248	11	US-09-880-748-1727	Sequence 1727, Ap
32	493.5	71.7	251	11	US-09-880-748-1756	Sequence 1756, Ap
33	493.5	71.6	123	15	US-10-269-805-3	Sequence 3, Appl1
34	492	71.5	120	15	US-10-269-805-15	Sequence 15, Appl
35	492	71.5	248	11	US-09-880-748-1955	Sequence 1717, Ap
36	491.5	71.4	248	11	US-09-880-748-1717	Sequence 1717, Ap
37	490.5	71.3	123	15	US-10-269-805-17	Sequence 1717, Ap
38	490.5	71.3	239	15	US-10-151-882-23	Sequence 23, Appl
39	490.5	71.2	252	11	US-09-880-748-1666	Sequence 1666, Ap
40	490	71.2	253	11	US-09-880-748-1813	Sequence 1813, Ap
41	489.5	71.1	253	11	US-09-880-748-1813	Sequence 1813, Ap
42	489	71.1	120	15	US-10-269-805-37	Sequence 37, Appl
43	488.5	71.0	248	11	US-10-151-882-17	Sequence 17, Appl
44	488	70.9	250	15	US-09-880-748-7	Sequence 1915, Ap
45	486.5	70.7	242	11	US-09-880-748-1915	Sequence 1915, Ap

ALIGNMENTS

RESULT 1
US-10-269-805-19
; Sequence 19, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLIVER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-7722
; CURRENT APPLICATION NUMBER: US/10/269,805
; PRIOR FILING DATE: 2002-10-10
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-19

Query Match 76.2%; Score 524.5; DB 15; Length 121;
Best Local Similarity 78.5%; Pred. No. 7e-41;
Matches 102; Conservative 9; Mismatches 10; Indels 9; Gaps 1;

QY	1	QVOLVSGAEYKAKKPGSSVKVSCKASGDTFNSPISWVRQAPGQLEWVGIIPIFGSTKY 60
DB	1	QVOLVSGAEYKAKKPGSSVKVSCKASGDTFNSPISWVRQAPGQLEWVGIIPIFGTANY 60
QY	61	AOKRGVMTADGTSSTAYMELNSRSEDATATYCAQONGGMYEGPPLLEPRPDLDIW 120
DB	61	AOKRGVMTADGTSSTAYMELNSRSEDATATYCAQONGGMYEGPPLLEPRPDLDIW 120
QY	121	GQGTMTVSS 130
DB	112	GQGTMTVSS 121

RESULT 2

DR WPI: 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1: Page 2470-2471, 3148pp; English.

XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX Sequence 248 AA;

SQ Query Match 73.0%; Score 502.5; DB 23; Length 248;

Best Local Similarity 75.2%; Pred. No. 2.8e-40;

Matches 100; Conservative 9; Mismatches 13; Indels 11; Gaps 2;

QY 1 QVQLVDSGAEAKKPKGSSVKVSCAKASGDTFNSPFIWVROAPGGGLEWGGITPIFGSTKY 60
DB 1 QVQLVDSGAEVKKPKGSSVKVSCAKASGDTFSSVYISWVROAPGGGLEWGGITPIFGTANY 60
QY 61 AOKFQGRVTMTADGSTAYAMELNSLRSEDTAIYYCARQONG---GWYEGPLLEPRPDAL 117
DB 61 AOKFQGRVTITADESTAYAMELSLRSEDTAVYYCARMEDILTYGYOG-----YF 112
QY 118 DIWGQGTWTVSS 130
DB 113 DYWGQGTITVSS 125

Search completed: December 30, 2003, 10:54:29
Job time : 41.903 secs

PT treating cancer -
 XX
 PS Claim 3; Fig 2; 51pp; English.
 CC The present invention relates to human anti-epidermal growth factor
 CC receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a
 CC human IgM phage display library using EGFR as antigen. Two isolates
 CC with different amino acid sequences were identified. The
 CC anti-EGFR-scFvs are useful for treating cancer, and for the
 CC diagnostic location and assessment of tumor growth, where the
 CC anti-EGFR-scFv is radiolabelled. The present sequence represents
 CC human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
 XX
 SQ Sequence 270 AA;
 Query Match 73.3%; Score 504; DB 23; Length 270;
 Best Local Similarity 74.6%; Pred. No. 2.2e-40;
 Matches 100; Conservative 10; Mismatches 12; Indels 12; Gaps 2;
 QY 1 QVQLVSGAFAKPGSSVSKVSCKASGDTFNSPISWVROAPGQLEMMGIIPIFGSTRY 60
 Db 1 QVQLVSGAEVKKRPGSSVSKVSCKASGTFSSYALISWVROAPGQLEMMGIIPIFGTANY 60
 QY 61 AQKFGKRVITMTADGSTSTAYMELNSLRSDTAIYYCARQ---NGWYEGPLLEPRDA 116
 Db 61 AQKFGKRVITMTADESTSTAYMELNSLRSDTAIYYCARPDYVYGGSY-----PNW 112
 QY 117 LDIWGQGMVTVSS 130
 Db 113 FDPWGGTLTVSS 126
 RESULT 14
 ABR01518
 ID ABR01518 standard; Protein; 229 AA.
 AC ABR01518;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human anti-TIMP-1 antibody heavy chain #16.
 XX
 KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCD3;
 KW matrix metalloproteinase; MMP; variable heavy chain; VHCDB3; hepatotropic;
 KW variable light chain; cytotactic; nephrotropic; cardiant; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002WO-US12801.
 XX
 PR 24-APR-2001; 2001US-285683P.
 XX
 PA (FARB) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;
 XX
 XX WPI; 2003-129114/12.
 DR N-PSDB; AB274789.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 PT hypertrophy or lung cancer -
 PS Claim 20; Page 158-159; 228pp; English.

XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
 CC chain regions of a human anti-TIMP-1 antibody of the invention.
 XX
 SQ Sequence 229 AA;
 Query Match 73.0%; Score 502.5; DB 24; Length 229;
 Best Local Similarity 75.8%; Pred. No. 2.6e-40;
 Matches 100; Conservative 10; Mismatches 13; Indels 9; Gaps 2;
 QY 1 QVQLVSGAFAKPGSSVSKVSCKASGDTFNSPISWVROAPGQLEMMGIIPIFGSTRY 60
 Db 1 QVQLVSGAEVKKRPGSSVSKVSCKASGTFSSYALISWVROAPGQLEMMGIIPIFGTANY 60
 QY 61 AQKFGKRVITMTADGSTSTAYMELNSLRSDTAIYYCAR--QNGWYEGPLLEPRDALD 118
 Db 61 AQKFGKRVITMTADESTSTAYMELNSLRSDTAIYYCARSDQSYHYVHPY-----FD 113
 QY 119 IWGQGMVTVSS 130
 Db 114 IWGQGMVTVSS 125
 RESULT 15
 ABP45722
 ID ABP45722 standard; Protein; 248 AA.
 AC ABP45722;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1733.
 XX
 KW Blye; B lymphocyte stimulator; TNF superfamily; human; cytotactic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS.
 XX
 OS common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 PN Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX

XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX PA Edwards BM, Main SH, Vaughan TJ;
 XX PI WPI: 2001-282031/29.
 XX DR N-PSDB; AAS03455.
 XX PT Panel of specific binding members of antibody molecules which bind to
 XX PT whole adipocytes is used in the treatment of obesity and obesity
 XX PT related diseases -
 XX PS Claim 1; Page 127; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
 CC chain, and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease.
 CC Sequence 125 AA;
 SQ
 Query Match 73.3%; Score 504.5; DB 22; Length 125;
 Best Local Similarity 75.9%; Pred. No. 8.4e-41;
 Matches 101; Conservative 10; Mismatches 11; Indels 11; Gaps 2;
 QY 1 QVQLVSGAEAKKRGSSVYKVSCKASGDTFNSPISWVROAPGQGLEWMGIIPIFGSTKY 60
 D1 1 QVQLVSGAEVKKRGSSVKVSCKASGDTFSSYALSWVROAPGQGLEWMGIIPIFGTANY 60
 QY 61 AOKRQGRVTMTADGSTTAYMELNSLRSEDTAIYYCARQONGMYEGPLRPD---AL 117
 D1 AOKRQGRVTITADGSTTAYMELSLRSEDTAYVYCARQNSRRTITFGC-----GARDIW 113
 QY 118 DIMGGTMTVTSS 130
 D1 113 DIMGRGTLVTSS 125
 DB
 RESULT 12
 AAB36083
 ID AAB36083 standard; Protein; 249 AA.
 XX AAB36083;
 XX AC 16-FEB-2001 (first entry)
 XX DT
 XX DE Recombinant human antibody scFv TN11.
 XX KM Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
 XX KW CTN-C.
 XX OS Homo sapiens.
 XX PA W0200063699-A1.
 XX PN 26-OCT-2000.
 XX PD 19-APR-2000; 2000WO-EP03550.
 XX PF 20-APR-1999; 99IT-FI00094.
 XX PR

XX (PHIL-) PHILLOGEN SRL.
 XX PA Zardi L;
 XX PI WPI: 2000-687225/67.
 XX DR N-PSDB; AAC67868.
 XX PT Ligands used for diagnosis and treatment of human neoplasias, are
 XX PT capable of identifying the tenascin-C isoform containing domain C of
 XX PT tenascin-C -
 XX PS Disclosure; Page 5-6; 31pp; English.
 XX The present sequence is a recombinant human antibody scFv. Antibody
 CC TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
 CC recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
 CC only capable of recognising TN-C isoforms containing domain C (CTN-C).
 CC TN11 is useful for detecting the presence of TN-C isoforms in vitro or
 CC in vivo for diagnosing pathologies expressing the CTN-C isoforms of TN-C.
 CC It is useful for the preparation of formulations for the treatment of
 CC human neoplasias.
 CC Sequence 249 AA;
 SQ
 Query Match 73.3%; Score 504.5; DB 21; Length 249;
 Best Local Similarity 76.9%; Pred. No. 1.8e-40;
 Matches 100; Conservative 9; Mismatches 14; Indels 7; Gaps 1;
 QY 1 QVQLVSGAEAKKRGSSVYKVSCKASGDTFNSPISWVROAPGQGLEWMGIIPIFGSTKY 60
 D1 1 QVQLVSGAEVKKRGSSVKVSCKASGDTFSSYALSWVROAPGQGLEWMGIIPIFGTANY 60
 QY 61 AOKRQGRVTMTADGSTTAYMELNSLRSEDTAIYYCARQONGMYEGPLRPDALDIW 120
 D1 61 AOKRQGRVTITADGSTTAYMELSLRSEDTAYVYCARQNSRRTITFGC-----GARDIW 113
 QY 121 GGGTMTVTSS 130
 D1 114 GRGTMTVTSS 123
 DB
 RESULT 13
 AAU97198
 ID AAU97198 standard; protein; 270 AA.
 XX AAU97198;
 XX AC 27-AUG-2002 (first entry)
 XX DT
 XX DE Human anti-EGFR single-chain antibody isolated from clone pSEX81-63.
 XX KM Human; anti-epidermal growth factor receptor single-chain antibody;
 XX KW anti-EGFR-scFv; IGM; cancer; tumour growth; clone pSEX81-63; cytostatic.
 XX OS Homo sapiens.
 XX PA W02000230984-A1.
 XX PN 18-APR-2002.
 XX PD 12-OCT-2001; 2001WO-US31857.
 XX PF 13-OCT-2000; 2000US-240353P.
 XX PR (UABR-) UAB RES FOUND.
 XX PA Ralsch KP, Curiel DT, Bonner JA;
 XX PI WPI: 2002-463261/49.
 XX DR Novel human anti-epidermal growth factor receptor single-chain antibody
 XX PT useful for diagnostic location and assessment of tumour growth, and in

DR WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 2645-2646; 3148pp; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineuritic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 253 AA:
 Query Match 73.9%; Score 508.5; DB 23; Length 253;
 Best Local Similarity 74.6%; Pred. No. 7.6e-41;
 Matches 100; Conservative 11; Mismatches 12; Indels 11; Gaps 2;
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 DB 1 QVQLVSGAEVKKPGSSVYVSCKASGTFSSVAISMVRAPQGLEWNGIIPFGTANY 60
 QY 61 AOKFGRVMTADGSTSTAYMELNSLRSEDTAIYYCARQO-----GCGYEGPLLEPPDA 116
 DB 61 AOKFGRVITITADKSTSTAYMELSSLRSEDTAVYICARSHYDILTYGYPGGMF-----S 113
 QY 117 LDINWGGTMYTVSS 130
 DB 114 FDIWGRGTMYTVSS 127
 RESULT 10
 ABP45855
 ID ABP45855 standard; Protein; 254 AA.
 AC ABP45855;
 XX
 XX 19-AUG-2002 (first entry)
 DT
 DE Human BLyS binding scFv SEQ ID 1866.
 XX
 KW BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineuritic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XX MO200202641-A1.
 XX
 XX 10-JAN-2002.
 PD
 PF 15-JUN-2001; 2001WO-US19110.
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 XX 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 2628-2629; 3148pp; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineuritic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 254 AA:
 Query Match 73.8%; Score 508; DB 23; Length 254;
 Best Local Similarity 71.4%; Pred. No. 8.5e-41;
 Matches 100; Conservative 10; Mismatches 8; Indels 22; Gaps 2;
 QY 1 QVQLVSGAEAKKPGSSVYVSCKASGDTFNSFPISWVRAPQGLEWNGIIPFGSTKY 60
 DB 1 QVQLVSGAEVKKPGSSVYVSCKASGTFSSVAISMVRAPQGLEWNGIIPFGTANY 60
 QY 61 AOKFGRVMTADGSTSTAYMELNSLRSEDTAIYYCARQO-----GCGYEGPLL 110
 DB 61 AOKFGRVITITADKSTSTAYMELSSLRSEDTAVYICARSHYDILTYGYPGGMF----- 115
 QY 111 ERPPDALDIWGGTMYTVSS 130
 DB 116 -----DPWGRGTMYTVSS 128
 RESULT 11
 AAU02555
 ID AAU02555 standard; Protein; 125 AA.
 AC AAU02555;
 XX
 XX 29-AUG-2001 (first entry)
 DT
 DE Anti-adipocyte monoclonal antibody heavy chain, FAT 41.
 XX
 KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX
 XX Homo sapiens.
 XX
 XX MO200127279-A1.
 XX
 XX 19-APR-2001.
 PD
 PF 11-OCT-2000; 2000WO-GB03900.
 XX
 XX 12-OCT-1999; 99US-0158812.

CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 220 AA;

Query Match 74.4%; Score 512; DB 24; Length 220;

Best Local Similarity 76.9%; Pred. No. 3e-41;

Matches 100; Conservative 9; Mismatches 7; Indels 14; Gaps 2;

QY 1 QVQLVQSGAEAKKPPSSVKKVSCKASGDTFNSFPISWYRQAPGQGLEWMGIIPIFGSTKY 60

DB 1 QVQLVQSGAEVKKPKSSSVKVSCKASGCTFSSVAISWYRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCARQNGWYEGPLLEPRDADLIW 120

DB 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYICAROE---WT-----MDYW 106

QY 121 GQGTMVTSS 130

DB 107 GQGLTVTVSS 116

RESULT 8

ABP45498 ABR45498 standard; Protein; 253 AA.

XX ABP45498;

AC 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1509.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 PS Claim 1; Page 2203-2204; 3148pp; English.
 XX

CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 253 AA;

Query Match 74.3%; Score 511; DB 23; Length 253;

Best Local Similarity 72.1%; Pred. No. 4.4e-41;

Matches 101; Conservative 9; Mismatches 8; Indels 22; Gaps 2;

QY 1 QVQLVQSGAEAKKPPSSVKKVSCKASGDTFNSFPISWYRQAPGQGLEWMGIIPIFGSTKY 60

DB 1 QVQLVQSGAEVKKPKSSSVKVSCKASGCTFSSVAISWYRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCARO-----NGWYEGPL 110

DB 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYICAROEQYDILTGYPEGWF----- 115

QY 111 EPRDADLIWGQGMVTSS 130

DB 116 -----DPMKGTMVTSS 128

RESULT 9

ABP45869 ABR45869 standard; Protein; 253 AA.

XX ABP45869;

AC 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1880.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 XX
 XX
 XX

CC with high affinity against a wide range of antigens and having no or
 CC minimum immunogenicity to human subjects treated with antibody
 CC therapeutics. This sequence represents a protein region of an antibody
 CC relating to the novel antibody library construction method of the
 CC invention.

XX
 XX
 SQ Sequence 120 AA;

Query Match 74.4%; Score 512; DB 24; Length 120;
 Best Local Similarity 76.9%; Pred. No. 1.5e-41;
 Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVSGAELAKKPGSSVSKVSCASGDTFNSPFIISWROAPGQGLMMGGIIPFGSTKY 60
 DB 1 QVQLVSGAELAKKPGSSVSKVSCASGDTFNSPFIISWROAPGQGLMMGGIIPFGSTKY 60
 QY 61 AQRFGKRVITMTADGSTSTAYMELNSLRSEDTAIYYCAEQNGWEGPLLEPRPALDIW 120
 DB 61 AQRFGKRVITMTADGSTSTAYMELNSLRSEDTAIYYCAEQNGWEGPLLEPRPALDIW 120
 QY 121 GGGTMTVTVSS 130
 DB 121 GGGTMTVTVSS 130
 QY 111 GGGTMTVTVSS 120
 DB 111 GGGTMTVTVSS 120

RESULT 6

ABJ18718
 ID ABJ18718 standard; Protein; 120 AA.

AC ABJ18718;

DT 06-MAR-2003 (first entry)

DE Antibody library related VH protein region 1DMA.

KW Library; recombinant antibody; clustering variable region; in silico;
 KM immunogenicity; antibody therapeutic.

XX Unidentified.

OS

XX WO200284277-A1.

XX 24-OCT-2002.

XX 17-APR-2002; 2002WO-US12202.

XX 17-APR-2001; 2001US-284407P.

XX (ABMA-) ABMAXIS INC.

XX Luo P;

XX WPI; 2003-093043/08.

PT Constructing a library of recombinant antibodies useful as source of
 PT antibody candidates for screening antigens comprises clustering
 PT variable regions of antibodies having known 3-dimensional structures
 PT into structural ensembles -

XX Disclosure; Fig 13B; 119pp; English.

XX The invention relates to a novel method for the construction of a library
 CC of recombinant antibodies. The novel method comprises clustering variable
 CC regions of a collection of antibodies having known 3D structures into at
 CC least two families of structural ensembles, each comprising at least two
 CC different antibody sequences but with substantially identical main chain
 CC conformations. The method is useful for constructing a library of
 CC artificial antibodies in silico which provides a structurally diverse and
 CC yet functionally more relevant source of antibody candidates which can
 CC then be screened for binding a wide variety of target molecules,
 CC including small molecules, and biomacromolecules such as proteins,
 CC peptides and nucleic acids. The libraries constructed are useful as a
 CC source of antibody candidates for further screening for novel antibodies

CC with high affinity against a wide range of antigens and having no or
 CC minimum immunogenicity to human subjects treated with antibody
 CC therapeutics. This sequence represents a protein region of an antibody
 CC relating to the novel antibody library construction method of the
 CC invention.

XX
 XX
 SQ Sequence 120 AA;

Query Match 74.4%; Score 512; DB 24; Length 120;
 Best Local Similarity 76.9%; Pred. No. 1.5e-41;
 Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVSGAELAKKPGSSVSKVSCASGDTFNSPFIISWROAPGQGLMMGGIIPFGSTKY 60
 DB 1 QVQLVSGAELAKKPGSSVSKVSCASGDTFNSPFIISWROAPGQGLMMGGIIPFGSTKY 60
 QY 61 AQRFGKRVITMTADGSTSTAYMELNSLRSEDTAIYYCAEQNGWEGPLLEPRPALDIW 120
 DB 61 AQRFGKRVITMTADGSTSTAYMELNSLRSEDTAIYYCAEQNGWEGPLLEPRPALDIW 120
 QY 121 GGGTMTVTVSS 130
 DB 121 GGGTMTVTVSS 130
 QY 111 GGGTMTVTVSS 120
 DB 111 GGGTMTVTVSS 120

RESULT 7

ABR01538
 ID ABR01538 standard; Protein; 220 AA.

XX ABR01538;

DT 16-APR-2003 (first entry)

DE Human anti-TIMP-1 antibody heavy chain #36.

XX

KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
 KM matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatocellular;
 KM variable light chain; cytoskeletal; nephrotropic; cardiac; liver fibrosis;
 KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KM lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KM idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX

XX Homo sapiens.

XX WO200286085-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-US12801.

XX 24-APR-2001; 2001US-285683P.

XX (FARB-) BAYER CORP.

XX (MORP-) MORPHOSYS AG.

XX Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;
 XX WPI; 2003-129114/12.

XX N-PSDB; AB274809.

PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 PT hypertrophy or lung cancer -

XX

XX Claim 20; Page 173; 228pp; English.

XX The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralizes a matrix metalloproteinase (MMP)-inhibiting activity of
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiac

PS Claim 1; Page 2646-2647; 3148bp; English.

XX This invention describes novel antibodies that immunospecifically bind to

CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS

CC and so may be used to detect and quantitate the presence of BLyS in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BLyS. They may also be

CC administered to treat diseases associated with aberrant BLyS expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent

CC the antibodies and fragments of the antibodies described in the method

CC of the invention.

XX

SO Sequence 244 AA;

Query Match 74.8%; Score 514.5; DB 23; Length 244;
Best Local Similarity 76.9%; Pred. No. 1.9e-41;
Matches 100; Conservative 9; Mismatches 12; Indels 9; Gaps 1;

QY 1 QVQLVQSGAEAKRPGSSVYKVCCKASGDTFNSPFIISWRQAPQGGLMMGIIPIFGSTKY 60
DB 1 QVQLVQSGAEVKKPGSSSVYKVCCKASGDTFSSYVAISWRQAPQGGLMMGIIPIFGTANY 60
QY 61 AOKFGQRTMTADGSTAYAMELNSLRSEDTAIYYCARQONGWYEGPLERPDALDIW 120
DB 61 AOKFGQRTVITTDKSTAYAMELSLRSDTAIVYICARWGSQSY-----DAFDIW 111
QY 121 GCGTMTVYSS 130
DB 112 GKGITMTVYSS 121

RESULT 4
AAW27550
ID AAW27550 standard; Protein; 120 AA.

AAW27550;
23-JAN-1998 (first entry)

Human Ab heavy chain variable region VH1A consensus.

Human; antibody; preparation; library; VH1A; variable region;
heavy chain; consensus.

Homo sapiens.

MO9708320-A1.

06-MAR-1997.

19-AUG-1996; 96WO-EP03647.

18-AUG-1995; 95EP-0113021.

(MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.

Ge L, Ilag V, Knapplik A, Moroney S, Pack P, Plueckthun A;

WPI; 1997-179277/16.

N-PSDB; AAT87948.

Preparation of human derived antibody gene library - using synthetic
consensus sequences, and signal consensus antibody gene as universal
framework for highly diverse antibody libraries

PS Example 1; Fig 5A; 436bp; English.

XX The present sequence is the human antibody heavy chain

CC variable region synthetic sequence VH1A, used in the preparation of

CC a human derived antibody gene library.

XX

SO Sequence 120 AA;

Query Match 74.4%; Score 512; DB 18; Length 120;
Best Local Similarity 76.9%; Pred. No. 1.5e-41;
Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVQSGAEAKRPGSSVYKVCCKASGDTFNSPFIISWRQAPQGGLMMGIIPIFGSTKY 60
DB 1 QVQLVQSGAEVKKPGSSSVYKVCCKASGDTFSSYVAISWRQAPQGGLMMGIIPIFGTANY 60
QY 61 AOKFGQRTMTADGSTAYAMELNSLRSEDTAIYYCARQONGWYEGPLERPDALDIW 120
DB 61 AOKFGQRTVITTDKSTAYAMELSLRSDTAIVYICARWGSQSY-----AMDYW 110
QY 121 GCGTMTVYSS 130
DB 111 GCGTLTVYSS 120

RESULT 5
ABJ18672
ID ABJ18672 standard; Protein; 120 AA.

ABJ18672;
06-MAR-2003 (first entry)

Antibody library related heavy variable chain protein region SEQ ID No 1.

Library; recombinant antibody; clustering variable region; in silico;
immunogenecity; antibody therapeutic.

Unidentified.

MO200284277-A1.

24-OCT-2002.

17-APR-2002; 2002WO-US12202.

17-APR-2001; 2001US-284407P.

(ABMA-) ABMAXIS INC.

Luo P;

WPI; 2003-093043/08.

Constructing a library of recombinant antibodies useful as source of
antibody candidates for screening antigens comprises clustering
variable regions of antibodies having known 3-dimensional structures
into structural ensembles -

Disclosure; Page 98-99; 119pp; English.

The invention relates to a novel method for the construction of a library
of recombinant antibodies. The novel method comprises clustering variable
regions of a collection of antibodies having known 3D structures into at
least two families of structural ensembles, each comprising at least two
different antibody sequences but with substantially identical main chain
conformations. The method is useful for constructing a library of
artificial antibodies in silico which provides a structurally diverse and
yet functionally more relevant source of antibody candidates which can
then be screened for binding a wide variety of target molecules,
including small molecules, and biomacromolecules such as proteins,
peptides and nucleic acids. The libraries constructed are useful as a
source of antibody candidates for further screening for novel antibodies

XX Example 4; Fig 4A; 61pp; English

CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specifically which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody clone EL-14 protein which is used in the method
CC of the invention.

SQ Sequence 130 AA;

Query Match	100.0%	Score 688	DB 21	length 130;
Best Local Similarity	100.0%	Pred. No. 2.2e-58;		
Matches 130; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 QVQLVQSGAEAAKPGGSSVAVCSKASDITFNSFPISWVRQAPEGGLMGIIIPFSTKY 60

Db 1 QVQLVQSGAEAAKPGGSSVAVCSKASDITFNSFPISWVRQAPEGGLMGIIIPFSTKY 60

QY 61 AOKPQGRVLTMDGSGSTAYMELNLSRSEDTAIYYCARQONGWYGGPPLLEPPPDALDIW 120

Db 61 AOKPQGRVLTMDGSGSTAYMELNLSRSEDTAIYYCARQONGWYGGPPLLEPPPDALDIW 120

RESULT 2

ID AAY99558 standard; Protein; 118 AA

AC AAY99558 ;

DT 20-SEP-2000 (first entry)

DE Human LH13 monoclonal antibody heavy chain variable region.

KM Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;
KM cytostatic; cytotoxic; heavy chain variable region.

OS Homo sapiens.

PN WO200032635-A2.

PD 08-JUN-2000

PF 01-DEC-1999; 99WO-US28485.

PR 02-DEC-1998; 98US-0203768.

PA (IXSY-) IXSYS INC.

PI Watkins JD, Hulse WD;

DR WPI; 2000-412293/35.

XX

PT and diagnosis of cancer, comprises at least one complementarity

2
-
3
3
2
2
2
2
2

CC The present sequence is the heavy chain variable region of a human
CC tumour-specific monoclonal antibody. Neoplastic cells selectively express
CC antigens which are not present on normal cells. Thus monoclonal
CC antibodies can be produced that are specifically directed against

CC tumour-specific antigens. The antibodies can be conjugated to cytotoxic
CC or cytostatic agents and used to selectively target cancer cells for the
CC elimination of tumours. They can also be linked to diagnostic moieties
CC that allow the imaging of neoplastic cells. Nucleic acids encoding human
CC tumour-specific monoclonal antibodies can be used to express the
CC antibodies and can be recombinantly engineered to produce modified
CC antibodies with higher affinity or higher selectivity for tumour cells.
CC Tumour-specific antibodies were produced by hybridomas that were
CC generated by *in vitro* immunisation of human spleen cell cultures with
CC breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
CC was then isolated from the hybridoma by RT-PCR. The present sequence
CC was produced by DH1S hybridoma cell line.

SQ Sequence 118 AA;

Query Match	75.1%	Score 517	DB 21	Length 118
Best Local Similarity	76.2%	Pred. No. 5e-42		
Matches 99	Conservative 9	Mismatches 10	Indels 12	Gaps 1

OY	61 AOKRGRTMTADSGTSTAYAMELNSLRSEDTIYYCAROONGCAWEGPLLEPRDALDITM 120
Dd	61 AOKRGRATLTITADESTAYMEHLSLRSEDVAVYICAREDDSGWTH-----YW 108
OY	1 OVOLVOSGAEMKKPKSSVKVSCASGDPFNPSPISMWRAPQOGLEMMKGIIPIFESTINY 60
Dd	1 OVOLVOSGAEMKKPKSSVKVSCASGCTFFSSVAISMVRAPQOGLEMMKGIIPIFETANY 60

RESULT 3
ABP45870

ID ABP45870 standard; Protein; 244 AA.

AC ABP45870;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1881.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytokostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antithematic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.

PN WO200202641-A1

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 16-MAR-2001; 2001US-276248P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC

XX: 3

XX

XX

PT the diagnosis and treatment

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 41.8197 Seconds
(without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 1 QVVLVSGAAKKKPGSSVKV.....EPRPDLDIWGGTMTVSS 130

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
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- 22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688	100.0	130	21	AAVS0948 Human anti-factor
2	517	75.1	118	21	AAVS0958 Human LHT3 monoclo
3	514.5	74.8	244	23	ABP45870 Human anti-EGFR s1
4	512	74.4	120	18	AAW27550 Human Ab heavy cha
5	512	74.4	120	24	ABJ18672 Antibody library r
6	512	74.4	120	24	ABJ18718 Antibody library r
7	512	74.4	220	24	ABR01538 Human anti-TIMP-1
8	511	74.3	253	23	ABP45498 Human Blys binding
9	508.5	73.9	253	23	ABP45869 Human Blys binding

10	508	73.8	254	23	ABP45855 Human Blys binding
11	504.5	73.3	125	22	AAU02555 Anti-adipocyte mon
12	504.5	73.3	249	21	AAB36083 Recombinant human
13	504	73.0	270	23	AAU97198 Human anti-EGFR s1
14	502.5	73.0	228	24	ABR01518 Human anti-TIMP-1
15	502.5	73.0	248	23	ABP45722 Human Blys binding
16	502.5	73.0	248	23	ABP45723 Human Blys binding
17	501.5	72.9	245	24	ABP60521 Human Blys binding
18	501.5	72.9	248	23	ABP45707 Human Blys binding
19	501.5	72.9	248	23	ABP45868 Human Blys binding
20	500.5	72.7	231	24	ABR01524 Human anti-TIMP-1
21	500.5	72.7	481	13	AAK24442 Sequence of antibo
22	500	72.7	257	23	ABP45542 Human Blys binding
23	499	72.5	222	24	ABR01531 Human Blys binding
24	498.5	72.5	248	23	ABP45708 Human Blys binding
25	498.5	72.5	248	23	ABP45721 Human Blys binding
26	498.5	72.5	248	23	ABP45726 Human Blys binding
27	497.5	72.3	248	23	ABP45730 Human Blys binding
28	497.5	72.3	250	23	ABP46055 Human Blys binding
29	497	72.2	254	23	ABP45439 Human Blys binding
30	496.5	72.2	219	24	ABR01523 Human anti-TIMP-1
31	495.5	72.0	248	23	ABP45716 Human Blys binding
32	495.5	72.0	248	23	ABP45717 Human Blys binding
33	494.5	71.9	271	23	AAK66039 scFv 1b4 antibody
34	493.5	71.7	245	22	AAK67617 Human leukocyte an
35	493.5	71.7	251	23	ABP45745 Human Blys binding
36	492.5	71.6	115	23	ABK57559 HLA-DR-specific pr
37	492.5	71.6	225	24	ABR01510 Human anti-TIMP-1
38	492.5	71.6	245	22	AAK67618 Human leukocyte an
39	492	71.5	248	23	ABP45944 Human Blys binding
40	491.5	71.4	223	24	ABR01535 Human anti-TIMP-1
41	491.5	71.4	248	23	ABP45706 Human Blys binding
42	491	71.4	220	24	ABR01512 Human anti-TIMP-1
43	490.5	71.3	239	24	ABP60529 APRIL binding scFv
44	490	71.2	252	23	ABP45655 Human Blys binding
45	490	71.2	253	23	ABP45471 Human Blys binding

ALIGNMENTS

RESULT 1	AAVS0948 standard; Protein; 130 AA.
AAVS0948	
XX	AAVS0948;
XX	
DT	23-MAR-2000 (first entry)
XX	
DB	Human anti-factor VIII antibody VH clone EL-14 encoded protein.
XX	
KW	Human; heavy chain; antibody; factor VIII; hemostatic;
KM	hemophilia A; VH gene.
XX	
OS	Homo sapiens.
XX	
PN	W0958680-A2.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-NL00285.
XX	
PR	08-MAY-1998; 98EP-0201543.
XX	
RA	(SAND-) STRICHTING SANQUIN BLOEDVOORZIENING.
XX	
PI	Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX	
DR	WPI; 2000-053102/04.
XX	
PT	New polynucleotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -

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Db      80 NEKFKGKTLTLADKSSSTAYMFLSLTSDSAVYFCTR--GGGW-----AFDYM 126
QY      121 GGGTMTVSS 130
Db      127 GGGTTLTVSS 136

RESULT 14
ID      092401      PRELIMINARY;      PRT;      142 AA.
AC      092401;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      V23-D-J-C mu protein (Fragment).
GN      V23-D-J-C MU.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1] _TaxID=10090;
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6;
RA      Kozono Y., Kozono H., Azuma T.;
RT      "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT      Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT      Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL      Submitted (MUG-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB069913; BAB63929.1; -.
DR      InterPro: IPR007110; IG_1like.
DR      InterPro: IPR003006; IG_MHC.
DR      InterPro: IPR003596; IG_v.
DR      Pfam: PF00047; IG_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER 1
FT      TER 142
SQ      SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match      55.7%; Score 383.5; DB 11; Length 142;
Best Local Similarity 57.7%; Pred. No. 3.5e-32;
Matches 75; Conservative 18; Mismatches 24; Indels 13; Gaps 2;

QY      1 OVOLVOSGAEGAKKPGSSVVKSCKASGDTFNSFPISWVROAPGQGLEWMGGLIPFGSTKY 60
Db      1 OVOLVOSGAEGAKKPGSSVVKSCKASGDTFNSFPISWVROAPGQGLEWMGGLIPFGSTKY 60
QY      61 AOKFGQRTVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
Db      61 NEKFKSKATLTVDKSSSTAYMQLSLTSDSAVYCAR--GW-----EAMDYV 107
QY      121 GGGTMTVSS 130
Db      108 GGGTSTVSS 117

RESULT 15
ID      095978      PRELIMINARY;      PRT;      157 AA.
AC      095978;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      VHL protein precursor (Fragment).
GN      VHL.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      [1] _TaxID=9606;
RP      SEQUENCE FROM N.A.
RC      TISSUE=PerIPHERAL blood;
RA      Jox A., Zander T., Kuepers R., Irsch J., Kanzler H., Kornacker M.,

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RA      Bohlen H., Diehl V., Wolf J.;
RT      "Absence of Immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT      patient with mixed cellularly Hodgkin's disease is associated with
RT      somatic mutations within the untranslated regions of rearranged and
RT      class switch recombined Ig genes."
RL      Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ005570; CA06599.1; -.
DR      HSP; P01772; 2F84.
DR      InterPro: IPR007110; IG_1like.
DR      InterPro: IPR003006; IG_MHC.
DR      InterPro: IPR003596; IG_v.
DR      Pfam; PF00047; IGV_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      SIGNAL.
FT      SIGNAL 1
FT      NON_TER 157
FT      TER 157
SQ      SEQUENCE 157 AA; 17304 MW; 86986EDDA4D88B5 CRC64;

Query Match      55.6%; Score 382.5; DB 4; Length 157;
Best Local Similarity 60.4%; Pred. No. 5e-32;
Matches 81; Conservative 10; Mismatches 26; Indels 17; Gaps 3;

QY      1 OVOLVOSGAEGAKKPGSSVVKSCKASGDTFNSFPISWVROAPGQGLEWMGGLIPFGSTKY 60
Db      20 OVOLVOSGAEGAKKPGSSVVKSCKASGDTFNSFPISWVROAPGQGLEWMGGLIPFGSTKY 79
QY      61 AOKFGQRTVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 116
Db      61 AOKFGQRTVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 129
QY      117 LDIMGGTMTVSS 130
Db      130 ---WGQGTPTVSS 140

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Search completed: December 30, 2003, 11:01:02
 Job time : 32.6816 secs

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OY 61 AOKFGRTVTADGSTATAYMELNSLRSEPTAIYYCARQONGWYEGPPLLEPRDADIW 120
DB 80 NEKFGATFTADSTMTATWQSLTSLSBDSAVYYCARRL-GRWY-----FDW 127
OY 121 GGGTMTVSS 130
DB 128 GAGTTTVSS 137

RESULT 11
OY 09GYZ2 PRELIMINARY; PRT; 119 AA.
ID 09GYZ2;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2003 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5F6AB CRC64;

Query Match 57.0%; Score 392.5; DB 5; Length 119;
Best Local Similarity 60.8%; Pred. No. 3.2e-33;
Matches 79; Conservative 14; Mismatches 26; Indels 11; Gaps 1;

OY 1 OVOLVQSGAEAKKRGSSVYKSCASGDTFNSFWYRQAPGQGLEWNGGIPIFGSTKY 60
DB 1 OVOLVESGAELVRKPGASVRSCKASGYFTGYMMWVRQAPGHLGIEWINPGRGTYN 60
OY 61 AOKFGRTVTADGSTATAYMELNSLRSEPTAIYYCARQONGWYEGPPLLEPRDADIW 120
DB 61 NOKFDRVTMTTDSFSFYAVMDLSLSADSAYVYCARYYDDHY-----CLDYW 109
OY 121 GGGTMTVSS 130
DB 110 GGGTTTVSS 119

RESULT 12
OY 09ZIC4 PRELIMINARY; PRT; 118 AA.
ID 09ZIC4;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Anti-porcine VCAW mab 3f4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Balb/c;
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RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mats L.M., Evans M.U.;
RT "Humanized porcine VCAW-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR HSSP; P01810; 2F8J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 118 AA; 13036 MW; 90EECS59D31EC4FC CRC64;

Query Match 57.0%; Score 392; DB 11; Length 118;
Best Local Similarity 57.7%; Pred. No. 3.6e-33;
Matches 75; Conservative 20; Mismatches 23; Indels 12; Gaps 1;

OY 1 OVOLVQSGAEAKKRGSSVYKSCASGDTFNSFWYRQAPGQGLEWNGGIPIFGSTKY 60
DB 1 OVQVQSGAEIARPMASVSKLSCASGYFNFWMMVKORPGQGLEWIGAIYFGDDTST 60
OY 61 AOKFGRTVTADGSTATAYMELNSLRSEPTAIYYCARQONGWYEGPPLLEPRDADIW 120
DB 61 TOKRGAATLTAKSSSTAYMQLSLASBDSAVYYCARRTVGIF-----DWT 108
OY 121 GGGTMTVSS 130
DB 109 GGGTTTVSS 118

RESULT 13
OY 09IWT1 PRELIMINARY; PRT; 481 AA.
ID 09IWT1;
AC 09IWT1;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 56.5%; Score 388.5; DB 11; Length 481;
Best Local Similarity 59.2%; Pred. No. 4.8e-32;
Matches 77; Conservative 17; Mismatches 23; Indels 13; Gaps 2;

OY 1 OVOLVQSGAEAKKRGSSVYKSCASGDTFNSFWYRQAPGQGLEWNGGIPIFGSTKY 60
DB 20 OVOLLQSGPELVKRGASVKSCKASGYFTSYIHWKORPGQLVWIGWIPGDGNTKY 79
OY 61 AOKFGRTVTADGSTATAYMELNSLRSEPTAIYYCARQONGWYEGPPLLEPRDADIW 120
DB 1 AOKFGRTVTADGSTATAYMELNSLRSEPTAIYYCARQONGWYEGPPLLEPRDADIW 120
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Db      1 EVOLVESGAEEVKKPGASVSKVSCASGTYFTGYMHWROAPGQGLEMMGMINPNSWTNY 60
QY      61 AAKFGQRYMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPULLEPRPALDI 119
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 AAKFGQRYMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPULLEPRPALDI 108
QY      120 WGGQGTWTVSS 130
        |||||:|||||
Db      109 WGGQGTWTVSS 119

RESULT 8
Q96DKO PRELIMINARY; PRT; 496 AA.
AC Q96DKO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoetical protein FLJ25298.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Gastric mucosa;
RA Ishihashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotta T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK058027; BAB71633.1; -.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypoetical protein_
SQ SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;

Query Match 59.4%; Score 409; DB 4; Length 496;
Best Local Similarity 61.9%; Pred. No. 3.6e-34;
Matches 83; Conservative 11; Mismatches 26; Indels 14; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEMMGIIPIFGSTKY 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVHLVDSGAEELKMGSSVSKVSCASAMFISYAFITWROAQGLQMMGIIPIFGAPNY 79
QY 61 AAKFGQRYMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPULLEPRPALDI 116
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AAKFGQRYMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPULLEPRPALDI 129
QY 117 LDINGQGTWTVSS 130
        |||||:|||||
Db 130 LDINGQGTWTVSS 143

RESULT 9
Q9BRVO PRELIMINARY; PRT; 500 AA.
AC Q9BRVO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=prostate;
RA Struaberg R.;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypoetical protein_
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF41F2A3CC6D9 CRC64;

Query Match 59.2%; Score 407; DB 4; Length 500;
Best Local Similarity 59.1%; Pred. No. 6e-34;
Matches 81; Conservative 17; Mismatches 23; Indels 16; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEMMGIIPIFGSTKY 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVHLVDSGAEVMSPGASVSVCKTSGYAFHTYSIIWROAPGQGLEMMGIIPIFGSTNYF 79
QY 61 AAKFGQRYMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPULLEPR 113
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AAKFGQRYMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPULLEPR 132
QY 114 PDALDIWQGTWTVSS 130
        |||||:|||||
Db 133 --YMDVWGKGTITVTVSS 147

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypoetical 67.9 kDa protein.
GN IGH-6.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Salivary gland;
RA Struaberg R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR MGD; MGI:96448; IGH-6.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypoetical protein_
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 57.7%; Score 397; DB 11; Length 613;
Best Local Similarity 59.2%; Pred. No. 8.5e-33;
Matches 77; Conservative 19; Mismatches 22; Indels 12; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEMMGIIPIFGSTKY 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVDSGAEELKMGSSVSKVSCASGDTFNSFPISWVROAPGQGLEMMGIIPIFGSTNY 79

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Db      20 OMVLQVSGAEAKKGGSSVYKVCCKASGDTFTYRYLWVWQAPQALQEMWGIIPFGSTKY 79
Qy      61 AOKFGRYVTMTADGSTSTAYMELNSLRSEDPTAIYYCARQONGWYEGPLLEPRPDALDIW 120
Db      80 AOKFGDRVTITRRDRSMNTAYMELSLRSEDPTAIYYCARQONGWYEGPLLEPRPDALDIW 130
Qy      121 GCGTMTVTVSS 130
Db      131 GCGTMTVTVSS 140

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RESULT 5

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Q96QSO0 PRELIMINARY; PRT; 159 AA.
AC Q96QSO0;
DT 01-DEC-2001 (TREMBlrel. 19, Last Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilsen M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

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Query Match 63.1%; Score 434; DB 4; Length 159;
 Best Local Similarity 61.9%; Pred. No. 2.2e-37;
 Matches 86; Conservative 18; Mismatches 17; Indels 18; Gaps 2;

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Qy      1 QVQLVQSGAEAKKGGSSVYKVCCKASGDTFNSFPISWVRQAPGQGLEWMGIIPIFGSTKY 60
Db      20 QVQLVQSGAEVKKPKASVYVCKASGYTFSNYVMVWGAPQGGPEWMGVINPSGGSARY 79
Qy      61 AOKFGRYVTMTADGSTSTAYMELNSLRSEDPTAIYYCARQONGWYEGPLLE 111
Db      80 AOKFGDRVTITRRDRSMNTAYMELSLRSEDPTAIYYCARQONGWYEGPLLE 135
Qy      112 PRPDALDIWCGTMTVTVSS 130
Db      136 -----MDVWVGQGITVTVSS 149

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RESULT 6

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Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE IGG VH protein precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacquemin M.G., Vander Elst L.P.L.;

```

```

RT      "Mechanism and kinetics of factor VIII inactivation: study with an
RT      IgG4 monoclonal antibody derived from a hemophilia A patient with
RT      inhibitor."
RL      Blood 92:496-506(1998).
DR      EMBL; AJ224083; CAA11829.1; -.
DR      HSSP; P01772; 2FB4.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KM      Signal.
FT      SIGNAL.
FT      NON_TER
SQ      SEQUENCE 150 AA; 16031 MW; 563D164AB2802D5 CRC64;

```

Query Match 61.7%; Score 424.5; DB 4; Length 150;
 Best Local Similarity 64.6%; Pred. No. 2e-36;
 Matches 84; Conservative 10; Mismatches 23; Indels 13; Gaps 1;

```

Qy      1 QVQLVQSGAEAKKGGSSVYKVCCKASGDTFNSFPISWVRQAPGQGLEWMGIIPIFGSTKY 60
Db      20 QVQLVQSGAEVKKPKASVYVCKASGYTLTLPVHWGAPQGGPEWMGVINPSGGSARY 79
Qy      61 AOKFGRYVTMTADGSTSTAYMELNSLRSEDPTAIYYCARQONGWYEGPLLEPRPDALDIW 120
Db      80 AOKFGDRVTITRRDRSMNTAYMELSLRSEDPTAIYYCARQONGWYEGPLLEPRPDALDIW 126
Qy      121 GCGTMTVTVSS 130
Db      127 GCGTMTVTVSS 136

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RESULT 7

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Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus."
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035020; AAD56256.1; -.
DR      HSSP; P01810; 2FBJ.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE 119 AA; 13205 MW; 13B64F5345FA16E CRC64;

```

Query Match 61.1%; Score 420.5; DB 4; Length 119;
 Best Local Similarity 64.9%; Pred. No. 3.9e-36;
 Matches 85; Conservative 12; Mismatches 21; Indels 13; Gaps 2;

```

Qy      1 QVQLVQSGAEAKKGGSSVYKVCCKASGDTFNSFPISWVRQAPGQGLEWMGIIPIFGSTKY 60

```

```

Db      1 V0SGAEVKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPILIGIANYAOKF 60
QY      65 QGRVTMTADGSTSTAYVMEI...
Db      61 QGRVTTTADGSTSTAYVMEI...
QY      124 TMTVTSS 130
Db      110 TLVTVSS 116

RESULT 2
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95
AC Q9UL95;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -
DR HSP; P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match      65.8%; Score 452.5; DB 4; Length 125;
Best Local Similarity 69.2%; Pred. No. 1.9e-39;
Matches 90; Conservative 10; Mismatches 25; Indels 5; Gaps 1;

QY      1 QVOLV0SGAEAKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPFGSTKY 60
Db      1 EVOLVESAEVKKPGASVKVSCKASGYFTGYVMHWVROAPGQGLEWMGWIINPSGCTNY 60
QY      61 AOKFGQGVMTADGSTSTAYVMEI...
Db      61 AOKQGRVMTTRDTTISTAYVMEI...
QY      121 GGGTMTVSS 130
Db      116 GGGTMTVSS 125

RESULT 3
Q9UL92 PRELIMINARY; PRT; 124 AA.
ID Q9UL92
AC Q9UL92;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

OX      NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035022; AAD56258.1; -
DR HSP; P01772; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match      64.4%; Score 443; DB 4; Length 124;
Best Local Similarity 70.2%; Pred. No. 1.8e-38;
Matches 92; Conservative 11; Mismatches 20; Indels 8; Gaps 3;

QY      1 QVOLV0SGAEAKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPFGSTKY 60
Db      1 EVOLVESAEVKKPGASVKVSCKASGYFTSSYVMHWVROAPGQGLEWMGIIINPSGCTSY 60
QY      61 AOKFGQGVMTADGSTSTAYVMEI...
Db      61 AOKQGRVMTTRDTTISTAYVMEI...
QY      120 WGGTMTVSS 130
Db      114 WGGTMTVSS 124

RESULT 4
Q96GA6 PRELIMINARY; PRT; 614 AA.
ID Q96GA6
AC Q96GA6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009851; AAH09851.1; -
DR InterPro: IPR000005; HTHARAC.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00406; Ig; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
DR Hypothetical protein.
FT SEQUENCE 614 AA; 67921 MW; 55EP536E77AA9BBB CRC64;

Query Match      63.7%; Score 438.5; DB 4; Length 614;
Best Local Similarity 68.5%; Pred. No. 4e-37;
Matches 89; Conservative 8; Mismatches 24; Indels 9; Gaps 1;

QY      1 QVOLV0SGAEAKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPFGSTKY 60

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OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paekind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL: J00539; AAA8172.1; -
DR PIR: A02038; G2MG43.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL.
FT CHAIN 1 19
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 50 54 FRAMEWORK-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match
Best Local Similarity 51.5%; Score 354; DB 1; Length 137;
Matches 70; Conservative 19; Mismatches 29; Indels 12; Gaps 1;

OY 1 QVQLVQSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPQGLEWMGIIPIFGSTKY 60
DB 20 QVQLQPGAEFVKPGASVYLSCKASGYFTSYLMHVNRPGRGLEWIGRIDPNNGCTTY 79
OY 61 AOKFGRTVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPILPRPDALDIW 120
DB 80 NEHFRSKATLITIDKPSSTAYMQLSSLTSEDSAVYCARILGRYF-----DYM 127
OY 121 GGGTMTVSS 130
DB 128 GGGTTLTVSS 137

RESULT 15
HY48_MOUSE
ID HY48_MOUSE STANDARD; PRT; 138 AA.
AC P03880;
DT 23-OCT-1986 (rel. 02, Created)
DT 23-OCT-1986 (rel. 02, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG heavy chain V region TBPc 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HWSST7.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL.
FT CHAIN 1 20
FT DOMAIN 21 138 IG HEAVY CHAIN V REGION TBPc 1017.
FT DOMAIN 50 54 FRAMEWORK-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 FRAMEWORK-4.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match
Best Local Similarity 50.1%; Score 344.5; DB 1; Length 138;
Matches 69; Conservative 21; Mismatches 29; Indels 11; Gaps 2;

OY 1 QVQLVQSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPQGLEWMGIIPIFGSTKY 60
DB 20 QVQLQPGAEFVKPGASVYLSCKASGYFTSYLMHVNRPGRGLEWIGRIDPNNGRSNY 79
OY 61 AOKFGRTVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPILPRPDALDIW 120
DB 80 NEHFRSKATLITIDKPSSTAYMQLSSLTSEDSAVYCARILGRYF-----DYM 128
OY 121 GGGTMTVSS 130
DB 129 GGGTTLTVSS 138

Search completed: December 30, 2003, 10:55:49
Job time : 7.96994 secs

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=8620377; PubMed=3084950;
RA Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RL Immunoglobulin (Mol) having unusual papain cleavage sites.";
Mol. Immunol. 23:169-174(1986).
DR PIR: A02025; HVHMO.
DR HSSP: P01772; 2P84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 107 D SEGMENT.
FT DOMAIN 108 125 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 52.5%; Score 361.5; DB 1; Length 125;
Best Local Similarity 56.3%; Pred. No. 2.6e-30;
Matches 76; Conservative 12; Mismatches 32; Indels 15; Gaps 3;

OY 1 QVQLVQSAEAKKPKSSVYKVSCKASGDTFNSFPISWNRQAPGQGLEMMGIIPIFGSTRY 60
DB 1 QVQLVQSAEAKKPKSSARLSCKVSGDDFNTYDHWVRQAPRGLEMAVVPSSDRITTY 60
OY 61 AOKFQGRVTMTADGSTAYVWELNSLRSEDPATYYCARQNGWY-----EGPLLEPRPD 115
DB 61 GPRSGARTVTRDSTTYVWELTLISADPATYYCAR---GAHYSDPDDSGTSLGP--- 114
OY 116 ALDIWGQGTMTVSS 130
DB 115 -----WGQGTLLIVSS 125

RESULT 10
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RN STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bohwell A.L.M., Peakind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribuent to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NIB ANTIBODIES).
CC -----
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CC -----
DR EMBL: J00529; AAA38170.1; -.
DR PIR: A90809; MEMS18.
DR PDB: 1A6U; 27-MAY-98.
DR PDB: 1A6W; 15-JUL-98.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3d-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 52.5%; Score 361; DB 1; Length 139;
Best Local Similarity 56.2%; Pred. No. 3.3e-30;
Matches 73; Conservative 17; Mismatches 30; Indels 10; Gaps 2;

OY 1 QVQLVQSAEAKKPKSSVYKVSCKASGDTFNSFPISWNRQAPGQGLEMMGIIPIFGSTRY 60
DB 20 QVQLVQSAEALVYKGSVYKLSCKASGYTFSTYMWVWVQRPGRGLEWGRIDPNSGSTRY 79
OY 61 AOKFQGRVTMTADGSTAYVWELNSLRSEDPATYYCARQNGWYEGPLLEPRPDALDIW 120
DB 61 NEKFKSKATLVDPSSATYVWLSLTSEDSAVYYCARDY-----SSYPFW 129
OY 121 GQGTMTVSS 130
DB 130 GQGTTLIVSS 139

RESULT 11
HV00_MOUSE STANDARD; PRT; 114 AA.
ID HV00_MOUSE
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RN STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RL mice bearing a cross-reactive idiotype.";
J. Immunol. 123:279-284(1979).
CC -I- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGH1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.

```

SQ SEQUENCE 117 AA; 12983 MW; 3CF9ACB4BE447E41 CRC64;

Query Match 53.4%; Score 367.5; DB 1; Length 117;

Best Local Similarity 55.4%; Pred. No. 5.9e-31;

Matches 72; Conservative 18; Mismatches 27; Indels 13; Gaps 2;

QY 1 OVQLVSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPGOGLWMGGIIPFGSTKY 60

DB 1 EVQLQDSGPELVKPGASVMSCKASGYTFTDYMKVKVSHKSLRWIGDINPNNGSTSY 60

QY 61 AOKFGQVMTADGSTATYMLNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120

DB 61 NQKFKGATLTVDKSSSTAYMQNLSTSEDSAVYVCARDRY--WY-----FDVW 107

QY 121 GGGTMTVSS 130

DB 108 GAGTTVTSS 117

RESULT 7

HV13_MOUSE STANDARD; PRT; 117 AA.

ID HV13_MOUSE P01757;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region J558.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI_TaxId=10090;

CC [1]

CC SEQUENCE.

CC MEDLINE=80078170; PubMed=6765983;

CC Schilling J., Clevinger B., Davie J.M., Hood L.;

CC "Amino acid sequence of homogeneous antibodies to dextran and DNA

CC rearrangements in heavy chain V-region gene segments.";

CC Nature 283:35-40(1980)

CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO

CC WHICH OCCUR IN THE D AND J SEGMENTS.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC PIR: A26242; MEMSJS.

CC HSSP: P01789; IMCPS.

CC InterPro: IPR007110; Ig-like.

CC InterPro: IPR003006; Ig_MHC.

CC InterPro: IPR003596; Ig_V.

CC Pfam: PF00047; Ig_1.

CC SMART: SM00406; IGV_1.

CC PROSITE: PS50835; IG LIKE; 1.

CC Immunoglobulin V region.

CC DOMAIN 1 116 IG-LIKE.

CC DISULFID 22 96 BY SIMILARITY.

CC NON_TER 117 117

SO SEQUENCE 117 AA; 13024 MW; 292E2AFA4BE447E41 CRC64;

Query Match 53.3%; Score 366.5; DB 1; Length 117;

Best Local Similarity 55.4%; Pred. No. 7.4e-31;

Matches 72; Conservative 18; Mismatches 27; Indels 13; Gaps 2;

QY 1 OVQLVSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPGOGLWMGGIIPFGSTKY 60

DB 1 EVQLQDSGPELVKPGASVMSCKASGYTFTDYMKVKVSHKSLRWIGDINPNNGSTSY 60

QY 61 AOKFGQVMTADGSTATYMLNSLRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120

DB 61 NQKFKGATLTVDKSSSTAYMQNLSTSEDSAVYVCARDRY--WY-----FDVW 107

QY 121 GGGTMTVSS 130

DB 108 GAGTTVTSS 117

RESULT 8

HV02_MOUSE STANDARD; PRT; 140 AA.

ID HV02_MOUSE P01746;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region J3G7 precursor.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI_TaxId=10090;

CC [1]

CC SEQUENCE FROM N.A.

CC STRAIN=A/J;

CC MEDLINE=82152818; PubMed=6801765;

CC Sims J., Rabbits T.H., Estees P., Slaughter C., Tucker P.W.,

CC Capra J.D.,

CC "Somatic mutation in genes for the variable portion of the

CC immunoglobulin heavy chain.";

CC Science 216:309-311(1982).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

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CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC CC

CC EMBL J00493; AAA38128.1; -

CC PIR: A94264; HYMSG7.

CC HSSP: P01810; 2FBU.

CC InterPro: IPR007110; Ig-like.

CC InterPro: IPR003006; Ig_MHC.

CC InterPro: IPR003596; Ig_V.

CC Pfam: PF00047; Ig_1.

CC SMART: SM00406; IGV_1.

CC PROSITE: PS50835; IG LIKE; 1.

CC Immunoglobulin V region; Hybridoma; Signal.

CC SIGNAL 1 19

CC FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.

CC FT DOMAIN 20 139 IG-LIKE.

CC FT NON_TER 140 140

SO SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 52.8%; Score 363.5; DB 1; Length 140;

Best Local Similarity 56.5%; Pred. No. 1.9e-30;

Matches 74; Conservative 18; Mismatches 28; Indels 11; Gaps 2;

QY 1 OVQLVSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPGOGLWMGGIIPFGSTKY 60

DB 20 EVQLQDSGAEVLVRASSVYKMSCKASGYTFTSYGINVAVQKPGGLEWGYINPNNGYINY 79

QY 61 AOKFGQVMTADGSTATYMLNSLRSEDTAIYYCARQ--NGWYEGPLLEPRPDALDI 119

DB 80 NEKFKGATLTVDKSSSTAYMQNLSTSEDSAVYFCARSHYGGSYD-----FDY 129

QY 120 WGGTMTVSS 130

DB 130 WGGTMTVSS 140

RESULT 9

HV1F_HUMAN STANDARD; PRT; 125 AA.

ID HV1F_HUMAN P06326;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-I region Mcc.

DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296408; PubMed=2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
 RA Ohno H., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 RT heavy-chain locus".
 RL EMO J. 7:1047-1051(1988).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X07448; NOT_ANNOTATED_CDS.
 DR PIR: S00476; HVH03.
 DR HSSP: P01772; 2FB4.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; F:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IgV_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
 Query Match 55.2%; Score 380; DB 1; Length 117;
 Best Local Similarity 75.5%; Pred. No. 3e-32;
 Matches 74; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
 QY 1 QVQLVQSGAEAKKPGSSVYVSCKASGDTFNSPISWVROAPQGLEEMNGILPIFGSTKY 60
 DB 20 QVQLVQSGAEVAKKPGASVYVSCKASGYFTFTGYMHVROAPQGLEEMGRINPNSGCTNY 79
 QY 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIYYCAR 98
 DB 80 AOKFGQRYVTSTRTDSTISTAYMELSLRSDDTIVYYCAR 117
 RESULT 5
 HY03_MOUSE
 ID HY03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 36-65.
 DE Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83131846; PubMed=6186498;
 RA Silevitz M., Gelfer M.L., Brodeur P., Riblet R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenate

RT Idiotypic response of the strain A mouse.";
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 CC SEGMENT, JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 DR HSSP: P01789; 1MCP.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IgV_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 111
 FT NON_TER 120 120 IG-LIKE.
 SQ SEQUENCE 120 AA; 13307 MW; F04E4A167B654AF CRC64;
 Query Match 53.9%; Score 370.5; DB 1; Length 120;
 Best Local Similarity 57.3%; Pred. No. 3e-31;
 Matches 75; Conservative 17; Mismatches 26; Indels 13; Gaps 2;
 QY 2 VQLVQSGAEAKKPGSSVYVSCKASGDTFNSPISWVROAPQGLEEMNGILPIFGSTKYA 61
 DB 1 VQLVQSGAEVRAKSSVYVSCKASGYFTFTSYGINVVKORPQGLEWIGYINPGNYKYN 60
 QY 62 OKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ--QNGWYSGPLLEPPDLDI 119
 DB 61 EKFKGKTLITVDKSSSTAIRMQRLSLRSEDSAVYFCARSYVYGSSY-----FDY 109
 QY 120 WGGCTMTVSS 130
 DB 110 WGGCTTLTVSS 120
 RESULT 6
 HY12_MOUSE
 ID HY12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 104E.
 DE Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424(1982).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN HAS ALSO BEEN DETERMINED.
 CC -1- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 DR HSSP: P01789; 1MCP.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Glycoprotein.
 FT DOMAIN 1 116
 FT NON_TER 117 117 IG-LIKE.
 FT CARBOHYD 22 96 BY SIMILARITY.
 FT NON_TER 117 117 N-LINKED (GLCNAC. . .) (COMPLEX).

[illegible]

DT	21-JUL-1986	(Rel. 01, Created)
AC	P01744;	
DT	16-OCT-2001	(Rel. 40, Last sequence update)
DT	15-SEP-2003	(Rel. 42, Last annotation update)
DE	1g heavy chain V-I region ND precursor (Fragments).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=83065234; PubMed=6815656;	
RA	Kerten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J.,	
RA	Bell L.O., Gould H.J.;	
RT	"Cloning and sequence determination of the gene for the human	
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).	
RN	[2]	
RP	SEQUENCE OF 20-147.	
RA	Bernihl H.H., Johansson S.G.O., von Bahr-Blindstrom H.;	
RL	(In) Bach M.K. (eds.);	
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,	
RL	Marcel Dekker, New York (1978).	
CC	-1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA	
CC	PROTEIN.	
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.	
CC	HSSP; P01789; IMCP.	
DR	GO; GO:0005576; C:extracellular; NAS.	
DR	GO; GO:0003823; F:antigen binding activity; NAS.	
DR	GO; GO:0006955; P:immune response; NAS.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003006; IG_MHC.	
DR	InterPro; IPR003596; IG_V.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG_LIKE; 1.	
KW	Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.	
FT	SIGNAL	1 19
FT	CHAIN	20 147
FT	DOMAIN	20 131
FT	MOD RES	20 20
FT	DISTUFD	41 115
FT	CONFLICT	21 21
FT	CONFLICT	53 54
FT	CONFLICT	67 68
FT	CONFLICT	125 125
FT	NON TER	147 147
SO	SEQUENCE	147 AA; 14691 MM; 9489F72A5366C20 CRC64;
Query Match	56.2%;	Score 387; DB 1; Length 147;
Best Local Similarity	59.8%;	Pred. No. 7.5e-33;
Matches	79; Conservative	14; Mismatches 33; Indels 6; Gaps 2
OY	1	OVOLVQSABAKKPPSSVKVSCSKASGDFNFPISMWVAQGGQLEMMGGIIPFGSTKY 60
DB	20	QTQLVQSABAKKPPKASVRSVCSKASGTFIDISYIMIMIQAGHGLEMMGWINPNSGGINY 79
OY	61	AQKFGGRVTMTADSGTSTAYMELNSLRSEDTAIYCAQON--GGWYEGPLIEPPDALD 118
DB	80	APRFGRGRTMRDASFTAYMDLRSLRSDSDAVFYCAKSDPFWSDYVNFY----SYTLDD 135
OY	119	IWGGGTMVTYVS 130
DB	136	VWGCGITVTYVS 147
RESULT 4		
ID	HVIG_HUMAN	STANDARD; PRT; 117 AA.
AC	P23083;	
DT	01-NOV-1991	(Rel. 20, Created)
DT	01-NOV-1991	(Rel. 20, Last sequence update)
DT	15-SEP-2003	(Rel. 42, Last annotation update)

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.96994 Seconds
(without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688
Sequence: 1 QVOLVSGAEVKKRGSSVVKV.....EPRPDALDIMCGTIVTVSS 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420.5	61.1	117	1	HV1A_HUMAN
2	412	59.9	117	1	HV1B_HUMAN
3	387	56.2	117	1	HV1C_HUMAN
4	380	55.2	117	1	HV1G_HUMAN
5	370.5	53.9	120	1	HV03_MOUSE
6	367.5	53.4	117	1	HV12_MOUSE
7	366.5	53.3	117	1	HV13_MOUSE
8	363.5	52.8	140	1	HV02_MOUSE
9	361.5	52.5	125	1	HV1F_HUMAN
10	361	52.5	139	1	HV07_MOUSE
11	360	52.3	114	1	HV00_MOUSE
12	358	52.0	120	1	HV50_MOUSE
13	354	51.5	118	1	HV51_MOUSE
14	344.5	50.1	137	1	HV11_MOUSE
15	344.5	50.1	138	1	HV48_MOUSE
16	342	49.7	117	1	HV52_MOUSE
17	339.5	49.3	121	1	HV01_MOUSE
18	338	49.1	124	1	HV1E_HUMAN
19	329	47.8	117	1	HV09_MOUSE
20	328	47.7	117	1	HV05_MOUSE
21	324	47.1	117	1	HV06_MOUSE
22	322	46.8	117	1	HV04_MOUSE
23	319	46.4	120	1	HV1H_HUMAN
24	317	46.1	117	1	HV49_MOUSE
25	316	45.9	117	1	HV14_MOUSE
26	314	45.6	117	1	HV10_MOUSE
27	313.5	45.6	121	1	HV3J_HUMAN
28	313.5	45.6	116	1	HV15_MOUSE
29	310.5	45.1	135	1	HV4D_HUMAN
30	310	45.1	136	1	HV16_MOUSE
31	308	44.8	116	1	HV3T_HUMAN
32	308	44.8	122	1	HV3G_HUMAN
33	307	44.6	124	1	HV1D_HUMAN

34	303.5	44.1	119	1	HV3I_HUMAN	P01770 homo sapien
35	303	44.0	122	1	HV3A_HUMAN	P01762 homo sapien
36	303	44.0	122	1	HV3H_HUMAN	P01769 homo sapien
37	301	43.8	114	1	HV3B_HUMAN	P01763 homo sapien
38	301	43.8	120	1	HV3U_HUMAN	P01782 homo sapien
39	295	42.9	126	1	HV3K_HUMAN	P01772 homo sapien
40	292	42.4	114	1	HV01_CANFA	P01784 canis fam11
41	291	42.3	117	1	HV3C_HUMAN	P01764 homo sapien
42	291	42.3	119	1	HV38_MOUSE	P01808 mus musculu
43	286.5	41.6	117	1	HV02_CANFA	P01785 canis fam11
44	286	41.6	119	1	HV40_MOUSE	P01810 mus musculu
45	283.5	41.2	142	1	HV01_RAT	P01805 rattus norv

ALIGNMENTS

RESULT 1	ID	HV1A_HUMAN	STANDARD	PRT	117 AA.
AC	P01742				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Ig heavy chain V-I region EU.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=71064024; PubMed=5489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RA	Waxdal M.V., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino				
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."				
RL	Biochemistry 9:3161-3170(1970).				
RN	[2]				
RP	DISULFIDE BOND.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X.				
RT	Intrachain disulfide bonds."				
RL	Biochemistry 9:3188-3196(1970).				
CC	-I- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS				
CC	MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.				
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A90563; G1HUEU.				
DR	HSSP; P01772; 2FB4.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding activity; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Immunoglobulin V region; Pyroliidone carboxylic acid.				
FT	DOMAIN 1 112 IG-LIKE.				
FT	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.				
FT	DISULFID 22 96				
FT	NON TER 117 117				
SO	SEQUENCE 117 AA; 12472 MW; 99D60ADAE8D52818 CRC64;				
Qy	Query Match	61.1%; Score 420.5; DB 1; Length 117;			
Db	Best Local Similarity	67.4%; Pred. No. 2.1e-36;			
	Matches	89; Conservative 11; Mismatches 15; Indels 17; Gaps 4;			
	1 QVOLVSGAEVKKRGSSVVKVSCASGDTFNSWYRQAGCGLEWGGIIPFGSTKY 60				
	1 QVOLVSGAEVKKRGSSVVKVSCASGDTFNSWYRQAGCGLEWGGIIPFGSTKY 60				

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 6.75548 Seconds
(without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120

Sequence: 1 QQNGWYEGPLERPDLDI 21

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

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7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

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15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	21	AAV50956	Human anti-factor
2	120	100.0	21	AAV50948	Human anti-factor
3	52	43.3	265	ABG00057	Novel human diagno
4	51.5	42.9	118	AAU43195	Proionibacterium
5	51	42.5	132	ABP33553	Human ORF256 prot
6	50	41.7	341	AAU35179	Enterococcus faeca
7	50	41.7	348	ABP57025	Enterococcus faeca
8	50	41.7	358	ABP57024	Enterococcus faeci
9	49	40.8	549	ABG99970	Human novel polyPe

10	48	40.0	993	20	AAV49897
11	47	39.2	172	22	AAU23343
12	47	39.2	564	22	ABG24835
13	47	39.2	816	22	ABG24833
14	47	39.2	858	22	ABG04046
15	47	39.2	897	22	ABG25828
16	47	39.2	4150	22	AAV92707
17	47	39.2	7068	22	AAE10142
18	47	39.2	9477	22	AAE10144
19	46	38.3	70	23	ABP04042
20	46	38.3	355	22	AAE09457
21	46	38.3	429	22	ABG2412
22	46	38.3	1062	22	ABG2412
23	46	38.3	1235	21	AAAB4163
24	45.5	37.9	472	22	AAU39938
25	45	37.5	77	22	AAO13758
26	45	37.5	186	21	AAO2083
27	45	37.5	186	21	AAO2087
28	45	37.5	314	21	AAO60872
29	45	37.5	325	21	AAO60963
30	45	37.5	329	21	AAO60962
31	45	37.5	338	21	AAO60961
32	45	37.5	340	21	AAO60870
33	45	37.5	346	21	AAO60870
34	45	37.5	349	21	AAO60869
35	45	37.5	352	21	AAO60869
36	45	37.5	352	21	AAO60880
37	45	37.5	363	21	AAO60880
38	45	37.5	369	21	AAO60879
39	45	37.5	369	21	AAO60879
40	45	37.5	375	21	AAO60879
41	45	37.5	382	21	AAO60879
42	45	37.5	382	21	AAO60879
43	45	37.5	463	22	ABG25348
44	45	37.5	772	22	AAU44927
45	45	37.5	1729	22	AAAB2331

ALIGNMENTS

RESULT 1

AAV50956

AAV50956 standard; Protein; 21 AA.

AAV50956;

23-MAR-2000 (first entry)

Human anti-factor VIII antibody VH protein VH EU-14 CDR3 fragment.

Human; heavy chain; antibody; factor VIII; hemostatic;

hemophilia A; VH protein.

OS Homo sapiens.

XX MO958680-A2.

PN 18-NOV-1999.

PD 07-MAY-1999; 99WO-NL00285.

PP 08-MAY-1998; 98EP-0201543.

PR (SANO-) STICHTING SANQUIN BLOEDVOORZIENTING.

PA Voorberg JJ, Van Den Brink EN, Turenhout EAM;

PI WPT; 2000-053102/04.

DR New polynucleotide, polypeptide and antibody useful for diagnosing the

XX presence of neutralizing antibodies against factor VIII and for

PT treatment of hemophilia A patients with these antibodies -

XX Example 4; Fig 4C; 61pp; English.
PS
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful as a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody A EL-14 protein CDR3 fragment which is used
CC in the method of the invention.
XX
SQ Sequence 21 AA;
Query Match 100.0%; Score 120; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QONGWYEGPLLEPRPDALDI 21
Db 1 QONGWYEGPLLEPRPDALDI 21
RESULT 2
ID AAY50948 standard; Protein; 130 AA.
XX
AC AAY50948;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH clone EL-14 encoded protein.
XX
KW Human; heavy chain; antibody; factor VIII; hemostatic;
XX hemophilia A; VH gene.
XX
OS Homo sapiens.
XX
PN WO958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
PS Example 4; Fig 4A; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful as a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody clone EL-14 protein which is used in the method
CC of the invention.
XX
SQ Sequence 130 AA;

Query Match 100.0%; Score 120; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QONGWYEGPLLEPRPDALDI 21
Db 99 QONGWYEGPLLEPRPDALDI 119
RESULT 3
ID ABG00057 standard; Protein; 265 AA.
XX
AC ABG00057;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #48.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PDB; AAS64244.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 30416; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 265 AA;
Query Match 43.3%; Score 52; DB 22; Length 265;
Best Local Similarity 69.2%; Pred. No. 7.2;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCMYEGPLLEPR 16
 |||||
 Db 24 GGAHGGPALLEPR 36

RESULT 4

AAU43195
 ID AAU43195 standard; Protein; 118 AA.

AC AAU43195;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #4091.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 XX dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

XX (COR1-) CORIXA CORP.

PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI: 2001-616774/71.

XX N-PSDB; AAS59520.

PS Example 1; SEQ ID NO 4390; 1069bp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 118 AA;

Query Match 42.9%; Score 51.5; DB 22; Length 118;
 Best Local Similarity 71.4%; Pred. No. 3.5;

Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 NGCMYEG-PLLEPR 15
 |||||
 Db 74 NGCMYHGHPLLEPR 87

RESULT 5

ABP33553
 ID ABP33553 standard; Protein; 132 AA.

AC ABP33553;

DT 09-JUL-2002 (first entry)

DE Human ORF2526 protein, SEQ ID NO:5052.

XX Human; ORF; open reading frame; ORF; drug screening; diagnosis;
 XX disease monitoring; cytokine; cell proliferation; cell differentiation;
 XX immune modulation; haematopoiesis regulation; tissue growth;
 XX angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 XX behaviour; cancer; proliferative disorder; neurological disorder;
 XX cardiovascular disease; immune system disorder; organ transplantation;
 XX tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 XX hypothyroidism; cholesterol ester storage disease; infection; vulvar;
 XX vasotrophic; antipsoriatic; antidiabetic; cytostatic; nocotropic;
 XX neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 XX cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 XX dermatological; analgesic; vitruide; antibacterial; fungicide.

OS Homo sapiens.

PN WO200190366-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US17076.

PR 24-MAY-2000; 2000US-206690P.

XX (CURA-) CURAGEN CORP.

PI Leach MD, Shinkete RA;

DR WPI: 2002-106200/14.

XX N-PSDB; ABN77579.

PS Novel human polypeptides and polynucleotides useful for diagnosing,
 CC preventing and treating cardiovascular disease, neurodegenerative,
 CC hyperproliferative disorders and disorders related to organ
 CC transplantation -
 CC Claim 10; Page 1516; 2508bp; English.

CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX proteins, antibodies
 CC polypeptides, methods of screening for modulators of ORFX expression and
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antifibrotic activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,

CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases.

SO Sequence 132 AA;

Query Match 42.5%; Score 51; DB 23; Length 132;
 Best Local Similarity 64.3%; Pred. No. 4.7;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 NSGMYGPILEPRP 16
 Db 24 NSGMYTPTSLCRP 37

RESULT 6
 AAU35179
 ID AAU35179 standard; Protein; 341 AA.

AC AAU35179;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis cellular proliferation protein #466.

KW Antisense; prokaryotic cellular proliferation protein;

OS antibiotic; antibacterial; drug design.

PN Enterococcus faecalis.

MO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US09180.

21-MAR-2000; 2000US-191078P.

23-MAY-2000; 2000US-206848P.

26-MAY-2000; 2000US-207727P.

23-OCT-2000; 2000US-242578P.

27-NOV-2000; 2000US-253625P.

22-DEC-2000; 2000US-257931P.

16-FEB-2001; 2001US-269308P.

(ELIT-) ELITRA PHARM INC.

Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;

Yamamoto RT, Xu HH;

WPI; 2001-611495/70.

N-PSDB; AAS53038.

New polynucleotides for the identification and development of

antibiotics, comprise sequences of antisense nucleic acids -

Example 3; Seq ID No 10772; 511pp; English.

CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 341 AA;

Query Match 41.7%; Score 50; DB 22; Length 341;
 Best Local Similarity 40.0%; Pred. No. 20;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 2 ONGMYGPILEPRPADI 21
 Db 27 KDGQWVGPILEPRPQKEV 46

RESULT 7
 ABP57025
 ID ABP57025 standard; protein; 348 AA.

AC ABP57025;

DT 10-APR-2003 (first entry)

DE Enterococcus faecalis D-Ala-D-Ala ligase enzyme SEQ ID NO:31.

KW D-Ala-D-Ala ligase; enzyme; bacterial; structure-based drug design;

OS protein co-ordinate data; D-Ala-D-Ala ligase inhibitor; antibacterial.

PN Enterococcus faecalis.

MO2003002063-A2.

09-JAN-2003.

28-JUN-2002; 2002WO-US20465.

28-JUN-2001; 2001US-301676P.

(ESSE-) ESSENTIAL THERAPEUTICS INC.

(PLIV) PLIVA DD ZAGREB.

Navia MA, Ala PJ, Griffith JP, Ali JA, Faerman CH, Moe ST;

Magee AS, Connelly PR, Perola E;

WPI; 2003-201458/19.

Evaluating association potential of chemical entity to complex having

binding pocket defined by structural coordinates, by employing

computational unit for entity-pocket fitting operation and analyzing

the results -

Example 8; Fig 10; 115pp; English.

The present invention describes a method (M1) of evaluating the potential

of a chemical entity (CE) to associate with a molecule or molecular

complex comprising a binding pocket (BP) defined by specific structural

coordinates (SC) of D-Ala-D-Ala ligase (II) E. coli amino acids Lys144,

Glu180, Lys181, Leu183, Glu187, Asp257 and Glu270, by employing a

computational unit to perform a fitting operation between CE and BP

defined by SC and analysing the results of the fitting operation to

CC (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes,
CC atopic dermatitis). Sequences ABG9888-ABG9989 and ABU0010-ABU0433
CC represent human polypeptides of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied by the
CC European Patent Office.

XX Sequence 549 AA;

Query Match 40.8%; Score 49; DB 24; Length 549;

Best Local Similarity 47.6%; Pred. No. 48;

Matches 10; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 QONG--GWYEGPILPPEDAL 19
DB 515 EGTGAQOWLSGPTLSPYEDIL 535

RESULT 10

AA49897 ID AA49897 standard; Protein; 993 AA.

XX AA49897;

DT 27-JAN-2000 (first entry)

DE Rat TAO2 kinase.

XX

KW TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation;

KW p38; protein kinase; cancer; inflammation; autoimmune disease;

KW degeneration; insulin-resistant diabetes; metabolic disorder;

KW neurodegeneration; MAP kinase; MAP/ERK kinase.

OS Rattus sp.

XX WO9953076-A1.

XX 21-OCT-1999.

XX 14-APR-1999; 99WO-US08165.

XX 14-APR-1998; 98US-0060410.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Cobb M, Hutchison M, Chen Z, Berman K;

XX WPI; 1999-633831/54.

DR N-PSDB; AA232436.

PT New polypeptides that phosphorylate kinase, used to screen for

PT modulators for treating e.g. cancer or inflammation

XX Claim 7; Page 84-87; 95pp; English.

XX The present sequence represents rat TAO2 protein kinase, which is capable
CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related
CC polypeptides, are used to screen for modulators of stress-responsive
CC mitogen activated protein (MAP) kinase pathways. These modulators are
CC potentially useful for treating or preventing: (1) inflammation,
CC autoimmune disease, cancer and degeneration (inhibitors of
CC phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders
CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are
CC also used to raise specific antibodies, useful therapeutically as
CC modulators and as immunoassay reagents for detecting TAO kinases.
CC TAO kinase polynucleotides can be used: (a) for recombinant expression
CC of TAO kinases; and (b) in the form of fragments, for detecting TAO
CC kinase polynucleotides in standard hybridisation and amplification
XX tests. TAO kinases are highly specific for MEK3.

SQ Sequence 993 AA;

Query Match 40.0%; Score 48; DB 20; Length 993;

Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 GWYEGPILPPEDAL 17
DB 888 GWYEGPILPPEDAL 900

RESULT 11

AAU23343

ID AAU23343 standard; Protein; 172 AA.

XX AAU23343;

DT 18-DEC-2001 (first entry)

DE Novel human enzyme polypeptide #429.

XX

KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;

KW ligase; hyperproliferative disorder; immunodeficiency disorder;

KW autoimmune disorder; neurological disorder; metabolic disorder;

KW inflammatory disorder; cardiovascular disorder; reproductive disorder;

KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;

KW nephrotropic; anticoagulant.

XX

OS Homo sapiens.

XX WO20015301-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01239.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 15-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205155.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 14-AUG-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.

	PR	05-SEP-2000;	2000US-0229509.
	PR	05-SEP-2000;	2000US-0229513.
	PR	06-SEP-2000;	2000US-0230437.
	PR	06-SEP-2000;	2000US-0230438.
	PR	08-SEP-2000;	2000US-0231242.
	PR	08-SEP-2000;	2000US-0231243.
	PR	08-SEP-2000;	2000US-0231244.
	PR	08-SEP-2000;	2000US-0231413.
	PR	08-SEP-2000;	2000US-0231414.
	PR	08-SEP-2000;	2000US-0232080.
	PR	12-SEP-2000;	2000US-0232081.
	PR	14-SEP-2000;	2000US-0232397.
	PR	14-SEP-2000;	2000US-0232398.
	PR	14-SEP-2000;	2000US-0232399.
	PR	14-SEP-2000;	2000US-0232400.
	PR	14-SEP-2000;	2000US-0233063.
	PR	14-SEP-2000;	2000US-0233064.
	PR	14-SEP-2000;	2000US-0233065.
	PR	21-SEP-2000;	2000US-0234423.
	PR	21-SEP-2000;	2000US-0234424.
	PR	25-SEP-2000;	2000US-0234977.
	PR	25-SEP-2000;	2000US-0234998.
	PR	26-SEP-2000;	2000US-0235484.
	PR	27-SEP-2000;	2000US-0235834.
	PR	27-SEP-2000;	2000US-0235836.
	PR	29-SEP-2000;	2000US-0236327.
	PR	29-SEP-2000;	2000US-0236367.
	PR	29-SEP-2000;	2000US-0236368.
	PR	29-SEP-2000;	2000US-0236369.
	PR	29-SEP-2000;	2000US-0236370.
	PR	02-OCT-2000;	2000US-0237037.
	PR	02-OCT-2000;	2000US-0237038.
	PR	02-OCT-2000;	2000US-0237039.
	PR	02-OCT-2000;	2000US-0237040.
	PR	13-OCT-2000;	2000US-0239335.
	PR	13-OCT-2000;	2000US-0239337.
	PR	20-OCT-2000;	2000US-0240960.
	PR	20-OCT-2000;	2000US-0241221.
	PR	20-OCT-2000;	2000US-0241785.
	PR	20-OCT-2000;	2000US-0241786.
	PR	20-OCT-2000;	2000US-0241787.
	PR	20-OCT-2000;	2000US-0241808.
	PR	20-OCT-2000;	2000US-0241809.
	PR	20-OCT-2000;	2000US-0241826.
	PR	01-NOV-2000;	2000US-0246617.
	PR	08-NOV-2000;	2000US-0246477.
	PR	08-NOV-2000;	2000US-0246475.
	PR	08-NOV-2000;	2000US-0246476.
	PR	08-NOV-2000;	2000US-0246477.
	PR	08-NOV-2000;	2000US-0246523.
	PR	08-NOV-2000;	2000US-0246527.
	PR	08-NOV-2000;	2000US-0246528.
	PR	08-NOV-2000;	2000US-0246532.
	PR	08-NOV-2000;	2000US-0246609.
	PR	08-NOV-2000;	2000US-0246610.
	PR	08-NOV-2000;	2000US-0246611.
	PR	17-NOV-2000;	2000US-0249207.
	PR	17-NOV-2000;	2000US-0249208.
	PR	17-NOV-2000;	2000US-0249209.
	PR	17-NOV-2000;	2000US-0249210.
	PR	17-NOV-2000;	2000US-0249211.
	PR	17-NOV-2000;	2000US-0249212.
	PR	17-NOV-2000;	2000US-0249213.
	PR	17-NOV-2000;	2000US-0249214.
	PR	17-NOV-2000;	2000US-0249215.
	PR	17-NOV-2000;	2000US-0249216.
	PR	17-NOV-2000;	2000US-0249217.
	PR	17-NOV-2000;	2000US-0249218.
	PR	17-NOV-2000;	2000US-0249244.
	PR	17-NOV-2000;	2000US-0249245.
	PR	17-NOV-2000;	2000US-0249264.
	PR	17-NOV-2000;	2000US-0249265.
	PR	17-NOV-2000;	2000US-0249297.
	PR	17-NOV-2000;	2000US-0249299.
	PR	17-NOV-2000;	2000US-0249300.
	PR	01-DEC-2000;	2000US-0250160.
	PR	01-DEC-2000;	2000US-0250391.
	PR	05-DEC-2000;	2000US-0251030.
	PR	05-DEC-2000;	2000US-0251988.
	PR	05-DEC-2000;	2000US-0251989.
	PR	06-DEC-2000;	2000US-0251979.
	PR	06-DEC-2000;	2000US-0251986.
	PR	08-DEC-2000;	2000US-0251856.
	PR	08-DEC-2000;	2000US-0251868.
	PR	08-DEC-2000;	2000US-0251869.
	PR	08-DEC-2000;	2000US-0251899.
	PR	11-	


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AC  ABG24835;
XX
DT  18-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #24826.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US08631.
XX
PR  31-MAR-2000; 2000US-0540217.
XX  23-AUG-2000; 2000US-0649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
XX  N-PSDB; AAS89022.
XX
DR  N-PSDB; AAS89022.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits and to assess
XX  biodiversity -
XX
PS  Claim 20; SEQ ID No 55194; 103bp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and
XX  polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX  and gene mapping, and in recombinant production of (II). The
XX  polynucleotides are also used in diagnostics as expressed sequence tags
XX  for identifying expressed genes. (I) is useful in gene therapy techniques
XX  to restore normal activity of (II) or to treat disease states involving
XX  (II). (II) is useful for generating antibodies against it, detecting or
XX  quantitating a polypeptide in tissue, as molecular weight markers and as
XX  a food supplement. (II) and its binding partners are useful in medical
XX  imaging of sites expressing (II). (I) and (II) are useful for treating
XX  disorders involving aberrant protein expression or biological activity.
XX  The polypeptide and polynucleotide sequences have applications in
XX  diagnostics, forensics, gene mapping, identification of mutations in
XX  and to produce other types of data and products dependent on DNA and
XX  amino acid sequences. ABG00010-ABG30377 represent novel human
XX  diagnostic amino acid sequences of the invention.
XX  Note: The sequence data for this patent did not appear in the printed
XX  specification, but was obtained in electronic format directly from WIPO
XX  at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 564 AA;
XX
Query Match 39.2%; Score 47; DB 22; Length 564;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 6 WYEGPLEPPDALDI 21
Db 163 WYEAIVLAPQPEPLPL 178

```

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RESULT 13
ID  ABG24833 standard; Protein; 816 AA.
XX
AC  ABG24833;
XX
DT  13-FEB-2002 (first entry)
XX

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DT  18-FEB-2002 (first entry)
XX
DE  Novel human diagnostic protein #24824.
XX
KW  Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX  food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200175067-A2.
XX
PD  11-OCT-2001.
XX
PF  30-MAR-2001; 2001WO-US08631.
XX
PR  31-MAR-2000; 2000US-0540217.
XX  23-AUG-2000; 2000US-0649167.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Drmanac RT, Liu C, Tang YT;
XX
DR  WPI; 2001-639362/73.
XX  N-PSDB; AAS89020.
XX
DR  N-PSDB; AAS89020.
XX
PT  New isolated polynucleotide and encoded polypeptides, useful in
XX  diagnostics, forensics, gene mapping, identification of mutations
XX  responsible for genetic disorders or other traits and to assess
XX  biodiversity -
XX
PS  Claim 20; SEQ ID No 55192; 103bp; English.
XX
CC  The invention relates to isolated polynucleotide (I) and
XX  polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX  and gene mapping, and in recombinant production of (II). The
XX  polynucleotides are also used in diagnostics as expressed sequence tags
XX  for identifying expressed genes. (I) is useful in gene therapy techniques
XX  to restore normal activity of (II) or to treat disease states involving
XX  (II). (II) is useful for generating antibodies against it, detecting or
XX  quantitating a polypeptide in tissue, as molecular weight markers and as
XX  a food supplement. (II) and its binding partners are useful in medical
XX  imaging of sites expressing (II). (I) and (II) are useful for treating
XX  disorders involving aberrant protein expression or biological activity.
XX  The polypeptide and polynucleotide sequences have applications in
XX  diagnostics, forensics, gene mapping, identification of mutations in
XX  and to produce other types of data and products dependent on DNA and
XX  amino acid sequences. ABG00010-ABG30377 represent novel human
XX  diagnostic amino acid sequences of the invention.
XX  Note: The sequence data for this patent did not appear in the printed
XX  specification, but was obtained in electronic format directly from WIPO
XX  at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 816 AA;
XX
Query Match 39.2%; Score 47; DB 22; Length 816;
Best Local Similarity 43.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 6 WYEGPLEPPDALDI 21
Db 97 WYEAIVLAPQPEPLPL 112

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RESULT 14
ID  ABG04046 standard; Protein; 858 AA.
XX
AC  ABG04046;
XX
DT  13-FEB-2002 (first entry)
XX

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Novel human diagnostic protein #25819.

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6 WYEGPLEPPRALDI 21
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91 WYEAVALPQPETPL 106

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Job time : 7.83882 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 4.50366 Seconds
(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120
Sequence: 1 QONGGWYEGPLLEPPDALDI 21

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.5	42.1	1427	12 US-10-369-493-3841	Sequence 3841, Ap
2	50	41.7	1421	9 US-09-815-242-10772	Sequence 10772, A
3	50	41.7	348	15 US-10-186-886-31	Sequence 30, Appl
4	50	41.7	358	15 US-10-186-886-30	Sequence 30, Appl
5	50	41.7	555	15 US-10-156-761-8003	Sequence 8003, Ap
6	47.5	39.6	451	12 US-10-369-493-20793	Sequence 20793, A
7	47	39.2	362	12 US-10-369-493-748	Sequence 748, App
8	46	39.2	4150	11 US-09-808-880-2	Sequence 2, Appl1
9	46	38.3	355	11 US-10-203-708-44	Sequence 44, Appl1
10	45	37.5	163	15 US-10-156-761-11806	Sequence 11806, A
11	44.5	37.1	76	9 US-09-815-242-11403	Sequence 11403, A
12	44	36.7	358	15 US-10-186-886-29	Sequence 29, Appl
13	44	36.7	492	15 US-10-369-493-22963	Sequence 22963, A
14	44	36.7	583	12 US-10-156-761-12356	Sequence 12356, A
15	43.5	36.2	515	12 US-10-369-493-16825	Sequence 16825, A

16	43	35.8	35	11 US-09-983-802-409	Sequence 409, App
17	43	35.8	74	9 US-09-917-340-71	Sequence 71, Appl
18	43	35.8	82	15 US-10-106-698-5387	Sequence 5387, Ap
19	43	35.8	88	11 US-09-764-891-3296	Sequence 3296, Ap
20	43	35.8	318	12 US-10-369-493-1856	Sequence 1856, Ap
21	43	35.8	425	12 US-10-320-769-7	Sequence 7, Appl1
22	43	35.8	526	10 US-09-738-626-6454	Sequence 6454, Ap
23	43	35.8	862	8 US-08-556-422-2	Sequence 2, Appl1
24	43	35.8	862	12 US-10-261-049-2	Sequence 2, Appl1
25	43	35.8	862	12 US-10-320-769-2	Sequence 2, Appl1
26	42.5	35.4	57	11 US-09-355-815-3	Sequence 3, Appl1
27	42.5	35.4	89	12 US-10-340-578-22	Sequence 22, Appl
28	42.5	35.4	231	15 US-10-156-761-12903	Sequence 12903, A
29	42.5	35.4	742	12 US-10-297-022-15	Sequence 15, Appl
30	42.5	35.4	752	12 US-10-297-022-20	Sequence 20, Appl
31	42	35.0	33	9 US-09-864-761-39151	Sequence 39151, A
32	42	35.0	48	9 US-09-864-761-42742	Sequence 42742, A
33	42	35.0	172	15 US-10-101-482-16	Sequence 16, Appl
34	42	35.0	210	10 US-09-738-626-4654	Sequence 4654, Ap
35	42	35.0	238	10 US-09-738-626-5311	Sequence 5311, Ap
36	42	35.0	295	10 US-09-965-529-31	Sequence 31, Appl
37	42	35.0	295	11 US-09-969-680A-31	Sequence 31, Appl
38	42	35.0	324	10 US-09-816-095-4	Sequence 4, Appl1
39	42	35.0	419	9 US-09-741-669-415	Sequence 415, App
40	42	35.0	419	12 US-10-369-493-23477	Sequence 23477, A
41	42	35.0	436	15 US-10-081-872-40	Sequence 40, Appl
42	42	35.0	590	14 US-10-042-417-52	Sequence 52, Appl
43	42	35.0	888	9 US-09-826-752-6	Sequence 6, Appl1
44	42	35.0	985	15 US-10-205-823-76	Sequence 76, Appl
45	42	35.0	985	15 US-10-177-293-94	Sequence 94, Appl

ALIGNMENTS

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RESULT 1
US-10-369-493-3841
; Sequence 3841, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3841
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3841

Query Match      42.1%  Score 50.5;  DB 12;  Length 1427;
Best Local Similarity 58.8%  Pred. No. 1.2e+02;
Matches 10;  Conservative 1;  Mismatches 5;  Indels 1;  Gaps 1;

QY      1 QONGGWYEGPLLEPPD 17
DB      1099 QONGGWYEGPLLEPPD 1114

RESULT 2
US-09-815-242-10772
; Sequence 10772, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
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; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10772
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10772

Query Match
Best Local Similarity 41.7%; Score 50; DB 9; Length 341;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QNGWYEGPLERPPDALDI 21
Db 27 KDGQWVGPLSERPQNKV 46

RESULT 3
US-10-186-886-31
; Sequence 31, Application US/10186886
; Publication No. US20030119061A1
; GENERAL INFORMATION:
; APPLICANT: Navia, Manuel A.
; APPLICANT: Ala, Paul J.
; APPLICANT: Griffith, James P.
; APPLICANT: All, Janid A.
; APPLICANT: Faerman, Carlos H.
; APPLICANT: Magee, Andrew S.
; APPLICANT: Moe, Scott T.
; APPLICANT: Connolly, Patrick R.
; APPLICANT: Perola, Emanuele
; TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
; TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 10283-014001
; CURRENT APPLICATION NUMBER: US/10/186,886
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/301,676
; PRIOR FILING DATE: 2001-06-28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-186-886-31
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Query Match
Best Local Similarity 41.7%; Score 50; DB 15; Length 348;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QNGWYEGPLERPPDALDI 21
Db 42 KDGQWVGPLSERPQNKV 61
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RESULT 4
US-10-186-886-30
; Sequence 30, Application US/10186886
; Publication No. US20030119061A1
; GENERAL INFORMATION:
; APPLICANT: Navia, Manuel A.
; APPLICANT: Ala, Paul J.
; APPLICANT: Griffith, James P.
; APPLICANT: All, Janid A.
; APPLICANT: Faerman, Carlos H.
; APPLICANT: Magee, Andrew S.
; APPLICANT: Moe, Scott T.
; APPLICANT: Connolly, Patrick R.
; APPLICANT: Perola, Emanuele
; TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
; TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 10283-014001
; CURRENT APPLICATION NUMBER: US/10/186,886
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/301,676
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-186-886-30

Query Match
Best Local Similarity 41.7%; Score 50; DB 15; Length 358;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QNGWYEGPLERPPDALDI 21
Db 42 KEGQWVGPLTERPKSKDV 61
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RESULT 5
US-10-156-761-8003
; Sequence 8003, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAMIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8003
; LENGTH: 555
; TYPE: PRT
US-10-156-761-8003
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ORGANISM: Streptomyces avermitilis
US-10-156-761-8003

Query Match 41.7%; Score 50; DB 15; Length 555;
Best Local Similarity 58.3%; Pred. No. 56;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QONGWEGPPL 12
DB 434 QERGWHRGPVL 445

RESULT 6
US-10-369-493-20793

Sequence 20793, Application US/10369493
Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20793

LENGTH: 451

TYPE: PRT

ORGANISM: Rhodopseudomonas palustris

US-10-369-493-20793

Query Match 39.6%; Score 47.5; DB 12; Length 451;
Best Local Similarity 40.0%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

QY 4 GGMWEG-----PLLEPPDALDI 21
DB 74 GGYEGFANSALWLPALHSRDLIRV 98

RESULT 7
US-10-369-493-748

Sequence 748, Application US/10369493
Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 748

LENGTH: 362

TYPE: PRT

ORGANISM: Escherichia coli

US-10-369-493-748

Query Match 39.2%; Score 47; DB 12; Length 362;
Best Local Similarity 43.8%; Pred. No. 98;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 WYEGPPLPPDALDI 21
DB 178 WYEAVALPQPELPL 193

RESULT 8
US-09-808-880-2

Sequence 2, Application US/09808880
Publication No. US20030027287A1

GENERAL INFORMATION:

APPLICANT: Betlach, Mary C.

APPLICANT: Shah, Sanjay Krishnakant

APPLICANT: McDaniel, Robert

APPLICANT: Tang, Li

TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REFERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/808,880

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: US/09/428,517

PRIOR FILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: 60/120,254

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/106,100

PRIOR FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 2

LENGTH: 4150

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Recombinant

OTHER INFORMATION: Oleandolide PKS

US-09-808-880-2

Query Match 39.2%; Score 47; DB 11; Length 4150;
Best Local Similarity 56.2%; Pred. No. 1.1e+03;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 QONGWEGPPLPPRD 17
DB 2583 QNRGMDLGRLYDPDPD 2598

RESULT 9
US-10-203-708-44

Sequence 44, Application US/10203708
Publication No. US20030149238A1

GENERAL INFORMATION:

APPLICANT: SMITHKLINE BEECHAM CORPORATION

APPLICANT: SMITHKLINE BEECHAM P.L.C.

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP50013

CURRENT APPLICATION NUMBER: US/10/203,708

PRIOR FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: PCT/US01/04703

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,172

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 60/186,084

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 44

LENGTH: 355

TYPE: PRT

ORGANISM: Homo sapiens

US-10-203-708-44

Query Match 38.3%; Score 46; DB 12; Length 355;
Best Local Similarity 45.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 2.13241 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 1 QONGWEGEPLEPPALDI 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6CTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6CFTUS.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	41.7	348	1	US-08-454-196-8 Sequence 8, Appli
2	50	41.7	348	1	US-08-454-196-17 Sequence 17, Appli
3	50	41.7	348	3	US-09-064-033-8 Sequence 8, Appli
4	50	41.7	348	3	US-09-064-033-17 Sequence 17, Appli
5	50	41.7	348	4	US-09-291-046-8 Sequence 8, Appli
6	50	41.7	348	4	US-09-291-046-17 Sequence 17, Appli
7	50	41.7	370	4	US-09-107-532A-5920 Sequence 5920, Ap
8	48	40.0	993	3	US-09-060-410-4 Sequence 4, Appli
9	48	40.0	993	4	US-09-723-458-4 Sequence 4, Appli
10	47	39.2	4150	3	US-09-428-517-2 Sequence 2, Appli
11	46	38.3	605	4	US-09-252-991A-11355 Sequence 11355, A
12	45	37.1	76	4	US-09-732-210-1438 Sequence 1438, Ap
13	44	36.7	396	4	US-09-252-991A-20263 Sequence 20263, A
14	43	35.8	35	4	US-09-227-357-409 Sequence 409, App
15	43	35.8	825	4	US-08-556-422A-7 Sequence 7, Appli
16	43	35.8	825	4	US-08-556-422A-2 Sequence 2, Appli
17	42.5	35.4	316	4	US-09-252-991A-22518 Sequence 22518, A
18	42.5	35.4	540	3	US-08-688-988-43 Sequence 43, Appli
19	42.5	35.4	791	4	US-09-252-991A-23201 Sequence 23201, A
20	42.5	35.4	1290	1	US-08-138-641-2 Sequence 2, Appli
21	42.5	35.4	1290	1	US-08-138-641-2 Sequence 2, Appli
22	42	35.0	153	4	US-09-252-991A-30437 Sequence 30437, A
23	42	35.0	172	1	US-08-471-058-16 Sequence 16, Appli
24	42	35.0	172	1	US-08-471-058-16 Sequence 16, Appli
25	42	35.0	172	3	US-08-471-057-16 Sequence 3, Appli
26	42	35.0	172	3	US-09-113-789-3 Sequence 3, Appli
27	42	35.0	172	4	US-08-470-865-16 Sequence 16, Appli

28	42	35.0	432	4	US-09-252-991A-21794 Sequence 21794, A
29	42	35.0	433	1	US-07-661-610C-2 Sequence 2, Appli
30	42	35.0	519	3	US-09-172-841-55 Sequence 55, Appli
31	42	35.0	519	4	US-08-951-621-55 Sequence 55, Appli
32	42	35.0	888	2	US-08-861-464-6 Sequence 6, Appli
33	42	35.0	888	2	US-08-396-001-6 Sequence 6, Appli
34	42	35.0	888	3	US-09-323-433A-6 Sequence 6, Appli
35	42	35.0	2710	2	US-08-568-459A-12 Sequence 12, Appli
36	42	35.0	2710	2	US-08-487-826B-12 Sequence 12, Appli
37	42	35.0	2710	4	US-09-210-288-12 Sequence 12, Appli
38	42	35.0	3060	2	US-08-487-826B-14 Sequence 14, Appli
39	41	34.2	16	1	US-08-248-819A-50 Sequence 50, Appli
40	41	34.2	16	1	US-08-798-897-42 Sequence 42, Appli
41	41	34.2	16	2	US-08-337-646A-68 Sequence 68, Appli
42	41	34.2	16	2	US-08-978-523-42 Sequence 42, Appli
43	41	34.2	16	3	US-08-927-326-68 Sequence 68, Appli
44	41	34.2	17	1	US-08-333-565-14 Sequence 14, Appli
45	41	34.2	17	2	US-08-661-479-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-454-196-8
Sequence 8, Application US/08454196
Patent No. 5770361
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUTKA-MALEN, SYLVIE
APPLICANT: EVERS, STEFAN
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,196
FILING DATE: 07-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/15671
FILING DATE: 18-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-O PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-454-196-8

Query Match 41.7%; Score 50; DB 1; Length 348;
Best Local Similarity 40.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYGPPLERPDALDI 21
Db 42 KDGQWVGPLSERPQNKVEV 61

RESULT 2

US-08-454-196-17
Sequence 17, Application US/08454196
Patent No. 570361
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUTKA-MALEN, SYLVIE
APPLICANT: EVERS, STEFAN
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,196
FILING DATE: 07-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/15671
FILING DATE: 18-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-O PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-196-17

Query Match 41.7%; Score 50; DB 1; Length 348;
Best Local Similarity 40.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYGPPLERPDALDI 21
Db 42 KDGQWVGPLSERPQNKVEV 61

RESULT 3
US-09-064-033-8

Sequence 8, Application US/09064033
Patent No. 6087106

GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUTKA-MALEN, SYLVIE
APPLICANT: EVERS, STEFAN
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,033
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-O PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-033-8

Query Match 41.7%; Score 50; DB 3; Length 348;
Best Local Similarity 40.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYGPPLERPDALDI 21
Db 42 KDGQWVGPLSERPQNKVEV 61

RESULT 4

US-09-064-033-17
Sequence 17, Application US/09064033
Patent No. 6087106
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUTKA-MALEN, SYLVIE
APPLICANT: EVERS, STEFAN
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,033
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-O PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-033-17

Query Match 41.7%; Score 50; DB 3; Length 348;
Best Local Similarity 40.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGGWEGPLLEPRPDALDI 21
DB 42 KDQGWKGPLSERPQKEV 61

RESULT 5
US-09-291-046-8
Sequence 8, Application US/09291046
Patent No. 6569622
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
DUTKA-MALEN, SYLVIE
EVERS, STEFAN
COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
RESISTANCE TO GLYCOPOLYMERIDES, PARTICULARLY IN GRAM-POSITIVE
BACTERIA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/291,046
FILING DATE: 14-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-O PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-291-046-8

Query Match 41.7%; Score 50; DB 4; Length 348;
Best Local Similarity 40.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGGWEGPLLEPRPDALDI 21
DB 42 KDQGWKGPLSERPQKEV 61

RESULT 6
US-09-291-046-17
Sequence 17, Application US/09291046
Patent No. 6569622
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
DUTKA-MALEN, SYLVIE
EVERS, STEFAN
COURVALIN, PATRICE
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE
RESISTANCE TO GLYCOPOLYMERIDES, PARTICULARLY IN GRAM-POSITIVE
BACTERIA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,046
FILING DATE: 14-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,196
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 93/08356
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-101-O PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-291-046-17

Query Match 41.7%; Score 50; DB 4; Length 348;
Best Local Similarity 40.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDALDI 21
DB 42 KDGQWVGPLLEPPKPKV 61

RESULT 7
US-09-107-532A-5920
Sequence 5920, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107.532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5920:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...370
SEQUENCE DESCRIPTION: SEQ ID NO: 5920:
US-09-107-532A-5920

Query Match 41.7%; Score 50; DB 4; Length 370;

Best Local Similarity 40.0%; Pred. No. 9.8;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDALDI 21
DB 54 KEGQWVGPLLEPPKPKV 73

RESULT 8
US-09-060-410-4
Sequence 4, Application US/09060410
Patent No. 6165461
GENERAL INFORMATION:
APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: 14-Apr-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-410-4

Query Match 40.0%; Score 48; DB 3; Length 993;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 GWYEGPLLEPPD 17
DB 888 GWQGVPLTPVPE 900

RESULT 9
US-09-723-458-4
Sequence 4, Application US/09723458
Patent No. 6586242
GENERAL INFORMATION:
APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

```

; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,458
; FILING DATE: 27-NO. 6586242-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-723-458-4

Query Match          40.0%; Score 48; DB 4; Length 993;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      5 GWYEGPLLEPRPD 17
Db      888 GWYGFVLTVPVE 900

RESULT 10
US-09-428-517-2
; Sequence 2, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Belilach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4150
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2

Query Match          39.2%; Score 47; DB 3; Length 4150;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
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Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      2 QNCGWYEGPLLEPRPD 17
Db      2583 QNRGMDLGRLYDBDPD 2598

RESULT 11
US-09-252-991A-31355
; Sequence 31355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31355
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31355

Query Match          38.3%; Score 46; DB 4; Length 605;
Best Local Similarity 52.6%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 QNCGWYEGPLLEPRPDAL 19
Db      340 QNVGAWYEIRPLDPLTDKL 358

RESULT 12
US-09-732-210-1438
; Sequence 1438, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mitcanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1438
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-732-210-1438

Query Match          37.1%; Score 44.5; DB 4; Length 76;
Best Local Similarity 36.0%; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY      1 QNCGW-----YEGPLLEPRPDALD 20
Db      27 RRDGMISIGYNNPLSEPKDIDKID 51

RESULT 13
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```
US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20263

Query Match
Best Local Similarity 36.7%; Score 44; DB 4; Length 396;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      5 GMYEGPLLEPPD 17
Db      96 GCEHPLSPRE 108

RESULT 14
US-09-227-357-409
; Sequence 409, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: US/09/227,357
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
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EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 409
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-409

Query Match
Best Local Similarity 35.8%; Score 43; DB 4; Length 35;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      2 QNGGWEGLLEPPD 16
Db      20 BGGGWPGRLEPPD 34

RESULT 15
US-08-556-422A-7
; Sequence 7, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: Hall, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vasileiki
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DPN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-7

Query Match      35.8%; Score 43; DB 4; Length 425;
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Best Local Similarity 45.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;
 Oy 1 QONGGM--YEGPILBPPDA 18
 | : | | | : | | |
 Db 180 QSHTKWRYNGFVFKRPDA 199

Search completed: December 30, 2003, 11:05:33
 Job time : 3.21575 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 2.20471 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-30

Sequence: 1 DGGGAGVEDVWSEGEPEYAMDV 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76: *
2: PIR1: *
3: PIR2: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	43.3	132	2	PH0954
2	56.5	42.2	131	2	S26792
3	53	39.6	1264	2	A36858
4	53	39.6	1896	2	B72175
5	53	39.6	1897	2	T28621
6	50.5	37.7	433	2	S26646
7	50	37.3	292	2	T26908
8	49.5	36.9	220	2	B64169
9	49	36.6	509	2	H87389
10	48.5	36.2	166	2	H96940
11	48	35.8	469	2	B70607
12	47.5	35.4	308	2	B47369
13	47.5	35.4	321	2	A47369
14	47.5	35.4	345	1	B41732
15	47.5	35.4	558	2	T40651
16	47	35.1	383	2	C96581
17	47	35.1	812	1	MMECOR
18	47	35.1	860	1	F86349
19	46.5	34.7	126	2	S44107
20	46.5	34.7	431	1	B69092
21	46.5	34.7	1307	2	T35944
22	46	34.3	136	2	A49047
23	46	34.3	248	2	T05080
24	46	34.3	344	2	AG3020
25	46	34.3	345	2	S75745
26	46	34.3	368	2	B98264
27	46	34.3	482	2	G71603
28	46	34.3	528	2	F64580
29	46	34.3	627	2	G88533

30	46	34.3	741	2	I48694	probable transcrip
31	46	34.3	826	1	T02753	S-receptor kinase
32	46	34.3	894	2	C86756	prophage p12 prote
33	45	33.6	172	1	MMVZTH	BamHI-ORF13 protei
34	45	33.6	276	2	G83304	chloroperoxidase P
35	45	33.6	276	2	UC4161	probable chloride
36	45	33.6	319	2	S54100	deacetylcephalop
37	45	33.6	449	2	AF0820	exodeoxyribonuclea
38	45	33.6	453	2	F71673	exodeoxyribonuclea
39	45	33.6	456	1	NCRC7	exonuclease VII 1a
40	45	33.6	456	2	C91050	exonuclease VII 1a
41	45	33.6	456	2	H85894	exonuclease VII 1a
42	45	33.6	457	2	B97828	hypothetical prote
43	45	33.6	459	2	AH0349	exodeoxyribonuclea
44	45	33.6	463	2	S29170	annexin VII - mous
45	45	33.6	528	2	F71931	outer membrane pro

ALIGNMENTS

RESULT 1

PH0954

Ig heavy chain V region (G6+ CUL-HEN) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0954

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0954

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-132 <MAR>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-50/Region: complementarity-determining 1

F:51-67/Region: complementarity-determining 2

F:68-98/Region: complementarity-determining 3

F:99-120/Region: complementarity-determining 3

Query Match Best Local Similarity 43.3%; Score 58; DB 2; Length 132;

Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Db 8 EDVWSGEYPE--YYAMDV 23

104 DDFWSGYVNNYYTGMDV 121

RESULT 2

S26792

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26792

R:Morfari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fan

A:Reference number: S26786; MUID:9211632; PMID:1730251

A:Accession: S26792

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <MOR>

A:Cross-references: EMBL:X61012; NID:932804; PIDN:CAA43346.1; PID:91335131

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.2%; Score 56.5; DB 2; Length 131;
 Best Local Similarity 56.5%; Pred. No. 0.92;
 Matches 13; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 1 DGGGAYEDVMSGEYPEYAMDV 23
 DB 99 DSRGYSYDFWMSG-YFYYYMDV 120

RESULT 3

A36858
 G2R protein - variola virus (strain India-1967)
 C/Species: variola virus

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
 C/Accession: A36858; S46886
 R:Blinov, V.M.
 submitted to GenBank, November 1992

A/Reference number: A36859
 A/Accession: A36858

A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-1264 <BLI>
 A/Cross-references: GB:X69198

A/Experimental source: strain India-1967, ssp. major, isolate Ind3
 R.Kolykhlov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chiznikov, V.E.; Frolo

submitted to the EMBL Data Library, April 1992
 A/Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P

A/Reference number: S46868
 A/Accession: S46886

A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-1264 <KOL>
 A/Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47538.1; PID:9516447

A/Experimental source: strain India-1967, isolate Ind3
 C/Supertfamily: variola virus protein G2R

Query Match 39.6%; Score 53; DB 2; Length 1264;
 Best Local Similarity 46.2%; Pred. No. 37;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVMSGEYPEY 18
 DB 927 SYEDIKSDMPDY 939

RESULT 4

D1SR protein - variola minor virus (strain Garcia-1966)
 C/Species: variola minor virus
 C/Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999

C/Accession: B72175
 R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safonov, P.F.; Maesung, R.F.; Lopar

submitted to GenBank, March 1998
 A/Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A/Reference number: A72150
 A/Accession: B72175

A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-1896 <SHC>
 A/Cross-references: GB:Y16780; NID:95830555; PIDN:CA854796.1; PID:el542752; PID:95830757

A/Experimental source: strain Garcia-1966
 C/Genetics:

A/Gene: D1SR

Query Match 39.6%; Score 53; DB 2; Length 1896;
 Best Local Similarity 46.2%; Pred. No. 58;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVMSGEYPEY 18
 DB 1559 SYEDIKSDMPDY 1571

RESULT 5

T28621
 hypothetical protein B22R - variola major virus

C/Species: variola major virus
 C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000

C/Accession: T28621
 R:Maesung, R.F.; Esposto, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aub

Nature 366, 748-751, 1993
 A/Title: Potential virulence determinants in terminal regions of variola smallpox viru

A/Reference number: Z20488; NUID:94088747; PMID:8264798
 A/Accession: T28621

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA

A/Residues: 1-1897 <MAS>
 A/Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60931.1; PID:9439100

A/Experimental source: strain Bangladesh 1975
 Query Match 39.6%; Score 53; DB 2; Length 1897;
 Best Local Similarity 46.2%; Pred. No. 58;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVMSGEYPEY 18
 DB 1560 SYEDIKSDMPDY 1572

RESULT 6

S26646
 transcription factor IIE - African clawed frog

C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C/Accession: S26646
 R:Ohkuma, Y.; Hashimoto, S.; Roeder, R.G.; Horikoshi, M.

Nucleic Acids Res. 20, 5838, 1992
 A/Title: Identification of two large subdomains in TFIIE-alpha on the basis of homology

A/Reference number: S26646; MUID:93087200; PMID:1454543
 A/Accession: S26646

A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-433 <OHK>
 A/Cross-references: EMBL:Z14131; NID:965130; PIDN:CAA78505.1; PID:965131

Query Match 37.7%; Score 50.5; DB 2; Length 433;
 Best Local Similarity 40.0%; Pred. No. 24;
 Matches 10; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

QY 2 GGGAYEDVMSGEYPEY---YAMDV 23
 DB 227 GASGTOKEWSSKGPSYEDLYTQDV 251

RESULT 7

T26908
 hypothetical protein Y45F10A.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C/Accession: T26908
 R:McMurray, A.

submitted to the EMBL Data Library, January 1998
 A/Reference number: Z20285
 A/Accession: T26908

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA

A/Residues: 1-292 <WIL>
 A/Cross-references: EMBL:AL021488; PIDN:CAA16365.1; GSPDB:GN00022; CESP:Y45F10A.1

A/Experimental source: clone Y45F10A
 C/Genetics:

A/Gene: CESP:Y45F10A.1
 A/Map position: 4

A/Introns: 228/2; 261/3
 C/Supertfamily: Caenorhabditis elegans hypothetical protein Y45F10A.1

Query Match 37.3%; Score 50; DB 2; Length 292;

```

CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2003-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0.
SEQ ID NO 325
LENGTH: 127
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-325
```

Query Match	73.8%	Score 524.5	DB 12	Length 127
Best Local Similarity	78.9%	Pred. No. 1.4e-42		
Matches 105	Conservative	6	Mismatches 15	Indels 7
				Gaps 3

QY 1 QVOLLQSAIEVKKPKGASMYVS CMAGGYPTSYDISEMVAQAQGGGLEMMGWISYSGTGY 60
 1 QVGLVSGAEVKKPKGASVAVSCKASGYPTTSYGISMVAQAQGGGLEMMGWISANGTNY 60
 Db 1 QVGLVSGAEVKKPKGASVAVSCKASGYPTTSYGISMVAQAQGGGLEMMGWISANGTNY 60
 QY 61 AAGCGGRTVMTTDTSTRTAYMELRSLRSBDTAVVYCCARDGGGCAIEDWMSGEY-PEYIAM 119
 Db 61 AAGLQGRVTMTTDTSTRTAYMELRSLRSBDTAVVYCCARD---HHYD--SSDYLYYYGGL 114

Qy	120	DVWGQCGT	132
Db	115	DVWGQCGT	127

RESULT 6
US-09-880-748-1674
; Sequence 1674, Application US/09880748
; Publication No. US2003005937A1

```

1 TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
2
3 FILE REFERENCE: P5523
4
5 CURRENT APPLICATION NUMBER: US/09/880,748
6
7 CURRENT FILING DATE: 2001-06-15
8
9 PRIOR APPLICATION NUMBER: 60/212,210
10
11 PRIOR FILING DATE: 2000-06-15
12
13 PRIOR APPLICATION NUMBER: 60/240,816
14
15 PRIOR FILING DATE: 2000-10-17
16
17 PRIOR APPLICATION NUMBER: 60/276,248
18
19 PRIOR FILING DATE: 2001-03-16
20
21 PRIOR APPLICATION NUMBER: 60/277,379
22
23 PRIOR FILING DATE: 2001-03-21
24
25 PRIOR APPLICATION NUMBER: 60/293,499
26
27 PRIOR FILING DATE: 2001-05-25
28
29 NUMBER OF SEQ ID NOS: 3239
30
31 SOFTWARE: PatentIn Ver. 2.0
32
33 SEQ ID NO 1674
34
35 LENGTH: 252
36
37 TYPE: PRT
38
39 ORGANISM: Homo sapiens
40
41 OS-09-880-748-1674

```

Query Match Similarity	73.7%;	Score 524;	DB 11;	Length 252;
Best Local Similarity	78.0%;	Pred.No. 3.2e-42;		
Matches 103; Conservative	7;	Mismatches 16;	Indels 6;	Gaps 2

```

Qy 1 QVQLLSAIEVKKKPGASMYVS CMAGYPTSDYDIEMWQAQGGGLEMMWGISYSGTDY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVQLQSGAEVRKRGASVAVSCKASGYPTFSYGISWVAQAGQGLEMMWGISYNDNTNY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 61 AAKFQGRVMTTDTSRRTAYMELRLSRDDTAVVYCAADGGGGAIEDWMSSEYERYAMD 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AAKLQGRVLTITDTSITAYMELRLSRDDTAVVYCAR-----GAYDILGTGYP--YGM 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 121 VMGGGTTTVVSS 132
   ||| ||| ||| |||
Db 115 VMGGGTLTVVSS 126
   ||| ||| ||| |||

```

RESULT 7

US-09-880-748-1921
; Sequence 1921, Application US/09880748
; Publication No. US20030059937A1

```

1  APPLICANT: Ruben et al.
2  TITLE OF INVENTION: Anticododies that Immunospecifically Bind Blys
3  FILE REFERENCE: PF523
4  CURRENT APPLICATION NUMBER: US/09/860,748

```

PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 3239
 SOFTWARE: PatentIn Ver. 2.0

```

; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1921

```

Query Match	73.6%	Score 523	DB 11	Length 251
Best Local Similarity	74.6%	Pred. No. 4e-42		
Matches 103	Conservative	5	Mismatches 14	Indels 16
				Gaps 2

[illegible]

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QY      115 EYYANDVWGQGTITVSS 132
          |||||:|||||||
Db      112 -YYGMDVWGRGTTVSS 128

```

RESULT 8
US-09-880-748-973
; Sequence 973, Application US/09880748
; Publication No. US20030059937A1

APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antidodies that Immunospecifically Bind Blyss
 FILE REFERENCE: P523
 CURRENT APPLICATION NUMBER: US/09/880,748

```

? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 60/240, 816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277, 379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293, 499
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3239
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 973
? LENGTH: 259
? TYPE: PRT
? ORGANISM: Homo sapiens
? OS-09-880-748-973

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Query Match	73.3%	Score 521.5	DB 11	Length 259
-------------	-------	-------------	-------	------------

Best Local Similarity 74.5%; Pred. No. 5.8e-42;
Matches 102; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

Qy 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQLEMMGMSISYSGNTDY 60
Db 1 QVOLLQSGAEVKKPGASVKSCKASGYFTSYGISWVRQAPGQLEMMGMSISYNGNTY 60
Qy 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 117
Db 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 116
Cy 118 --ANDVWGQGTMTVSS 132
Db 117 SDAFDIWGQGTMTVSS 133

RESULT 9

US-09-880-748-1777
Sequence 1777, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1777
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1777

Query Match 73.1%; Score 520; DB 11; Length 253;
Best Local Similarity 75.8%; Pred. No. 7.8e-42;
Matches 100; Conservative 12; Mismatches 18; Indels 2; Gaps 2;

Qy 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQLEMMGMSISYSGNTDY 60
Db 1 EVQLVQSGAEVKKPGASVKSCKASGYFTSYGISWVRQAPGQLEMMGMSISAYNGDTNY 60
Qy 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 120
Db 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 118
Qy 121 VMGQGTMTVSS 132
Db 119 VMGQGTMTVSS 130

RESULT 10

US-09-880-748-1778
Sequence 1778, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1778
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1778

Query Match 72.4%; Score 514.5; DB 11; Length 248;
Best Local Similarity 75.8%; Pred. No. 2.6e-41;
Matches 100; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

Qy 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQLEMMGMSISYSGNTDY 60
Db 1 QVOLLQSGAEVKKPGASVKSCKASGYFTSYGISWVRQAPGQLEMMGMSISAYNGNTY 60
Qy 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 120
Db 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 113
Qy 121 VMGQGTMTVSS 132
Db 114 VMGQGTMTVSS 125

RESULT 11

US-09-880-748-1610
Sequence 1610, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1610
LENGTH: 257
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1610

Query Match 72.4%; Score 514.5; DB 11; Length 257;
Best Local Similarity 77.0%; Pred. No. 2.7e-41;
Matches 104; Conservative 6; Mismatches 18; Indels 7; Gaps 3;

Qy 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQLEMMGMSISYSGNTDY 60
Db 1 QVOLLQSGAEVKKPGASVKSCKASGYFTSYGISWVRQAPGQLEMMGMSISAYNGNTY 60
Qy 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 117
Db 61 AOKFGQVMTTDTTSRTAYMELRSLSRSDTAAYVYCARDDGGGAYEDVMSGEYPEYAMD 116

QY 118 AMDWGGTIVTSS 132
| | | | |
Db 117 DMDWGGTIVTSS 131

RESULT 12

US-09-880-748-1425
; Sequence 1425, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1425
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1425

Query Match 72.2%; Score 513; DB 11; Length 249;
Best Local Similarity 76.9%; Pred. No. 3,6e-41;
Matches 103; Conservative 8; Mismatches 13; Indels 10; Gaps 4;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVQAQPGQGLEMMGWISYSGNTDY 60
| | | | |
Db 1 QVQLVSGAEVKKPKGASVAVSCASGYFTSYGISWVAQAPGQGLEMMGWISAYNGNTNY 60
QY 61 AOKFGQRYMTTDTSTRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWSGEPEY--A 118
| | | | |
Db 61 AOKLQGRVMTTDTSTSTAYMELSLRSDDTAVYYCAR---GGNT-DLTG---YIIGA 112
QY 119 MDWGGTIVTSS 132
| | | | |
Db 113 PDWGGTIVTSS 126

RESULT 13

US-09-880-748-1576
; Sequence 1576, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1576

; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1576

Query Match 72.1%; Score 512.5; DB 11; Length 257;
Best Local Similarity 75.9%; Pred. No. 4,1e-41;
Matches 101; Conservative 8; Mismatches 21; Indels 3; Gaps 2;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVQAQPGQGLEMMGWISYSGNTDY 60
| | | | |
Db 1 QVQLVSGAEVKKPKGASVAVSCASGYFTSYGISWVAQAPGQGLEMMGWISYNGNTNY 60
QY 61 AOKFGQRYMTTDTSTRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWSGEPEY--A 119
| | | | |
Db 61 POKLQGRVMTTDTSTSTAYMELSLRSDDTAVYYCAR--GRSLYDILGTGYARDYGM 118
QY 120 DWGGTIVTSS 132
| | | | |
Db 119 DMDGGTIVTSS 131

RESULT 14

US-09-880-748-1562
; Sequence 1562, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1562
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1562

Query Match 71.8%; Score 510.5; DB 11; Length 251;
Best Local Similarity 76.5%; Pred. No. 6,2e-41;
Matches 101; Conservative 7; Mismatches 17; Indels 7; Gaps 2;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVQAQPGQGLEMMGWISYSGNTDY 60
| | | | |
Db 1 QVQLVSGAEVKKPKGASVAVSCASGYFTSYGISWVAQAPGQGLEMMGWISAYNGNTNY 60
QY 61 AOKFGQRYMTTDTSTRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWSGEPEY--A 120
| | | | |
Db 61 AOKLQGRVMTTDTSTSTAYMELSLRSDDTAVYYCAR---MEYDILGTGYGYP--D 113
QY 121 VWGGTIVTSS 132
| | | | |
Db 114 YWGGTIVTSS 125

RESULT 15

US-09-880-748-1452
; Sequence 1452, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1452
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1452

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```

Query Match          71.8%; Score 510.5; DB 11; Length 259;
Best Local Similarity 73.9%; Pred. No. 6,4e-41;
Matches 99; Conservative 12; Mismatches 20; Indels 3; Gaps 2;

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QY      1 QVQLQSATEVKKPKGASKMKVSCMASGYPTSTYDISMVRQAPQGLEMMGWISISGNTDY 60
      1 QMQLVQSGAEVKKPKGASVYVSCKASGYFTFTNYGISWVRQAPQGLEMMGWISTYNGDTNY 60
Db      61 AQKPGQRYVTMTDTTSRRTAYMELRSLRSDDDTAIVYYCARDGGGAYEDVWSGEY--PEYYA 118
      61 AQKLGQRYVTMTDTTSTRTAYMELRSLRSDDDTAIVYYCARDGASNY-DILTGYVAPAQGVA 119
QY      119 MDVWGQGTIVTVSS 132
      120 FDIWGRGTLTVTVSS 133
Db

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Search completed: December 30, 2003, 11:45:22
 Job time : 28.3087 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 30, 2003, 10:47:45 ; Search time 13.4037 Seconds

(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711

Sequence: 1 QVQLQSGATEVKRPGASMKV.....YPERYAMDVWGQTTVTSS 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	68.2	120	4	US-09-025-769B-36 Sequence 36, Appl
2	485	68.2	120	4	US-09-025-769B-59 Sequence 59, Appl
3	484.5	68.1	117	4	US-09-025-769B-52 Sequence 22, Appl
4	478.5	67.3	121	1	US-08-264-093-3 Sequence 3, Appl
5	476.5	67.0	129	2	US-08-561-521-45 Sequence 45, Appl
6	476.5	67.0	129	4	US-08-525-539A-77 Sequence 77, Appl
7	476.5	67.0	129	5	PCT-US95-01219-45 Sequence 45, Appl
8	476	66.9	128	1	US-08-202-047-22 Sequence 22, Appl
9	476	66.9	128	3	US-08-964-690-22 Sequence 22, Appl
10	471.5	66.3	125	3	US-09-199-149-3 Sequence 3, Appl
11	464	65.3	120	2	US-08-652-816A-19 Sequence 19, Appl
12	452.5	63.6	139	3	US-08-933-983-21 Sequence 21, Appl
13	450	63.3	117	3	US-08-545-809A-105 Sequence 105, Appl
14	448	63.0	139	1	US-08-253-877C-19 Sequence 19, Appl
15	448	63.0	139	2	US-08-451-164A-19 Sequence 19, Appl
16	448	63.0	139	3	US-08-603-024-18 Sequence 18, Appl
17	448	63.0	139	4	US-08-450-809-14 Sequence 14, Appl
18	447	62.9	123	6	US-09-049-672A-13 Sequence 13, Appl
19	444	62.4	120	4	US-09-025-769B-35 Sequence 35, Appl
20	444	62.4	120	4	US-09-025-769B-57 Sequence 57, Appl
21	443.5	62.4	119	2	US-08-561-521-10 Sequence 10, Appl
22	443.5	62.4	119	5	PCT-US95-01219-10 Sequence 10, Appl
23	440.5	62.0	119	4	US-09-438-954-41 Sequence 41, Appl
24	440.5	62.0	146	1	US-08-276-852-155 Sequence 155, App
25	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
26	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
27	440.5	62.0	146	5	PCT-US95-08743-155 Sequence 155, App

28	438	61.6	116	2	US-08-561-521-41 Sequence 41, Appl
29	438	61.6	116	5	PCT-US95-01219-41 Sequence 41, Appl
30	438	61.6	135	1	US-08-137-117D-102 Sequence 102, App
31	438	61.6	135	2	US-08-436-717-102 Sequence 107, App
32	436.5	61.4	119	1	US-08-300-386A-65 Sequence 65, Appl
33	436.5	61.4	119	3	US-08-931-645-65 Sequence 65, Appl
34	436.5	61.4	119	5	PCT-US95-11235-65 Sequence 65, Appl
35	435.5	61.3	119	2	US-08-561-521-12 Sequence 12, Appl
36	435.5	61.3	119	5	PCT-US95-01219-12 Sequence 12, Appl
37	434.5	61.1	123	1	US-08-477-877B-94 Sequence 94, Appl
38	434.5	61.1	123	2	US-08-472-281A-94 Sequence 94, Appl
39	434.5	61.1	123	2	US-08-477-989B-94 Sequence 94, Appl
40	433.5	61.0	140	3	US-08-836-561-63 Sequence 63, Appl
41	433.5	61.0	140	4	US-09-434-122-63 Sequence 63, Appl
42	433	60.9	135	1	US-08-137-117D-100 Sequence 100, App
43	433	60.9	135	2	US-08-436-717-100 Sequence 100, App
44	432	60.8	135	1	US-08-137-117D-112 Sequence 112, App
45	432	60.8	135	2	US-08-436-717-112 Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-025-769B-36
Sequence 36, Application US/09025769B
Parent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Illeg, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36
Query Match 68.2%; Score 485; DB 4; Length 120;
Best Local Similarity 72.7%; Pred. No. 5.3e-39;
Matches 96; Conservative 7; Mismatches 17; Indels 12; Gaps 1;

[illegible]

```

Db          109 YWGQGLTVTVSS 120

RESULT 3
US-09-025-769B-22
Sequence 22, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-22

Query Match      68.1%; Score 484.5; DB 4; Length 117;
Best Local Similarity 72.7%; Pred. No. 5.7e-39;
Matches 96; Conservative 5; Mismatches 16; Indels 15; Gaps 1,

QY      1 QVOLIQSATEYVKKPKGASKVGSCMASGYFTSYDYSWTRQAQGQGLEMMGWISISGNTRYD 60
DB      1 QVLIQSGAEYKKPKPASKVSKASGYFTSYMHMWVAQAGQGLEMMGWIMPSNGNTNY 60
QY      61 AOKFGGRVTMTDTTDRRTATYAMELRSLRSDPTAVVYCARDDGGGAVEDVMGSGBEPXYAMD 120
DB      61 AOKFGGRVTMRDTSISTATIELSLRSDDTAIVYICARDGDG-----FD 105
QY      121 VMGGCTTVTVSS 132
DB      106 YWGQGLTVTVSS 117

RESULT 4
US-08-264-093-3
Sequence 3, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
```

APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-3

Query Match 67.3%; Score 478.5; DB 1; Length 121;
Best Local Similarity 72.0%; Pred. No. 2,2e-38;
Matches 95; Conservative 11; Mismatches 15; Indels 11; Gaps 3;

QY 1 QVQLQSGATEYVKKPGKASVKSCMASGYPTSTYDISWVRQAPQGLGEMNGWISISYSGNTDY 60
DB 1 QVQLVQSGAEYVKKPGASVYVSCKASGYFTFTYGLSWVRQAPQGLGEMNGWISAHNGTNS 60
QY 61 AOKFQGRVYMTTDTSRRTAYMELRSLRSDDTAVYYCARQGGGAYEDVWSGEYPEYYAM 120
DB 61 AOKFQGRVYMTTDTSRRTAYMELRSLRSDDTAVYYCARVGG-----VW--DLNLYF--D 109
QY 121 VMGGQITVTVSS 132
DB 110 YMGQITLVTVSS 121

RESULT 5
US-08-561-521-45
Sequence 45, Application US/08561521
Patent No. 5640299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-45

Query Match 67.0%; Score 476.5; DB 2; Length 129;
Best Local Similarity 71.4%; Pred. No. 3,7e-38;
Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

QY 1 QVQLQSGATEYVKKPGKASVKSCMASGYPTSTYDISWVRQAPQGLGEMNGWISISYSGNTD 59
DB 1 QVQLVQSGAEYVKKPGASVYVSCKASGYFTFTYGLSWVRQAPQGLGEMNGWISAHNGTNS 60
QY 60 YAKQFQGRVYMTTDTSRRTAYMELRSLRSDDTAVYYCARQGGGAYEDVWSGEYPEYYAM 119
DB 61 YAKQFQGRVYMTTDTSRRTAYMELRSLRSDDTAVYYCARARVGGGCGYRND---YXF 116
QY 120 DVMGQITVTVSS 132
DB 117 DVMGQITLVTVSS 129

RESULT 6
US-08-525-539A-77
Sequence 77, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERTANT, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: M63 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-77

Query Match 67.0%; Score 476.5; DB 4; Length 129;
Best Local Similarity 71.4%; Pred. No. 3,7e-38;
Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

QY 1 QVQLQSATVKKPKGASMKVSCMASGYPTFTSYDISWVRQAPQGLEMGMHISLY-SGNTD 59
DB 1 QVQLVQSGAEVKKPKGASVSKASGYFTSYAISWVRQAPQGLEMGMHINPYGNDTN 60

QY 60 YAKPFGGRVTMTDTSRRTAYMELRSRSDPTAVYVCARDGGGAYEDVMSGEYPERVYAM 119
DB 61 YAKPFGGRVTITADTSTAYMELSLRSEDTAVYCARAPGSGGCGCTRGD---YXF 116

QY 120 DWNGQGTIVTVSS 132
DB 117 DWNGQGTIVTVSS 129

RESULT 7
PCT-US95-01219-45
Sequence 45, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-45

Query Match 67.0%; Score 476.5; DB 5; Length 129;
Best Local Similarity 71.4%; Pred. No. 3,7e-38;
Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

QY 1 QVQLQSATVKKPKGASMKVSCMASGYPTFTSYDISWVRQAPQGLEMGMHISLY-SGNTD 59
DB 1 QVQLVQSGAEVKKPKGASVSKASGYFTSYAISWVRQAPQGLEMGMHINPYGNDTN 60

QY 60 YAKPFGGRVTMTDTSRRTAYMELRSRSDPTAVYVCARDGGGAYEDVMSGEYPERVYAM 119
DB 61 YAKPFGGRVTITADTSTAYMELSLRSEDTAVYCARAPGSGGCGCTRGD---YXF 116

QY 120 DWNGQGTIVTVSS 132
DB 117 DWNGQGTIVTVSS 129

RESULT 8
US-08-202-047-22
Sequence 22, Application US/08202047
Patent No. 5800815
GENERAL INFORMATION:
APPLICANT: CHESNOT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_I
US-08-202-047-22

RESULT 9
 US-08-964-690-22
 Sequence 22, Application US/08964690
 Patent No. 6033667
 GENERAL INFORMATION:
 APPLICANT: CHESNUT, Robert W.
 APPLICANT: POLEY, Margaret J.
 APPLICANT: PAULSON, James C.
 APPLICANT: JONES, S. Tarran
 APPLICANT: SALDANHA, Jose W.
 APPLICANT: BENDIG, Mary M.
 TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

Query Match	66.3%	Score 476;	DB 3;	Length 128;
Best Local Similarity	71.4%;	Pred. No. 4.1e-38;		
Matches 95;	Conservative 11;	Mismatches 21;	Indels 6;	Gaps 2

RESULT 10
 US-09-199-149-3
 : Sequence No, Application US/09199149
 : Patent No. 6160099
 : GENERAL INFORMATION:
 : APPLICANT: Jonak, Zdenka L.
 : APPLICANT: Taylor, Alexander H.
 : APPLICANT: Trull Jr., Stephen H.
 : APPLICANT: Johanson, Kyung O.
 : TITLE OF INVENTION: Humanized Monoclonal Antibodies
 : FILE REFERENCE: P50860
 : CURRENT APPLICATION NUMBER: US/09/159,149
 : CURRENT FILING DATE: 1998-11-24
 : NUMBER OF SEQ ID NOS: 37
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 3
 : :
 : LENGTH: 125
 : :
 : TYPE: PRT
 : :
 : ORGANISM: Kabat VH subgroup I
 : US-09-199-149-3

Query Match	66.3%	Score 471.5;	DB 3;	Length 125;
Best Local Similarity	71.1%	Pred. No. 1.1e-37;		
Matches	96;	Conservative 8;	Mismatches 18;	Indels 13; Gaps 3
QY	1 QVQLQSATTEVKKPGASMKVSCMASGYPFTSYDYSWROAPGGGLEMMGHISISYCNTRY			
	1 QVQLVQSGAEVKKPKQASVKYSCKASGTTFTSYAISWROAPGGGLEMMGHIN-PCGDTNYY			
QY	61 AOKFGGRVYTMDDTSRRATVWELSLRSDDTAVYYCARDG---GGGAYEDVMSGEVPEY			
Db	60 AOKFGGRVITADTSTSTAVWELSLRSEDTAVYYCARPEYIGGGCY-----GYW			
QY	118 AMDVWGSGTITVSS	132		
Db	111 YWGIVGSGTITVSS	125		

RESULT 11
US-08-652-816A-19
Sequence 19, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Oshourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JC
TITLE OF INVENTION: Specific binding members, materials and
METHODS OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David M. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-19

Query Match
Best Local Similarity 65.3%; Score 464; DB 2; Length 120;
Matches 94; Conservative 5; Mismatches 21; Indels 12; Gaps 2;

QY 1 QVQLQSGATEVYKKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTDY 60
DB 1 QVTLQSGAEVYKKGASVYKISCKASGYFTYVGNWVRQAPGQGLEWMGINIKSGEPY 80
QY 61 AQKFGQRYVTMTDTSRTAYMELRSLSDDTAVYYCARDDGGGAYEDVWSGEYPERYAMD 120
DB 60 AQKFGQRYVTMTDTSRTAYMELRSLSDDTAVYYCARDDGGGAYEDVWSGEYPERYAMD 120
QY 121 VMGGGTVTVSS 132
DB 109 VMGGGTVTVSS 120

RESULT 12
US-08-933-983-21
Sequence 21, Application US/08933983
Patent No. 6114506
GENERAL INFORMATION:
APPLICANT: REED, GUY L.
APPLICANT: HARRIS, LINDA
APPLICANT: BATORATH, JURGEN
APPLICANT: MATSUEDA, GARY
APPLICANT: HSU, MEI-YIN
APPLICANT: NOVOTNY, JIRI
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
```

```

STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,983
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,356
FILING DATE: 20-SEP-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.4320002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-933-983-21

Query Match
Best Local Similarity 63.6%; Score 452.5; DB 3; Length 139;
Matches 86; Conservative 14; Mismatches 19; Indels 13; Gaps 2;

QY 1 QVQLQSGATEVYKKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTDY 60
DB 21 QVTLQSGAEVYKKGASVYKISCKASGYFTYVGNWVRQAPGQGLEWMGINIKSGEPY 80
QY 61 AQKFGQRYVTMTDTSRTAYMELRSLSDDTAVYYCARDDGGGAYEDVWSGEYPERYAMD 120
DB 81 AEEFGKRTFTLDTSTAYLIELRSLSDTAVYFCAR-----W---VPGTYAMD 127
QY 121 VMGGGTVTVSS 132
DB 128 VMGGGTVTVSS 139

RESULT 13
US-08-545-809A-105
Sequence 105, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
```


APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/Jp93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-105

Query Match 63.3%; Score 450; DB 3; Length 117;
Best Local Similarity 86.7%; Pred. No. 1,1e-35;
Matches 85; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTSTYDISWVROAPGQGLEMMGMIISYSGNTDY 60
DB 20 QIOLVQSGAEVKKPGASVKVSCKASGYTFSTYDISWVROAPGQGLEMMGMIISYSGNTDY 79
QY 61 AOKFGQRYVTMTDTSRTATYMLSLRSDPTAVYYCAR 98
DB 80 AOKLQGRVTMTDTSRTATYMLSLRSDPTAVYYCAR 117

RESULT 14
US-08-253-877C-19
Sequence 19, Application US/08253877C
Patent No. 5773001
GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Halleck, William
APPLICANT: Tesou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-19

Query Match 63.0%; Score 448; DB 1; Length 139;
Best Local Similarity 65.2%; Pred. No. 2e-35;
Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTSTYDISWVROAPGQGLEMMGMIISYSGNTDY 60
DB 20 QIOLVQSGAEVKKPGASVKVSCKASGYTFSTYDISWVROAPGQGLEMMGMIISYSGNTDY 79
QY 61 AOKFGQRYVTMTDTSRTATYMLSLRSDPTAVYYCARDDGGGAYEDVWGSGEYEVYAMD 120
DB 80 NEKRGKRYVTMTDTSRTATYMLSLRSDPTAVYYCARDDGGGAYEDVWGSGEYEVYAMD 127
QY 121 VMGGQTVTVSS 132
DB 128 YMGQGLTVTVSS 139

RESULT 15
US-08-452-164A-19
Sequence 19, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Halleck, William
APPLICANT: Tesou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-19

Query Match 63.0%; Score 448; DB 2; Length 139;

Best Local Similarity 65.2%; Pred. No. 2e-35; Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

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QY      1 QVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMGISITSGNTDY 60
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      20 QIQLVQSGAEVKKPGSSVKVSCKASGYFTDYINMROAPGQGLEWGMIDPGSGNTKY 79
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      61 AQKFGQRYMTTDTSRRTAYMELRSLRSDDTAVYCGARDGGGAYEDVWSGEYPEYYAMD 120
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      80 NEKFKGRVTITVDTSNTAYMELSLRSEDTAFYFCARE-----KTTYYYAMD 127
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      121 VMGGGTTVTVSS 132
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      128 YMGQGTLTVTSS 139
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

Search completed: December 30, 2003, 11:05:31
Job time : 13.4871 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 (Search time 9.3939 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-27
Perfect score: 521
Sequence: 1 QVOLLQSAIEVKKKGASMKV.....AYMELRLSRSDPTAVYYCAR 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	87.5	98	2	S26919 Ig heavy chain V r
2	453	86.9	129	2	S36260 Ig heavy chain V r
3	451	86.6	122	2	S36271 Ig heavy chain V r
4	450	86.4	124	2	S19665 Ig heavy chain V r
5	432	82.9	131	2	S21924 Ig heavy chain V r
6	428	82.1	160	2	PI0105 anti-PR2 erythrocy
7	420	80.6	111	2	S21925 Ig heavy chain V r
8	407	78.1	98	2	S26918 Ig heavy chain V r
9	407	78.1	117	2	S18553 Ig heavy chain V r
10	407	78.1	136	2	S31600 Ig heavy chain V r
11	405	77.7	125	2	S68170 Ig heavy chain V r
12	401	77.0	98	2	S26938 Ig heavy chain V r
13	401	77.0	117	2	S31680 Ig heavy chain V r
14	401	77.0	117	2	S18551 Ig heavy chain V r
15	401	77.0	135	2	S49530 anti-5m antibody V
16	400	76.8	118	2	S36265 Ig heavy chain V r
17	397	76.2	104	2	S69899 Ig heavy chain V r
18	397	76.2	127	2	S34014 Ig heavy chain V r
19	393	75.4	98	2	S26912 Ig heavy chain V r
20	393	75.4	129	2	S46393 Ig heavy chain V r
21	391	75.0	117	2	S18552 Ig heavy chain V r
22	390	74.9	132	2	S31596 Ig heavy chain V r
23	389	74.7	110	2	PH1670 Ig heavy chain V r
24	389	74.7	123	2	D33548 Ig heavy chain V-1
25	388	74.5	98	2	S26920 Ig heavy chain V r
26	387	74.3	117	2	PT0371 Ig gamma chain pre
27	383	73.5	117	1	HVHUNG Ig heavy chain pre
28	383	73.5	148	2	S29257 Ig heavy chain V r
29	382	73.3	114	2	PH1667 Ig heavy chain V r

30	382	73.3	118	2	PH1666 Ig heavy chain V r
31	381	73.1	142	2	A32483 Ig heavy chain V r
32	380	72.9	171	2	S23623 Ig heavy chain V r
33	379	72.7	98	2	PH0871 Ig heavy chain V r
34	378	72.6	119	2	PH0295 Ig heavy chain V-D
35	377	72.4	116	2	S31667 Ig heavy chain V r
36	377	72.4	117	1	HVHJ35 Ig heavy chain pre
37	377	72.4	120	2	S31999 Ig heavy chain V r
38	377	72.4	135	2	B32374 Ig heavy chain pre
39	376	72.2	126	2	I44151 Ig heavy chain V r
40	372	71.4	98	2	S24680 Ig heavy chain V1
41	370	71.0	98	2	S26921 Ig heavy chain V r
42	369	70.8	104	2	PH1665 Ig heavy chain V r
43	369	70.8	109	2	PH1668 Ig heavy chain V r
44	367	70.4	98	2	S26915 Ig heavy chain V r
45	367	70.4	116	2	S31698 Ig heavy chain pre

ALIGNMENTS

RESULT 1

S26919 Ig heavy chain V region (DP-14) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S26919

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A/Reference number: S26885; MID:93021117; PMID:1404388

A/Accession: S26919

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 456; DB 2; Length 98;

Best Local Similarity 87.8%; Pred. No. 1.7e-39;

Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVOLLQSAIEVKKKGASMKVSCASGYPTSYISVVRQAPGGLGEMVGHISVNGNTNY 60

Db 1 QVOLLQSAIEVKKKGASMKVSCASGYPTSYISVVRQAPGGLGEMVGHISVNGNTNY 60

Qy 61 AOKFGQRTVTMTDTSRTAYMELRLSRSDPTAVYYCAR 98

Db 61 AOKFGQRTVTMTDTSRTAYMELRLSRSDPTAVYYCAR 98

RESULT 2

S36260 Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C/Accession: S36260

R/Giffiths, A.D.; Malngvict, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MID:93178448; PMID:7679990

A/Accession: S36260

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-129 <GR1>

A/Cross-references: EMBL:218651; NID:g33124; PIRN:CAA79303.1; PIR:9339903

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 453; DB 2; Length 129;

Db 20 QVQLV¹ASGAEV²YKPKASV³KVSCAKSG⁴YTF⁵TSY⁶SI⁷SWRQ⁸APGGL⁹ELM¹⁰GM¹¹ISV¹²ND¹³TNY¹⁴ 79

QY 61 AQRFG¹RV²MT³TD⁴TS⁵RR⁶TA⁷YME⁸LR⁹SL¹⁰RSDD¹¹TA¹²YY¹³CA¹⁴R 98

Db 80 AQNLG¹RV²MT³TD⁴TS⁵RR⁶TA⁷YME⁸LR⁹SL¹⁰RSDD¹¹TA¹²YY¹³CA¹⁴R 117

RESULT 7

ig heavy chain V region - human
 A:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 R:Friedman, D.F.
 Submitted to the EMBL Data Library, July 1991
 A:Reference number: S21923
 A:Accession: S21925
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-111 <PRT>
 A:Cross-references: EMBL:X6503; NID:g33626; PIDN:CAA43023.1; PID:g33627
 C:Genetics:
 A:Insertions: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match	Score	DB 2;	Length
80.6%;	420;		111;
Best Local Similarity	87.0%;		
Best Local Similarity	87.0%;		

Query Match	80.6%	Score 420;	DB 2;	Length 111;
Best Local Similarity	87.0%;	Pred. No. 9, 1e-36;		
Matches	80;	Conservative	4;	Mismatches 8;
				Indels 0;
				Gaps 0

[illegible]

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QY      61 A Q E F G R V T M T D T S R K T A Y M E L S L R S D D T A 92
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      80 A Q K L G R V T M T D T S T A Y M E L S L R S D D T A 111

```

RESULT 8

19 heavy chain V region (DP-15) - human (fragment)
 C.Species: Homo sapiens (man)
 C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C.Accession: S26918
 R.Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A.Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
 A.Reference number: S26885; MUID:93021117; PMID:1404388
 A.Accession: S26918
 A.Status: Preliminary
 A.Molecule type: DNA
 A.Residues: 1-98 <TOM>
 A.Cross-references: EMBL:Z12317; NID:G32857; PIDN:CAA78187.1; PID:q32858
 C.Superfamily: immunoglobulin V region; immunoglobulin homology
 C.Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	78.14	Score 407;	DB 2;	Length 98;
Best Local Similarity	78.64	Pred. No. 1.7e-34;		
Matches 77; Conservative	9;	Mismatches 12.	Indels 0.	Cuts 0

QY 1 QVOLLGSAATEVKKFKGASMKVSCMASGYPFTSYDII SWRQAPGGGLEWIGISAINGNTHY 60

Db 1 QVQLVSGGAELVKKPKGASVKSCKASGTYFTSYDII NWKQATGGLGELMGMNPNNSNTIY 60

61 AOKFOGRVMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
 ||||| : ||||| : |||||
 Db 61 AOKFOGRVMTTRNTSISTAYMELSLRSEDYAVYYCAR 98

RESULT 5

S18553
 Ig heavy chain V region precursor (VI-3b) - human (fragment)
 C.Species: Homo sapiens (man)
 C.Date: 13-Jan-1995 #sequence _revision 06-Jun-1997 #text _change 23-Jul-1999
 C.Accession: S18553: 526016
 R.Shin R.V. Marudá P. Virelizier M. Virelizier

EXBO J. 10, 3641-3645, 1991
A>Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: (A)Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18553

A/Status: translation not shown
A/Molecule type: DNA

A/Cross-references: EMBL:X62109
P.Tomlinson T W M J L

A:Title: The reproductive behavior of human cawling worm
J. Mol. Biol. 277, 776-798, 1992

A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26916

A;Molecule type: DNA
A;Residues: 20-117 <

Cross-References: EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID:g32872
C:Genetics:
Abstracts: 16/
Abstracts: 16/

C:Keywords: bet

F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (Vr-2b) #status predicted

P;34-117/Domain: immunoglobulin homology <IMM>

Query Match	Score 407;	DB 2;	Length 117;
Best Local Similarity	78.1%;	Pred. No. 2e-34;	
Water	78.6%;		

Matches	100	Conservative	8	Mismatches	13	Indels	0	Gaps	0
---------	-----	--------------	---	------------	----	--------	---	------	---

Db

20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGRLERMGWINAGNNTKY 79

61 AAGTGGATGTTTIDTSRRATAMELSSLRSDDTAVYYCAR 98
: ||||| : || ||||| ||||| : |||||
80 SQKFGKRVITITDTSASTAYMELSSLRSEDTAVYYCAR 117

RESULT 10

Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31600
R/Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL data library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31600
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1136 <GUI>
A/Cross-references: EMBL:214165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IRM>

Query Match	78.1%;	Score 407;	DB 2;	Length 136;
Best Local Similarity	78.6%;	Pred. No. 2.4e-34;		
Matches	77;	Conservative	9;	Mismatches 12;
				Indels 0;
				Cons 0;

27 L QVQLTQSLATELKKKPGASMKVSGCMASGYPFTSYDISWRQAPGQGLEWVGWISAYNGNTTHY 600
 ||||:| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
 Db 20 QVQLVSGAEVKKKPGASVKVCSRASGTYFTSYDINWYQATGGGLEWVGMMNPNNSGNTGY 79

```
QY      61 A Q F Q G R V T M T T D T S R R T A Y M E L R S L R S D D T A V Y Y C A R      98
      |||||
      ||||| : || ||||| ||||| : |||||
Db      80 A Q F Q G R V T M T R N T S I S T A Y M E L S L R S E D T A V Y Y C A R      117
```


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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 5.25426 Seconds
(without alignments) 877.119 Million cell updates/sec

Title: US-09-674-752-27
Perfect score: 521
Sequence: 1 QVQLQSGATEVKKPKGASMKV.....AYNELRLRSDDTAIVYCAR 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	73.5	117	1	HV1B_HUMAN
2	377	72.4	117	1	HV1G_HUMAN
3	359	68.9	147	1	HV1C_HUMAN
4	340	65.3	117	1	HV52_MOUSE
5	331	63.5	117	1	HV1A_HUMAN
6	326	62.6	114	1	HV00_MOUSE
7	326	62.6	117	1	HV14_MOUSE
8	326	62.6	120	1	HV03_MOUSE
9	325	62.4	117	1	HV04_MOUSE
10	324	62.2	140	1	HV02_MOUSE
11	319	61.2	117	1	HV09_MOUSE
12	315	60.5	118	1	HV51_MOUSE
13	314	60.3	117	1	HV06_MOUSE
14	314	60.3	120	1	HV50_MOUSE
15	313	60.1	117	1	HV05_MOUSE
16	313	60.1	117	1	HV12_MOUSE
17	313	60.1	117	1	HV07_MOUSE
18	307	58.9	139	1	HV13_MOUSE
19	300	57.6	136	1	HV15_MOUSE
20	298	57.2	117	1	HV3C_HUMAN
21	297	57.0	117	1	HV10_MOUSE
22	297	57.0	117	1	HV11_MOUSE
23	295	56.6	117	1	HV19_MOUSE
24	294	56.4	138	1	HV48_MOUSE
25	292	56.0	121	1	HV3J_HUMAN
26	290	55.7	125	1	HV1F_HUMAN
27	289	55.5	117	1	HV5E_MOUSE
28	284	54.5	119	1	HV3I_HUMAN
29	282	54.1	121	1	HV01_MOUSE
30	275.5	52.9	120	1	HV1H_HUMAN
31	274	52.6	119	1	HV3P_HUMAN
32	274	52.6	122	1	HV3G_HUMAN
33	272	52.2	136	1	HV1E_MOUSE

34	270	51.8	122	1	HV3A_HUMAN
35	270	51.8	122	1	HV3H_HUMAN
36	269	51.6	114	1	HV3B_HUMAN
37	268	51.4	119	1	HV3M_HUMAN
38	266	51.1	117	1	HV54_MOUSE
39	265.5	51.0	97	1	HV5E_MOUSE
40	265.5	51.0	116	1	HV05_CARAU
41	265	50.9	119	1	HV3L_HUMAN
42	264	50.7	126	1	HV3K_HUMAN
43	263.5	50.6	117	1	HV02_CARAU
44	263	50.5	117	1	HV03_CARAU
45	261.5	50.2	115	1	HV3F_HUMAN

ALIGNMENTS

RESULT 1

HV1B_HUMAN STANDARD; PRT; 117 AA.
ID HV1B_HUMAN
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region Hg3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144026; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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DR EMBL; J08240; AAA52988.1; -
DR PIR; A02024; HVH0HG.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V-I REGION Hg3.
FT NON_TER 117 IG-LIKE.
SQ SEQUENCE 117 AA; 12946 MW; 20DF92FC60CD1FE7 CRC64;

Query Match 73.5%; Score 393; DB 1; Length 117;
Best Local Similarity 75.5%; Pred. No. 1e-37;
Matches 74; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLQSGATEVKKPKGASMKVSPFYSYDTSWTRAPGGLGVNMGMSAYNGTTHY 60
DB 20 QVQLVQSGAEVKKRQASGVKSCKASGTTFSYHAWVRQAPGGGLEWVGIIINSGGSTSY 79

QY 61 AOKFOGRVTMTDTSRTAYMELRSLRSDDTAVYYCAR 98
 Db 80 AOKFOGRVTMTDTSRTAYMELRSLRSDDTAVYYCAR 117

RESULT 2
 HV1G_HUMAN STANDARD; PRT; 117 AA.
 ID P21083;
 AC 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=8296408; PubMed=2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,
 Ohno H., Fukushima S., Honjo T.,
 RT "Dispersed localization of D segments in the human immunoglobulin
 heavy-chain locus."
 RL EMBO J. 7:1047-1051 (1988).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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 CC
 DR EMBL, X07448; -; NOT_ANNOTATED_CDS.
 DR PIR, S00476; HVH035.
 DR HSSP: P01772; 2F84.
 DR GO, GO:0005576; C:extracellular; NAS.
 DR GO, GO:0003823; F:antigen binding activity; NAS.
 DR GO, GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-1-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
 FT DOMAIN 20 >117 IG-1-like.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 13009 MW; BE6ICE63F8CE97BD CRC64;

Query Match 72.4%; Score 377; DB 1; Length 117;
 Best Local Similarity 74.5%; Pred. No. 5,1e-37;
 Matches 73; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSAITEVKKKGASMKYSCMASGYPTFSYDISWTRQAPGGGLEWVGMIISAYNGNTHY 60
 Db 20 QVQLVQSGAEVKKRQASVKSCAKSGLTFGYYMHWVRQAPGGGLEWVGMIINPNSGCTNY 79

QY 61 AOKFOGRVTMTDTSRTAYMELRSLRSDDTAVYYCAR 98
 Db 80 AOKFOGRVTMTDTSRTAYMELRSLRSDDTAVYYCAR 117

RESULT 3
 HV1C_HUMAN STANDARD; PRT; 147 AA.
 ID P01744;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region ND precursor (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=83065234; PubMed=6815656;
 RA Kenten J.H., Moigard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.,
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).
 RN [12]
 RP SEQUENCE OF 20-147.
 RA Bennich H.H., Johanson S.G.O., von Bahr-Lindstrom H.,
 RL (In) Bach M.K. (ed.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN.
 CC
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC HSSP: P01789; 1MCP.
 DR GO, GO:0005576; C:extracellular; NAS.
 DR GO, GO:0003823; F:antigen binding activity; NAS.
 DR GO, GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-1-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
 FT DOMAIN 20 131 IG-LIKE
 FT MOD RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 41 115
 FT CONFLICT 21 21
 FT CONFLICT 53 54 T -> V (IN REF. 2).
 FT CONFLICT 67 68 IH -> HI (IN REF. 2).
 FT CONFLICT 125 125 VG -> GV (IN REF. 2).
 FT NON TER 147 147 MISSING (IN REF. 2).
 SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 68.9%; Score 359; DB 1; Length 147;
 Best Local Similarity 67.3%; Pred. No. 8.3e-35;
 Matches 66; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQSAITEVKKKGASMKYSCMASGYPTFSYDISWTRQAPGGGLEWVGMIISAYNGNTHY 60
 Db 20 QVQLVQSGAEVKKRQASVKSCAKSGLTFIDSYIHWIRQAGHGLEWVGMIINPNSGCTNY 79

QY 61 AOKFOGRVTMTDTSRTAYMELRSLRSDDTAVYYCAR 98
 Db 80 AOKFOGRVTMTDTSRTAYMELRSLRSDDTAVYYCAR 117

RESULT 4
 HV52_MOUSE STANDARD; PRT; 117 AA.
 ID P06327;
 AC 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region VH58 A1/A4 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=85099340; PubMed=2578321;
 RA Yancopoulos G.D., Alt F.W.;
 RT "Developmentally controlled and tissue-specific expression of
 RL unearanged VH gene segments."; Cell 40:271-281(1985).
 CC -----
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 CC -----
 DR EMBL: M13787; AAA3849.1; -
 DR PIR: A02029; HWSA1.
 DR HSSP: P01810; 2FB4.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
 FT DISULFID 41 115 FRAMEWORK-3.
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;
 Query Match 65.3%; Score 340; DB 1; Length 117;
 Best Local Similarity 62.2%; Pred. No. 1e-32;
 Matches 61; Conservative 17; Mismatches 20; Indels 0; Gaps 0;
 QY 1 QVQLQSGATEVKKPGKASMKVSCMASGYPTSTYDISWVRQAPQGLEWVGWISAYNGNTY 60
 DB 20 QVQLQSGPELVKPGALVKISCKASGYFTSYDINWVKRPGQGLEWIGWIRPGSGSTKY 79
 QY 61 AOKFGQGRVTMTTDSRTAYMELSLRSDDTAIVYCA 98
 DB 80 NEKFKGKATLTADKSSSTAYMOLSLTSNSAVYFCAR 117
 RESULT 5
 HVID_HUMAN STANDARD; PRT; 117 AA.
 ID P01742;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-1 region EU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=71064024; PubMed=5489771;
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RL acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; J.
 Biochemistry 9:3161-3170(1970).
 RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds";
 RL Biochemistry 9:3188-3196(1970).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
 CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
 CC -----
 DR PIR: A90563; GHUED.
 DR HSSP: P01772; 2FB4.
 DR GO: GO:0005576; Extracellular; NAS.
 DR GO: GO:0003823; Antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Pyrolydine carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12472 MW; 99D60ADABBD52818 CRC64;
 Query Match 63.5%; Score 331; DB 1; Length 117;
 Best Local Similarity 68.0%; Pred. No. 1.2e-31;
 Matches 66; Conservative 9; Mismatches 22; Indels 0; Gaps 0;
 QY 1 QVQLQSGATEVKKPGKASMKVSCMASGYPTSTYDISWVRQAPQGLEWVGWISAYNGNTY 60
 DB 1 QVQLQSGAEVKKPGSSSVKSCASGCTFSALTIWVRQAPQGLEWVGIVPMFCPPNY 60
 QY 61 AOKFGQGRVTMTTDSRTAYMELSLRSDDTAIVYCA 97
 DB 61 AOKFGQGRVTMTTDSRTAYMELSLRSDDTAIVYCA 97
 RESULT 6
 HVID_MOUSE STANDARD; PRT; 114 AA.
 ID P01741;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region (Anti-arsenate antibody).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=79195438; PubMed=109536;
 RA Capra J.D., Nisonoff A.;
 RT "Structural studies on induced antibodies with defined idiotypic
 RT specificities. VII. The complete amino acid sequence of the heavy
 RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
 RL mice bearing a cross-reactive idiotype."; J. Immunol. 123:279-284(1979).
 CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
 CC REGION SEQUENCE.
 CC -----
 DR PIR: A02022; GIMSAA.
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 106 IG-LIKE.
 FT NON_TER 114 114

SO SEQUENCE 114 AA; 12555 MW; 99DB8F0B6A69F4BE CRC64;

Query Match 62.6%; Score 326; DB 1; Length 114;
Best Local Similarity 63.9%; Pred. No. 4.4e-31;
Matches 62; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSGATEVKKPKGASMKVSCASGYPTSYDISVNRQAPQGLGEMVGMISAYNGNTHY 60
DB 1 EVQLQSGAEIVKAGSVKMSCKASGYTTSSTELVNRQAPQGLGLEDGISSSSAYPNY 60
QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 97
DB 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 97

RESULT 7
HIV4_MOUSE
ID HIV4_MOUSE STANDARD; PRT; 117 AA.

AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108a precursor.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE=81245215; Pubmed=6789211;
RA GIYOL D., Zakut R., Eifron K., Rechavi G., Ram D., Cohen J.B.;
RL Nature 292:426-430(1981).
-1- SIMILARITY: Contains 1 immunoglobulin-like gene."

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CC or send an email to license@sib-sib.ch).

DR EMBL; J00488; AAA38519.1; .

DR PIR; A02041; HVMS8A.

DR HSSP; P01810; ZFBJ.

DR MGD; MGI:96486; Igh-VJ558.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117

FT DOMAIN 20 >117

FT NON_TER 117 117

SO SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 62.6%; Score 326; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 4.5e-31;
Matches 59; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSGATEVKKPKGASMKVSCASGYPTSYDISVNRQAPQGLGEMVGMISAYNGNTHY 60
DB 20 EVQLQSGAEIVKAGSVKMSCKASGYTFTDYMHWKSHGKSLKEMIGIYIPYNGTGY 79

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 80 NOKFKSKATLTVDNSSSTAYMELSLTSEDSAVYCAR 117

RESULT 8
HIV3_MOUSE
ID HIV3_MOUSE STANDARD; PRT; 120 AA.

AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE=8131846; Pubmed=6186498;

RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,

RA Mathak-Rothstein A.;

RT "The genetic basis of antibody production: the dominant anti-arsenate

RT idotype response of the strain A mouse.";

RL Eur. J. Immunol. 12:1023-1032(1982).

CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER

CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J

CC SEGMENT. H2.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01789; IMCP.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Hybridoma.

FT DOMAIN 1 111

FT NON_TER 120 120

SO SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 62.6%; Score 326; DB 1; Length 120;
Best Local Similarity 60.8%; Pred. No. 4.6e-31;
Matches 59; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 2 VQLQSGATEVKKPKGASMKVSCASGYPTSYDISVNRQAPQGLGEMVGMISAYNGNTHY 61
DB 1 VQLQSGAEIVKAGSVKMSCKASGYTTSSTELVNRQAPQGLGLEDGISSSSAYPNY 60

QY 62 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

QY 61 AOKFGQGVMTTDTSTRAYMELRSLSRSDTAIVYCAR 98
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 DR PIR; A02030; HWM523.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;
 Query Match 62.4%; Score 325; DB 1; Length 117;
 Best Local Similarity 62.2%; Pred. No. 5.9e-31;
 Matches 61; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
 QY 1 QVQLQSGATEVKKKPGASMKVSCMASGYPTFSYDISWVROAPGGGLEWGMISAYNGNTY 60
 DB 20 QVQLQPGTELVKPGASVKLSCKASGYTFTSYMMHWKORPGGLEWIGINIPNGNGTNY 79
 QY 61 AOKFGQVMTTDTSRRTAYMELRLSRSDTAVYYCAR 98
 DB 80 NEKFKSKTTLVVDKSSSTAYTQLSLTSBDSAVYYCAR 117
 RESULT 10
 ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 93GT precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/7;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 RT immunoglobulin heavy chain.";
 RT Science 216:309-311(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 DR EMBL; J00493; AAA8128.1; -
 DR PIR; A94264; HWM5G7.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region; HyBridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93GT.
 FT DOMAIN 20 139 IG-LIKE.
 FT NON TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CB8E31DA5CE8 CRC64;
 Query Match 62.2%; Score 324; DB 1; Length 140;
 Best Local Similarity 59.2%; Pred. No. 9.5e-31;
 Matches 58; Conservative 20; Mismatches 20; Indels 0; Gaps 0;
 QY 1 QVQLQSGATEVKKKPGASMKVSCMASGYPTFSYDISWVROAPGGGLEWGMISAYNGNTY 60
 DB 20 EVQLQDSAGEELVRASSYVMSCKASGYTFTSYGINWVKORPGGLEWIGIINPGNGTNY 79
 QY 61 AOKFGQVMTTDTSRRTAYMELRLSRSDTAVYYCAR 98
 DB 80 NEKFKSKTTLVVDKSSSTAYTQLSLTSBDSAVYYCAR 117
 RESULT 11
 ID HV09_MOUSE STANDARD; PRT; 117 AA.
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 186-1 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botchwell A.L.M., Peakind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RT Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERM-LINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 CC PIR; D90809; HWM5G1.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A086CB17F5A CRC64;
 Query Match 60.2%; Score 319; DB 1; Length 117;
 Best Local Similarity 60.2%; Pred. No. 2.9e-30;
 Matches 59; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
 QY 1 QVQLQSGATEVKKKPGASMKVSCMASGYPTFSYDISWVROAPGGGLEWGMISAYNGNTY 60
 DB 20 QVQLQPGTELVKPGASVKLSCKASGYTFTSYMMHWKORPGGLEWIGINIPNGNGTNY 79
 QY 61 AOKFGQVMTTDTSRRTAYMELRLSRSDTAVYYCAR 98

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Db      :|||:|:|||||:|||||:|:|||||:|
          80 NEKFKGKATLTVDTSSSTAYMOLSHLTSSEDSAVYYCAR 117

RESULT 12
HV50_MOUSE STANDARD; PRT; 118 AA.
ID HV50_MOUSE
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN (1)
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match
Best Local Similarity 60.5%; Score 315; DB 1; Length 118;
Matches 58; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

Qy      1 QVQLQSGATEVKKPKGASMKVSCMASGYPTFSYDIISWVROAPGGGLEWGMISAYNGNTYIA 60
Db      1 EVQLQSGPELVKRGASVKISCKASGTFITDYIMNWVKSHGKSLWIGIDINNGATSY 60
Qy      61 AOKRQGRVMTTTSRTAYMELRSLRSDDTAVYYCAR 98
Db      61 NOKFKGKATLTVDKSSSATYMELRSLTSSEDSAVYYCAR 98

RESULT 13
HV06_MOUSE STANDARD; PRT; 117 AA.
ID HV06_MOUSE
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).

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CC      -1 MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR: A02032; HWS02.
DR HSSP: P01810; 2PBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 50 54 FRAMEWORK-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

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Query Match
Best Local Similarity 60.3%; Score 314; DB 1; Length 117;
Matches 59; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

Qy      2 VQLQLSGATEVKKPKGASMKVSCMASGYPTFSYDIISWVROAPGGGLEWGMISAYNGNTYIA 61
Db      21 VQLQPGALVLRGASVVKSCASGYTFTSYMMHWKRPQGGGLEWIGIRIHPSDDTYN 80
Qy      62 OKRQGRVMTTTSRTAYMELRSLRSDDTAVYYCAR 97
Db      81 OKRKGKATLTVDKSSSATYMELRSLTSSEDSAVYYCA 116

RESULT 14
HV50_MOUSE STANDARD; PRT; 120 AA.
ID HV50_MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN (1)
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR HSSP: P01810; 2PBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

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Query Match
Best Local Similarity 58.2%; Score 314; DB 1; Length 120;
Matches 57; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

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OY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGGLGIEWGWSAANGNTHY 60
Db 1 QVOLLQPGTELVRKPGASVNLSCKASGYFTFTSYMMHMIQRPGGGLGIEWGWSAANGNTHY 60
OY 61 AQKFGGRVMTTDTSRRTAYMEIPLRSLSDDTAAYVYCAR 98
Db 61 NEKFRSKATLTVDKSSSTAYVQLSTPTSEDSAVVYCAR 98

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OY 61 AQKFGGRVMTTDTSRRTAYMEIPLRSLSDDTAAYVYCAR 98
Db 80 NQKFKDKA LUTVDKSSSTAYVQLSTPTSEDSAVVYCAR 117

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Search completed: December 30, 2003, 10:55:49
Job time : 5.25426 secs

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RESULT 15
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981)
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
DR EMBL; J00536; AAA38605.1; -
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-V-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR KX Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 1 17
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 13016 MM; 427C861C53975EDC CRC64;

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Query Match 60.1%; Score 313; DB 1; Length 117;
Best Local Similarity 59.2%; Pred. No. 1.5e-29;
Matches 58; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

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OY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGGLGIEWGWSAANGNTHY 60
Db 20 QVOLLQPGTELVRKPGASVNLSCKASGYFTFTSYMMHMIQRPGGGLGIEWGWSAANGNTHY 79

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Db 1 EVOLVESGAEEVKKPGASVSKASGYTFTGYMAHWROAPGQGLEWGMWINSNGTNY 60
 QY 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98
 DB 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98

RESULT 2

Q9UL94 PRELIMINARY; PRT; 119 AA.

AC Q9UL94; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035020; AAD56258.1; -
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345FA16E CRC64;

Query Match 73.7%; Score 384; DB 4; Length 119;
 Best Local Similarity 73.5%; Pred. No. 8.9e-35;
 Matches 72; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWGMWINSNGTNY 60
 DB 1 EVOLVESGAEEVKKPGASVSKASGYTFTGYMAHWROAPGQGLEWGMWINSNGTNY 60
 QY 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98
 DB 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98

RESULT 3

Q9BRV0 PRELIMINARY; PRT; 500 AA.

AC Q9BRV0; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005951; AA05951.1; -
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig_1like.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 73.3%; Score 382; DB 4; Length 500;
 Best Local Similarity 72.4%; Pred. No. 8.2e-34;
 Matches 71; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWGMWINSNGTNY 60
 DB 20 QVQLVSGAEVMSPGASVSKASGYTFTGYMAHWROAPGQGLEWGMWINSNGTNY 79
 QY 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98
 DB 80 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 117

RESULT 4

Q9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF035022; AAD56258.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 124
 SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 72.6%; Score 378; DB 4; Length 124;
 Best Local Similarity 73.5%; Pred. No. 4.3e-34;
 Matches 72; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWGMWINSNGTNY 60
 DB 1 EVOLVESGAEEVKKPGASVSKASGYTFTGYMAHWROAPGQGLEWGMWINSNGTNY 60
 QY 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98
 DB 61 AOKFGGRVTMTTDSRTATYMLRSLSRSDDTAVYYCAR 98

RESULT 5

Q96GAG PRELIMINARY; PRT; 614 AA.

ID Q96GAG
 AC Q96GAG;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)


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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DB Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AA09851.1..
DR InterPro; IPR00005; HTHARC.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match
Best Local Similarity 71.2%; Score 371; DB 4; Length 614;
Matches 69; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFSYDISWROAPGQGLEWVGMISAYNGNTHY 60
Db 20 QVQLVSGAEVKKRQGSFVSVCKASGYTFTYLYKRWKRAQGLLEWGMITPRFGNINY 79

Qy 61 AOKFGQRYVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 80 AOKFQDRVTITDRSMNTAYMELSLRSEDYAVYYCAR 117

RESULT 6
Q960S0 PRELIMINARY; PRT; 159 AA.
ID Q960S0
AC Q960S0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RL mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AA082649.1..
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match
Best Local Similarity 69.4%; Score 363; DB 4; Length 159;
Matches 66; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFSYDISWROAPGQGLEWVGMISAYNGNTHY 60
Db 20 QVQLVSGAEVKKRQGSFVSVCKASGYTFTSNNYMNWVRAQPGQPEWGMVINSGGASARY 79

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Qy 61 AOKFGQRYVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 80 SQKFGRLTMTDTSRSTVYMQLSLRSDDTAVYYFCAR 117

RESULT 7
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
ID Q9GYZ2
AC Q9GYZ2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OK NCBI_TaxID=6182;
RN (1)
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.O., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAC01452.1..
DR HSPB; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

Query Match
Best Local Similarity 68.7%; Score 358; DB 5; Length 119;
Matches 67; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFSYDISWROAPGQGLEWVGMISAYNGNTHY 60
Db 1 QVQLVSGAEVKKRQGSFVSVCKASGYTFTGYNNWVRAQGLLEWIGYINPSRGYTNV 60

Qy 61 AOKFGQRYVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 61 NQKFPDRVTMTDTSFSTAYMQLSLRSDAUSAVYYCAR 98

RESULT 8
Q8WY24 PRELIMINARY; PRT; 497 AA.
ID Q8WY24
AC Q8WY24;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Pang Y., Dong Q.;
RT "Identification and characterization of SNC66, a Ig-like gene which is
RT down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1..
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 5365 MW; F24D08DFA5A63E5 CRC64;

Query Match
Best Local Similarity 68.5%; Score 357; DB 4; Length 497;
Matches 65; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 1 QVQLQSATEVKKPGASKVSCMASGYPTSYDISWVQAPQGLEWVGMISAVNGNTHY 60
Db 20 QGOLQSGAEVTKPGASVAVSCASGYFTFIADINWVQAPQGLEWGMNPGQTGNEF 79
Qy 61 AQKFGKRYMTTDSRTATYMLRSLRSDDTAVYYCA 98
Db 80 AQKFGKRLTFSDTISINATYMLVLSLSTEDSHYFCAR 117

RESULT 9

Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match
Best Local Similarity 72.0%; Pred. No. 6.3e-30;
Matches 67; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 5 LQSAIEYKPKGASKVSCMASGYPTSYDISWVQAPQGLEWVGMISAVNGNTHY 64
Db 1 VQGAIEYKPKGSSVSKASGCTFSYALSWVQAPQGLEWGMRIIPILGANYAKKF 60
Qy 65 QGRVMTTDSRTATYMLRSLRSDDTAVYYCA 97
Db 61 QGRVTTADKSTSTAYMELSLRSEDTAVYYCA 93

RESULT 10

Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MRP3
SQ Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX PubMed=1181679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."
RL World J. Gastroenterol. 6:709-717(2000).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match
Best Local Similarity 64.7%; Score 337; DB 11; Length 147;
Matches 63; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QVQLQSATEVKKPGASKVSCMASGYPTSYDISWVQAPQGLEWVGMISAVNGNTHY 60
Db 3 QVQLHQSPEVYKPGASKVSKASGYFTSYDISWVQAPQGLEWGMIFPEGSTY 62
Qy 61 AQKFGKRYMTTDSRTATYMLRSLRSDDTAVYYCA 98
Db 63 NEKFGKRYMTTDSRTATYMLRSLRSDDTAVYYCA 100

RESULT 11

Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Straubeberg R.;
RL Submitted (SRP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013480; AAH13490.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
DE Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match
Best Local Similarity 64.3%; Score 335; DB 11; Length 481;
Matches 62; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGQGLEWYGMISAVYNGNTHY 60
 Db 20 QVQLQSGPELVKPKGASVSKSCASGYFTSYIHMMVGRPGQGLVIGWITPPDGNTRY 79
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 98
 Db 80 NEKFKGKATLTADKSSSTAYMFLSLTSEDSAVYFCTR 117

RESULT 12

QY298 PRELIMINARY: PRT; 150 AA.
 AC QY298:

DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE IGG VH protein precursor (fragment).
 GN IGG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98322155; PubMed=9657749;
 RA Jacquemin M.G., Vander Elst L.P.U.,
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IGG4 monoclonal antibody derived from a hemophilia A patient with
 RT inhibitor."
 RL Blood 92:496-506 (1998).
 DR EMBL; AJ224083; CAA11829.1; -.
 DR HSSP; P01772; 2PB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Signal.
 FT SIGNAL.
 FT NON TER 150 150 POTENTIAL.
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB2280ZDS CRC64;

Query Match Best Local Similarity 64.1%; Score 334; DB 4; Length 150;
 Matches 65; Conservative 8; Mismatches 24; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGQGLEWYGMISAVYNGNTHY 60
 Db 20 QVQLQSGPELVKPKGASVSKSCASGYFTSYIHMMVGRPGQGLVIGWITPPDGNTRY 79
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 97
 Db 80 NEKFKGKATLTADKSSSTAYMFLSLTSEDSAVYFCTR 116

RESULT 13

Q8K024 PRELIMINARY: PRT; 480 AA.
 AC Q8K024:

DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to expressed sequence A1893585.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strauberg R.;

RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029188; AAH29188.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; IGV; 3.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; 2.
 SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match Best Local Similarity 63.5%; Score 331; DB 11; Length 480;
 Matches 59; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGQGLEWYGMISAVYNGNTHY 60
 Db 20 QVQLQSGPELVKPKGASVSKSCASGYFTSYIHMMVGRPGQGLVIGWITPPDGNTRY 79
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 98
 Db 80 NEKFKGKATLTADKSSSTAYMFLSLTSEDSAVYFCTR 117

RESULT 14

Q8V1J1 PRELIMINARY: PRT; 123 AA.
 AC Q8V1J1:

DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Anti-DNA heavy chain (fragment).
 GN J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C3H/HeJ-Ipr; PubMed=8814271;
 RA Wlodek M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among
 RT anti-DNA from C3H-Ipr mice and lupus mice with nephritis."
 RL Eur. J. Immunol. 26:2225-2233 (1996).
 DR EMBL; U59154; AAB02916.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON TER 123 123
 FT NON TER 123 123
 SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911B CRC64;

Query Match Best Local Similarity 63.3%; Score 330; DB 11; Length 123;
 Matches 59; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGQGLEWYGMISAVYNGNTHY 60
 Db 1 EQQLQSGPELVKPKGASVSKSCASGYFTSYIHMMVGRPGQGLVIGWITPPDGNTRY 60
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 98
 Db 61 SOKFKGKATLTADKSSSTAYMFLSLTSEDSAVYFCTR 98

```

RESULT 15
O9D8L4      PRELIMINARY;      PRT;      473 AA.
ID O9D8L4;
AC O9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1810060009RIK protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleisemann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guclincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007918; BAB25349.1; -.
DR HSSP: P01842; 7FAB.
DR MGD: MGI:96443; Igh-1.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FB8 CRC64;

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```

Query Match      63.3%; Score 330; DB 11; Length 473;
Best Local Similarity 61.2%; Pred. No. 4,3e-28;
Matches 60; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

```

```

QY 1 QVQLLQSGATEYVKRPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 20 QVQLKQSGALVLRKPGASVKISCKASGYFTFDYINWVKRPGQGLEWIGKIGPGSGSTYY 79
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 61 AQKFGAVTMTDTSRRTAYMELSLRSDDPVTAYTCAR 98
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 80 NEKFKGKATLTADKSSSTAYWQLSLTSEDSAVYFCAR 117
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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Search completed: December 30, 2003, 11:01:02
 Job time : 23.883 secs

PD 24-NOV-1994.
XX
PF 10-MAY-1993; 93WO-JP00603.
XX
PR 10-MAY-1993; 93WO-JP00603.
XX
PA (NIBS) JAPAN TOBACCO INC.
XX
PI Honjo T, Matsumura F;
XX
DR MPI; 1995-006791/01.
XX
PT N-PSDB; AAQ78956.
XX
PS DNA fragment comprising human immunoglobulin Vh genes - for the
XX production of human immunoglobulin in mammalian hosts
XX
PS Claim 27; Page 54-55; 130pp; Japanese.
XX
CC Protein sequences (AA66295-51) are novel human immunoglobulin heavy
CC chain sequences encoded by novel isolated genes. The genes
CC (AAQ78939-79002) were isolated and cloned from a series of cosmid
CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131. By PCR
CC amplification using primers AAQ78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TagI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridisation. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 117 AA;
Query Match 87.5%; Score 456; DB 16; Length 117;
Best Local Similarity 87.8%; Pred. No. 2.5e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGMSAYNGNTY 60
DB 20 QVQLVQSGAEVKKPKGASVSKVSCKASGYTFTSYGISWVRQAPGQGLEWVGMSAYNGNTY 79
QY 61 AOKFQGRVTMTDTTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 80 AOKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 117
RESULT 15
ABP45461
ID ABP45461 standard; Protein; 248 AA.
XX
AC ABP45461;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BlyS binding scFv SEQ ID 1472.
XX
XX BlyS: B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antitumour;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.

XX
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR MPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2159-2160; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antitumour, and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 248 AA;
Query Match 87.5%; Score 456; DB 23; Length 248;
Best Local Similarity 87.8%; Pred. No. 5.6e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGMSAYNGNTY 60
DB 1 QVQLVQSGAEVKKPKGASVSKVSCKASGYTFTSYGISWVRQAPGQGLEWVGMSAYNGNTY 60
QY 61 AOKFQGRVTMTDTTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

Search completed: December 30, 2003, 10:54:31
Job time : 32.6089 secs

DT 25-FEB-2003 (first entry)
 XX
 DE Human liver peptide, SEQ ID No 34543.
 XX
 KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KM hypercholesterolaemia; coronary heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157273-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00664.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488898/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human adult liver -
 XX
 PS Claim 27; SEQ ID No 34543; 658bp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (I) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 104 AA;
 XX
 Query Match 87.5%; Score 456; DB 22; Length 104;
 Best Local Similarity 87.8%; Pred. No. 2.2e-39;
 Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 XX
 QY 1 QVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTY 60
 DB 4 QVQLVQSGAEVKKPGASVKVSCKASGTFITISGISWVRQAPGQGLEWVGWISAYNGNTY 63
 QY 61 AOKFGQRYVTMTTDSRTAYWEELRSRSDTAIVYYCAR 98
 DB 64 AOKLQGRVTMTTDTSTSTAYWEELRSRSDTAIVYYCAR 101
 XX
 RESULT 13
 ID ABB40538 standard; Peptide; 104 AA.
 XX
 AC ABB40538;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #8044 encoded by human foetal liver single exon probe.

XX
 KM Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX
 PS Claim 27; SEQ ID NO 33173; 639pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 104 AA;
 XX
 Query Match 87.5%; Score 456; DB 22; Length 104;
 Best Local Similarity 87.8%; Pred. No. 2.2e-39;
 Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 XX
 QY 1 QVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTY 60
 DB 4 QVQLVQSGAEVKKPGASVKVSCKASGTFITISGISWVRQAPGQGLEWVGWISAYNGNTY 63
 QY 61 AOKFGQRYVTMTTDSRTAYWEELRSRSDTAIVYYCAR 98
 DB 64 AOKLQGRVTMTTDTSTSTAYWEELRSRSDTAIVYYCAR 101
 XX
 RESULT 14
 ID AAR66311 standard; Protein; 117 AA.
 XX
 AC AAR66311;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1995 (first entry)
 XX
 DE Human immunoglobulin variable heavy chain #17.
 XX
 KM Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KM cosmid; placenta; vector; pJB81; E.coli; mammalian.
 XX
 OS Homo sapiens.
 XX
 PN WO9426895-A1.
 XX

Human antibody fragment #46.

KM human; antibody; epitope; cancer; tumour; cell; rolling; inflammation;
KM metastasis; hypervariable region; autoimmune disease; thrombosis;
KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KM myocardial infarction; retinopathic disease; abnormal platelet function;
KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.
xy

PN WO200253700-A2
XX

PD 11-JUL-2002.
XY

31-DEC-2001; 2001WO-US49442.
XX

PR	29-DEC-2000; 2000US-258948P.
PR	29-DEC-2000; 2000US-0751181.
XX	

PR 29-DEC-2000; 2000US-0751181.
XY

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX

PI	Lazarovits J, Hagai Y,	Plaksin D, Vogel T,	Nimrod A,	Mar-Haim H
PI	Szantonu E, Richter T,	Amit B, Kooperman L,	Peretz T,	Levanon A,
XX	WPI; 2002-674776/72.			
DR				
XX				

PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX
XX
XX Disclosure: Page 246-247; 310pp; English.

The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of diseased cells or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention.

Sequence 98 AA;

Query Match	Score	DB	Length
87.5%	456	23	98
Best Local Similarity	87.8%	Prod	320

Matches	86;	Conservative	4;	Mismatches	8;	Indels	0;	Gaps	0
---------	-----	--------------	----	------------	----	--------	----	------	---

1 QVQLQSLATPEVKKKPGASMKYSCMASGYPPFTSYDISWVRQAPOGLEWVGWISAYNGNTYH
|||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLVSGAEVKKKPGASVKYSCKASGYTFTSYGISWVRQAPOGLEWMGWSIAYNGNTNY 60

RESULT 11
ABG78171

ID	ABG78171	standard; Protein; 98 AA.
XX		

AC ABG78171;
YY

DT 15-NOV-2002 (first entry)
XX

Human Fv molecule hypervariable region related peptide #46.

AM human; FV molecule; hypervariable region; single chain Fv; cytostatic;
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma
 KM Lymphoma; blastoma; seminoma; melanoma; acute myeloid leukaemia
 XX

US Homo sapiens.
XX

MOZ00259464-AZ
XX

01-AUG-2002
FD
XX

PT 31-DEC-2001; 2001MO-US49440.
XX

23-DEC-2000; 200005-0/51181.

(P) - BIO-TECHNOLOGY GEN CORP

WPI; 2002-619166/66.

PT novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favour of other
PT cells -

PS Claim 13; Page 169; 232pp; English
yy

The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma), and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention.

Sequence 98 AA;

Query Match	87.5%	Score 456;	DB 23;	Length 98,
Best Local Similarity	87.8%	Pred No 30		

Matches	86	Conservative	4	Mismatches	8	Indels	0	Gaps	0
---------	----	--------------	---	------------	---	--------	---	------	---

1 QVQLVQSAITEVKKPGASMKYSCMASGYPTFSYDLSWVRQAPOGGIEHWGVIISAYNGNTHY
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLVQSAGEVKKIPGASVYVSCKASGYPTFSYGISWVRQAPOGGIEMWGVIISAYNGNTNY
60

```

RESULT 12
ID      ABG55895
        ABG55895 standard; Peptide; 104 AA
XX
XX
XX      ABG55895;
XX
XX

```

RESULT 8
ABP45584
ID ABP45584 standard; Protein; 250 AA.
XX
AC ABP45584;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1595.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
XX
PR 17-OCT-2000; 2000US-240816P.
XX
PR 16-MAR-2001; 2001US-276248P.
XX
PR 21-MAR-2001; 2001US-277379P.
XX
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2306-2307; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 250 AA;
XX
Query Match 88.3%; Score 460; DB 23; Length 250;
Best Local Similarity 88.8%; Pred. No. 2.2e-39;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 QVOLLQSATVKKPKGASMKVSCMASGYPTFSYDISWVROAPQGLQLEWGMISAVNGNTHY 60
DB 1 QVOLLQSAEAEVKKPKGASVSVKSCASGYTTTSYGISWVROAPQGLQLEWGMISAVNGNTHY 60

OY 61 AOKFQGRVTMTTDSRRATVMELSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTISTATVMELSRSDDTAVYYCAR 98

RESULT 9
AAV50952
ID AAV50952 standard; Protein; 98 AA.
XX
AC AAV50952;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH clone DP-14 protein #2.
XX
KW Human; heavy chain; antibody; factor VIII; hemostatic;
KW hemophilia A; VH gene.
XX
OS Homo sapiens.
XX
PN WO958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SANO-) STICHTING SANQUIN BLOEDVOORZINNING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
XX presence of neutralizing antibodies against factor VIII and for
XX treatment of hemophilia A patients with these antibodies -
XX
PS Example 4; Fig 4B; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody clone DP-14 protein which is used in the method
XX of the invention.
XX
SQ Sequence 98 AA;
XX
Query Match 87.5%; Score 456; DB 21; Length 98;
Best Local Similarity 87.8%; Pred. No. 2e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVOLLQSATVKKPKGASMKVSCMASGYPTFSYDISWVROAPQGLQLEWGMISAVNGNTHY 60
DB 1 QVOLLQSAEAEVKKPKGASVSVKSCASGYTTTSYGISWVROAPQGLQLEWGMISAVNGNTHY 60

OY 61 AOKFQGRVTMTTDSRRATVMELSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTISTATVMELSRSDDTAVYYCAR 98

RESULT 10
ABG91862
ID ABG91862 standard; Protein; 98 AA.
XX
AC ABG91862;
XX
DT 04-DEC-2002 (first entry)

AC ABP45549;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 1560.
 XX
 KW BlyS: B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 PN
 XX 10-JAN-2002.
 PD
 XX 15-JUN-2001; 2001WO-US19110.
 PF
 XX 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 XX Claim 1; Page 2264-2265; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 250 AA;

Query Match 88.9%; Score 463; DB 23; Length 250;
 Best Local Similarity 89.8%; Pred. No. 1,1e-39;
 Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLQSATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWMGMSIAYNGNTY 60
 DB 1 QVQLQSAAEVKKPGASVKVSCKASGYTFSTYSISWVRQAPGQGLEWMGMSIAYNGNTY 60
 QY AOKFOGRVTMTDTSRTAYMELRSLSDDTAYYYCAR 98
 DB 61 AOKLQGRVTMTDTSRTAYMELRSLSDDTAYYYCAR 98

RESULT 7

ABP45727
 ID ABP45727 standard; Protein; 251 AA.
 XX
 AC ABP45727;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human BlyS binding scFv SEQ ID 1738.
 XX
 KW BlyS: B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 PN
 XX 10-JAN-2002.
 PD
 XX 15-JUN-2001; 2001WO-US19110.
 PF
 XX 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 XX Claim 1; Page 2476-2477; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 251 AA;

Query Match 88.9%; Score 463; DB 23; Length 251;
 Best Local Similarity 88.8%; Pred. No. 1,1e-39;
 Matches 87; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQSATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWMGMSIAYNGNTY 60
 DB 1 QVQLVSGAEVKKPGASVKVSCKASGYTFSTYSISWVRQAPGQGLEWMGMSIAYNGNTY 60
 QY AOKFOGRVTMTDTSRTAYMELRSLSDDTAYYYCAR 98
 DB 61 AOKLQGRVTMTDTSRTAYMELRSLSDDTAYYYCAR 98

```

OY 61 AOKFOGRVTMTTDSRTAYMELRSLSRSDTAAYYCAR 98
    |||||
DB 61 AOKFOGRVTMTTDSRTAYMELRSLSRSDTAAYYCAR 98

RESULT 4
ID AAY50955 standard; Protein; 98 AA.
XX
AC AAY50955;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH protein VH EL-25.
XX
KM Human; heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; VH protein.
XX
OS Homo sapiens.
XX
PN M0958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99MO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PI (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
PS Example 4; Fig 4B; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody VH EL-25 protein which is used in the method
CC of the invention.
XX
SQ Sequence 98 AA;
XX
Query Match 90.0%; Score 469; DB 21; Length 98;
Best Local Similarity 89.8%; Pred. No. 9,4e-41;
Matches 88; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY 1 QVOLLQSATEVKKPKGASMKVSCMASGYPTFSYDISWVRQAPGQLEWVGMSIYNGNTNY 60
DB 1 QVOLLQSAAEVRKPKGASVSKVSCKASGYPTFSYDISWVRQAPGQLEWVGMSIYSGNTDY 60
OY 61 AOKFOGRVTMTTDSRTAYMELRSLSRSDTAAYYCAR 98
DB 61 AOKFOGRVTMTTDSRTAYMELRSLSRSDTAAYYCAR 98

RESULT 5
ID ABP45105 standard; Protein; 247 AA.
XX
AC ABP45105;
XX
DT 19-AUG-2002 (first entry)
XX

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```

XX
DE Human Blys binding scFv SEQ ID 1116.
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulator; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN M0200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001MO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
XX
PR 17-OCT-2000; 2000US-240816P.
XX
PR 16-MAR-2001; 2001US-276248P.
XX
PR 21-MAR-2001; 2001US-277379P.
XX
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 1734-1735; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 247 AA;
XX
Query Match 88.9%; Score 463; DB 23; Length 247;
Best Local Similarity 89.8%; Pred. No. 1.1e-39;
Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
OY 1 QVOLLQSATEVKKPKGASMKVSCMASGYPTFSYDISWVRQAPGQLEWVGMSIYNGNTNY 60
DB 1 QVOLLQSAAEVRKPKGASVSKVSCKASGYTTTSGISWVRQAPGQLEWVGMSIYNGNTNY 60
OY 61 AOKFOGRVTMTTDSRTAYMELRSLSRSDTAAYYCAR 98
DB 61 AOKFOGRVTMTTDSRTAYMELRSLSRSDTAAYYCAR 98

RESULT 6
ID ABP45549 standard; Protein; 250 AA.
XX
AC ABP45549;
XX
DT 19-AUG-2002 (first entry)
XX

```

XX	Example 4; Fig 4B; 61pp; English.
PS	
CC	This invention describes a novel polynucleotide (I) (and complements and
XX	hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC	coding for a human antibody with factor VIII specifically which has
CC	hemostatic activity. (I) is useful a primer or probe for detecting the
CC	presence of inhibitory antibodies directed against factor VIII. The
CC	polypeptides of the invention and the antibodies generated from them
CC	are useful in compositions for neutralizing factor VIII inhibiting
CC	antibodies in hemophilia A patients. This sequence represents the human
CC	anti-factor VIII antibody VH EL-5 protein which is used in the method
CC	of the invention.
XX	
SQ	Sequence 98 AA;
Query Match	98.1%; Score 511; DB 21; Length 98;
Best Local Similarity	98.0%; Pred No. 4.5e-45;
Matches	96; Conservative 1; Mismatches 1; Indels 0; Gaps 0
Dd	1 QVOLLQSATEYKKKPGASMKFVSQMASGYPTTSYDISWVRQAPQGELWVGWISAYNGNTHY 60 1 QVQLVLSATNEVKKPGASMKVSCMASGYPTTSYDISWVRQAPQGELWVGWISAYNGNTHY 60
Dy	61 AQKFGGRVTMTDTTSRRITAYMELRSLRSDDTAVYYCAR 98 61 AQKFGGRVTMTDTTSRRITAYMELRSLRSDDTAVYYCAR 98
Db	61 AQKFGGRVTMTDTTSRRITAYMELRSLRSDDTAVYYCAR 98
RESULT 2	
ID	AAV50953 standard; Protein; 132 AA.
AC	AAV50953;
XX	AAV50953;
DT	23-MAR-2000 (first entry)
DE	Human anti-factor VIII antibody VH protein VH IT-2.
XX	
KM	Human; heavy chain; antibody; factor VIII; hemostatic;
XX	hemophilia A; VH protein.
XX	
OS	Homo sapiens.
XX	
PN	WO958680-A2.
PD	18-NOV-1999.
PF	07-MAY-1999; 99WO-NL00285.
XX	
PR	08-MAY-1998; 98EP-0201543.
PA	(SANO-) STICHTING SANOUTIN BLOEDVOORZIENING.
XX	
PI	Voorberg JJ, Van Den Brink EN, Turenhout EM;
DR	WPI; 2000-053102/04.
PT	New polynucleotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -
PS	
XX	Example 4; Fig 4B; 61pp; English.
XX	
CC	This invention describes a novel polynucleotide (I) (and complements and
CC	hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC	coding for a human antibody with factor VIII specificity which has
CC	hemostatic activity. (I) is useful a primer or probe for detecting the
CC	presence of inhibitory antibodies directed against factor VIII. The
CC	polypeptides of the invention and the antibodies generated from them
CC	are useful in compositions for neutralizing factor VIII inhibiting
CC	antibodies in hemophilia A patients. This sequence represents the human
CC	anti-factor VIII antibody VH IT-2 protein which is used in the method
CC	of the invention.

CC	of the invention.
XX	
SQ	Sequence 132 AA;
	Query Match 95.8%; Score 499; DB 21; Length 132; Best Local Similarity 95.9%; Pred. No. 1,1e-43; Matches 94; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY	1 QVOLLQSATEVKKFGQSMKVSCMASGYPFPTSYDISWTRAPGCGLEVMGMISAYNGNTH 60 :::
DB	1 QVOLLQSATEVKKFGQSMKVSCMASGYPFTSYDISWTRAPGCGGLEVMGMISAYSGNTDY 60 :::
QY	61 AAKFCGRVTMTTDSRRRAYMELSLRSDDTAVYYCAR 98 :::
DB	61 AAKFCGRVTMTTDSRRRAYMELSLRSDDTAVYYCAR 98 :::

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 31.5256 Seconds
(without alignments) 493.415 Million cell updates/sec

Title: US-09-674-752-27

Sequence: 1 QVQLQSATEVKKPGASKV.....AYWELRSLSRSDPTAVYYCAR 98

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: A_Geneseq_19Jun03:*
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- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	511	98.1	98	21	AA50954
2	499	95.8	132	21	AA50953
3	490	94.0	132	21	AA50950
4	469	90.0	98	21	AA50955
5	463	88.9	247	23	ABP45105
6	463	88.9	250	23	ABP45549
7	463	88.9	251	23	ABP45727
8	460	88.3	250	23	ABP45584
9	456	87.5	98	21	AA50952

10	456	87.5	98	23	ABG91862	Human antibody fra
11	456	87.5	98	23	ABG78171	Human Fv molecule
12	456	87.5	104	22	ABG55895	Human liver peptid
13	456	87.5	104	22	ABB40538	Peptide #8044 enco
14	456	87.5	117	16	AAR66311	Human Immunoglobul
15	456	87.5	248	23	ABP45461	Human Blys binding
16	456	87.5	251	23	ABP45551	Human Blys binding
17	456	87.5	251	23	ABP45561	Human Blys binding
18	456	87.5	251	23	ABP45910	Human Blys binding
19	456	87.5	255	23	ABP45179	Human Blys binding
20	456	87.5	259	23	ABP45345	Human Blys binding
21	453	86.9	247	23	ABP45662	Human Blys binding
22	453	86.9	249	23	ABP45814	Human Blys binding
23	453	86.9	250	23	ABP45550	Human Blys binding
24	453	86.9	250	23	ABP45582	Human Blys binding
25	453	86.9	251	23	ABP45867	Human Blys binding
26	452	86.8	248	23	ABP45860	Human Blys binding
27	452	86.8	251	23	ABP45575	Human Blys binding
28	452	86.8	251	23	ABP45859	Human Blys binding
29	451	86.6	257	23	ABP45668	Human Blys binding
30	450	86.4	251	23	ABP45544	Human Blys binding
31	450	86.4	254	23	ABP45394	Human Blys binding
32	449	86.2	253	23	ABP45953	Human Blys binding
33	448	86.0	248	23	ABP45866	Human Blys binding
34	447	85.8	98	21	AA50951	Human Blys binding
35	447	85.8	257	23	ABP45599	Human Blys binding
36	447	85.8	259	23	ABP45962	Human Blys binding
37	446	85.6	251	23	ABP44919	Human Blys binding
38	446	85.6	251	23	ABP45725	Human Blys binding
39	446	85.6	251	23	ABP45858	Human Blys binding
40	445	85.4	121	22	AAU02549	Human Blys binding
41	445	85.4	248	23	ABP45767	Human Blys binding
42	445	85.2	253	23	ABP45625	Human Blys binding
43	444	85.0	118	13	AAR22569	Human Blys binding
44	443	84.9	134	21	AA64688	Human 5' ESR relat
45	442.5	84.9	246	23	ABP45181	Human Blys binding

ALIGNMENTS

RESULT 1
AA50954
ID AA50954 standard; Protein: 98 AA.
AC AA50954;
XX
XX 23-MAR-2000 (first entry)
DT
DE Human anti-factor VIII antibody VH protein VH EU-5.
XX
XX Human; heavy chain; antibody; factor VIII; hemostatic;
KW hemophililia A; VH protein.
XX
XX OS Homo sapiens.
XX
XX WO9956860-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99MO-NU00285.
XX
XX 08-MAY-1998; 98EP-0201543.
XX
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
XX Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX WFI; 2000-053102/04.
XX
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
XX presence of neutralizing antibodies against factor VIII and for
XX treatment of hemophililia A patients with these antibodies -

Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 2

US-09-880-748-1560
; Sequence 1560, Application US/09880748
; Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 1560

LENGTH: 250

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1560

Query Match 88.9%; Score 463; DB 11; Length 250;
Best Local Similarity 89.8%; Pred. No. 7e-40;
Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWGMISAYNGNTHY 60
Db 1 OVQLQSAEYKPKGASVSKCKASGYFTSYGISWVRQAPQGLEWGMISAYNGNTHY 60

QY 61 AOKFOGRVTMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

US-09-880-748-1738
; Sequence 1738, Application US/09880748
; Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 1738

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1738

Query Match 88.9%; Score 463; DB 11; Length 251;

Best Local Similarity 88.8%; Pred. No. 7e-40;
Matches 87; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWGMISAYNGNTHY 60
Db 1 OVQLQSAEYKPKGASVSKCKASGYFTSYGISWVRQAPQGLEWGMISAYNGNTHY 60

QY 61 AOKFOGRVTMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 4

US-09-880-748-1595
; Sequence 1595, Application US/09880748
; Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 1595

LENGTH: 250

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1595

Query Match 88.3%; Score 460; DB 11; Length 250;
Best Local Similarity 88.8%; Pred. No. 1.4e-39;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWGMISAYNGNTHY 60
Db 1 OVQLQSAEYKPKGASVSKCKASGYFTSYGISWVRQAPQGLEWGMISAYNGNTHY 60

QY 61 AOKFOGRVTMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

US-10-041-860-2
; Sequence 2, Application US/10041860
; Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gad

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX-051A

CURRENT APPLICATION NUMBER: US/10/041,860

PRIOR FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSeq for Windows Version 4.0

Query Match 88.3%; Score 460; DB 11; Length 250;

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; SEQ ID NO 2
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-2
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```
Query Match      87.5%; Score 456; DB 12; Length 98;
Best Local Similarity 87.8%; Pred. No. 1.3e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 QVOLLQATVKKPGASMKVSCMASGYPTFSYDISWVROAPGCGLEWVGWISAYNGNTNY 60
DB 1 QVQLVDSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGCGLEWVGWISAYNGNTNY 60
QY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
```

RESULT 6

```
US-10-041-860-324
; Sequence 324, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-324
```

```
Query Match      87.5%; Score 456; DB 12; Length 98;
Best Local Similarity 87.8%; Pred. No. 1.3e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 QVOLLQATVKKPGASMKVSCMASGYPTFSYDISWVROAPGCGLEWVGWISAYNGNTNY 60
DB 1 QVQLVDSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGCGLEWVGWISAYNGNTNY 60
QY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
```

RESULT 7

```
US-10-041-860-326
; Sequence 326, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-326
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; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-326
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```
Query Match      87.5%; Score 456; DB 12; Length 98;
Best Local Similarity 87.8%; Pred. No. 1.3e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 QVOLLQATVKKPGASMKVSCMASGYPTFSYDISWVROAPGCGLEWVGWISAYNGNTNY 60
DB 1 QVQLVDSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGCGLEWVGWISAYNGNTNY 60
QY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
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RESULT 8

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US-10-041-860-355
; Sequence 355, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-355
```

```
Query Match      87.5%; Score 456; DB 12; Length 98;
Best Local Similarity 87.8%; Pred. No. 1.3e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 QVOLLQATVKKPGASMKVSCMASGYPTFSYDISWVROAPGCGLEWVGWISAYNGNTNY 60
DB 1 QVQLVDSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGCGLEWVGWISAYNGNTNY 60
QY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
```

RESULT 9

```
US-10-041-860-356
; Sequence 356, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
```

```

; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ARGENTIA.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 356
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-356

Query Match
Best Local Similarity 87.5%; Score 456; DB 12; Length 98;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVROAPQGLEWGWISAYNGNTY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYGISWVROAPQGLEWGMISAYNGNTY 60

QY 61 AOKFGQRYVTMTDTSRTAYMELRLSRDDTAIVYCAR 98
DB 61 AOKLQGRVTMTDTSRTAYMELRLSRDDTAIVYCAR 98

RESULT 10
US-10-308-817-44
; Sequence 44, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rocher, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-44

Query Match
Best Local Similarity 87.8%; Score 456; DB 12; Length 98;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVROAPQGLEWGWISAYNGNTY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYGISWVROAPQGLEWGMISAYNGNTY 60

QY 61 AOKFGQRYVTMTDTSRTAYMELRLSRDDTAIVYCAR 98
DB 61 AOKLQGRVTMTDTSRTAYMELRLSRDDTAIVYCAR 98

RESULT 11
US-10-194-975-4
; Sequence 4, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; PRIOR FILING DATE: 2001-07-12
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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-4

Query Match
Best Local Similarity 87.8%; Score 456; DB 15; Length 98;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVROAPQGLEWGWISAYNGNTY 60
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYGISWVROAPQGLEWGMISAYNGNTY 60

QY 61 AOKFGQRYVTMTDTSRTAYMELRLSRDDTAIVYCAR 98
DB 61 AOKLQGRVTMTDTSRTAYMELRLSRDDTAIVYCAR 98

RESULT 12
US-09-864-761-47285
; Sequence 47285, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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; SEQ ID NO 47285
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AM403728.1, EVALUE 4.00e-45
US-09-864-761-47285
```

```
Query Match      87.5%; Score 456; DB 9; Length 104;
Best Local Similarity 87.8%; Pred. No. 1.4e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 OVQLVQSGAEVKKPKASVSVCKASGYFTSYGISWROAPQGLEWGMISAYNGNTHY 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFOGRVTMTTDSRRTAYMELRSLSRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 AOKLOGRVMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 101
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```
RESULT 13
US-10-041-860-206
; Sequence 206, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 117
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-206
```

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Query Match      87.5%; Score 456; DB 12; Length 117;
Best Local Similarity 87.8%; Pred. No. 1.6e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLVQSGAEVKKPKASVSVCKASGYFTSYGISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFOGRVTMTTDSRRTAYMELRSLSRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 14
US-10-041-860-42
; Sequence 42, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
```

```
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-42
```

```
Query Match      87.5%; Score 456; DB 12; Length 125;
Best Local Similarity 87.8%; Pred. No. 1.7e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLVQSGAEVKKPKASVSVCKASGYFTSYGISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFOGRVTMTTDSRRTAYMELRSLSRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 15
US-10-041-860-207
; Sequence 207, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-207
```

```
Query Match      87.5%; Score 456; DB 12; Length 125;
Best Local Similarity 87.8%; Pred. No. 1.7e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLVQSGAEVKKPKASVSVCKASGYFTSYGISWROAPQGLEWGMISAYNGNTHY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFOGRVTMTTDSRRTAYMELRSLSRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98
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```

Search completed: December 30, 2003, 11:45:22
Job time : 21.0171 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45; Search time 9.95126 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-27

Perfect score: 521
Sequence: 1 QVQLQSTAVKPKGASMKV.....AYWEIRSLRSDPTAVYCAR 98

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	456	87.5	117	3	US-08-545-809A-105
2	436	83.7	121	1	US-08-264-093-3
3	418.5	80.3	128	1	US-08-202-047-22
4	418.5	80.3	128	3	US-08-964-690-22
5	418.5	80.3	129	2	US-08-561-521-45
6	418.5	80.3	129	4	US-08-525-539A-77
7	418.5	80.3	129	5	PCT-US95-01219-45
8	416	79.8	117	4	US-09-025-769B-96
9	407	78.1	119	4	US-08-561-521-10
10	407	78.1	119	2	US-09-438-954-41
11	407	78.1	119	4	US-09-438-954-41
12	407	78.1	119	5	PCT-US95-01219-10
13	406	77.9	120	4	US-09-025-769B-36
14	406	77.9	120	4	US-09-025-769B-59
15	405.5	77.8	120	2	US-08-652-816A-19
16	405.5	77.8	125	3	US-09-199-149-3
17	401	77.0	116	2	US-08-561-521-41
18	401	77.0	116	5	PCT-US95-01219-41
19	401	77.0	117	3	US-08-545-809A-90
20	400	76.8	135	1	US-08-137-117D-102
21	400	76.8	135	2	US-08-436-717-102
22	399	76.6	119	5	US-08-561-521-12
23	399	76.6	119	5	PCT-US95-01219-12
24	396	76.0	135	1	US-08-137-117D-100
25	396	76.0	135	2	US-08-436-717-100
26	393	75.4	121	1	US-08-202-047-23
27	393	75.4	121	3	US-08-964-690-23

28	391	75.0	110	4	US-09-899-896-5	Sequence 5, App1
29	391	75.0	117	3	US-08-545-809A-91	Sequence 91, App1
30	391	75.0	119	2	US-08-561-521-13	Sequence 13, App1
31	391	75.0	119	5	PCT-US95-01219-13	Sequence 13, App1
32	389	74.7	236	3	US-09-049-672A-13	Sequence 13, App1
33	388	74.5	108	4	US-09-899-896-3	Sequence 3, App1
34	388	74.5	117	3	US-08-545-809A-128	Sequence 128, App
35	388	74.5	135	1	US-08-137-117D-112	Sequence 112, App
36	388	74.5	135	2	US-08-436-717-112	Sequence 112, App
37	387	74.3	123	1	US-08-477-877B-94	Sequence 94, App1
38	387	74.3	123	2	US-08-472-281A-94	Sequence 94, App1
39	387	74.3	123	2	US-08-477-899B-94	Sequence 94, App1
40	385	73.9	140	3	US-08-836-561-63	Sequence 63, App1
41	385	73.9	140	4	US-09-434-122-63	Sequence 63, App1
42	381	73.1	118	1	US-08-491-845-14	Sequence 14, App1
43	381	73.1	137	3	US-08-513-968-38	Sequence 38, App1
44	380	72.9	108	4	US-09-899-896-1	Sequence 1, App1
45	380	72.9	121	3	US-08-579-378A-8	Sequence 8, App1

ALIGNMENTS

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RESULT 1
US-08-545-809A-105
; Sequence 105, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Taaku
; APPLICANT: Matsumoto, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545, 809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29, 066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-105
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; Query Match 87.5%; Score 456; DB 3; Length 117;
; Best Local Similarity 87.8%; Pred. No. 4,4e-42;
; Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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Db 20 QVVLVSGAEVKKPGASVKASCASGYFTSYGISWVRQAPGQGLEWMGMSAINGNTNY 79
QY 61 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAAYYCAR 98
Db 80 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAAYYCAR 117

RESULT 2
US-08-264-093-3
Sequence 3, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adeleide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-3

Query Match 83.7%; Score 436; DB 1; Length 121;
Best Local Similarity 82.7%; Pred. No. 6,6e-40;
Matches 81; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVVLVSGAEVKKPGASVKASCASGYFTSYGISWVRQAPGQGLEWMGMSAINGNTNY 60
Db 1 QVVLVSGAEVKKPGASVKASCASGYFTSYGISWVRQAPGQGLEWMGMSAINGNTNS 60
QY 61 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAAYYCAR 98
Db 61 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAAYYCAR 98

RESULT 3
US-08-202-047-22
Sequence 22, Application US/08202047
Patent No. 5800815
GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.

APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_1
US-08-202-047-22

Query Match 80.3%; Score 418.5; DB 1; Length 128;
Best Local Similarity 80.8%; Pred. No. 5,4e-38;
Matches 80; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVVLVSGAEVKKPGASVKASCASGYFTSYGISWVRQAPGQGLEWMGMSAINGNTNY 59
Db 1 QVVLVSGAEVKKPGASVKASCASGYFTSYGISWVRQAPGQGLEWMGMSAINGNDIN 60
QY 60 YAAKFGQGVMTTDTSRRTAYMELRSLSDDTAAYYCAR 98
Db 61 YAAKFGQGVMTTDTSRRTAYMELRSLSDDTAAYYCAR 99

RESULT 4
US-08-964-690-22
Sequence 22, Application US/08964690
Patent No. 6033667
GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_1
IS-08-964-690-22

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Query Match      80.3%  Score 418.5, DB 3, Length 128;
Best Local Similarity 80.8%  Pred No. 5,4e-38;
Matches 80; Conservative 8; Mismatches 10; Indels 1; Gaps 1

QY      1 QVOLLQSADEVKPKGASMKVSCMASGYFTSYDISWVQAPQGLEWGWISAY-NGNTH 59
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DB      1 QVQLVQSAEAEVKKPGASVKVSCKASGYFTSYAISWVQAPOGLEWMGWINPYNGDNT 60
      |||:||||:||||:||||:||||:||||:||||:||||:||||:

QY      60 YAAKFGGRVMTTIDTSRRATYAMELRSLSDDPAVYYCAR 98
      |||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      61 YAAKFGGRVTTIDTSTATYAMELSLSKSEDTAVYYCAR 99
      |||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
US-08-561-521--45
: Sequence 45, Application US/08561521
: Patent No. 5840299

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leiger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

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1  APPLICATION NUMBER:  US/08/186,265A
2
3  FILING DATE:  25-JAN-1994
4
5  ATTORNEY/AGENT INFORMATION:
6
7      NAME:  Smith, William L.
8
9      REGISTRATION NUMBER:  30,223
10
11     REFERENCE/DOCKET NUMBER:  15270-14
12
13     TELECOMMUNICATION INFORMATION:
14
15     TELEPHONE:  415-543-9600
16
17     TELEFAX:  415-543-5043
18
19     INFORMATION FOR SEQ ID NO:  45:
20
21     SEQUENCE CHARACTERISTICS:
22
23         LENGTH:  129 amino acids
24         TYPE:  amino acid
25         STRANDEDNESS:  single
26         TOPOLOGY:  linear
27
28     MOLECULE TYPE:  protein
29
30     US-08-561-521-45

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	Query Match	80.3%	Score 418.5;	DB 2;	Length 129;
	Best Local Similarity	80.8%;	Pred. No. 5.5e-38;		
	Matches	80;	Conservative	8;	Mismatches 10; Gaps 1
Oy	1 OVOLLGATATVKKKRGASAMKVSCMAQCPFTSYSDYSMPWRARCGGLEWGMISAY-NQUTH	59			
	:				
Dd	1 QVQLVDSGAELVKKGASGVKSCAKSGTFFTSYALSWAQAQGGGLERMGMINPVGNDTN	60			
	:				
Oy	60 YAAQFQGRVTMTDTISRRTAYMELSLRSDDTAVYYCAR	98			
	:				
Dd	61 YAQKFQGRVITLTADTSTSTAYMELSSLRSEDTAVYYCAR	99			
	:				

RESULT 6
 US-08-525-539A-77
 Sequence 77, Application US/08525539A
 Patent No. 6309636
 GENERAL INFORMATION:
 APPLICANT: DO COUTO, FERNANDO J. R.
 APPLICANT: CERIANI, ROBERTO L.
 APPLICANT: PETERSON, JERRY A.
 TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
 TITLE OF INVENTION: M33 ANTI-BA6 ANTIBODY, METHODS OF USE THEREOF, AND
 METHODS OF HUMANIZING ANTIBODY PEPTIDES
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/525,539A
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: DYLAN, TYLER
 REGISTRATION NUMBER: 37,612
 REFERENCE/DOCKET NUMBER: 27633-20001.21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear


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Query Match      78.1%; Score 407; DB 3; Length 117;
Best Local Similarity 78.6%; Pred. No. 8.5e-37;
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0.

QY      1  QVLLQSLATEYKKRQKASMKVSCMASGYFTSYDISMVRQAPQGLGVNWMISA YNGNTH 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20  QVLLVQSGAEYKKRQKASVKSCKASGYFTSYDIIMVVRQATGQGLENNGMNPNNSGNTGY 79
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61  AQKFGKRVTTTDTSRRTAYNELSLRSDDTAVYYCAR 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      80  AQKFGKRVTTTNTSISTAYNELSLRSEDYAVYYCAR 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-08-561-521-10
: Sequence 10, Application US/08561521
: Patent No. 5840299
: GENERAL INFORMATION:
: APPLICANT: Bendig, Mary M.
: APPLICANT: Leger, Olivier J.
: APPLICANT: Saldaña, Jose
: APPLICANT: Jones, S. Tarran
: TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
: TITLE OF INVENTION: Adhesion Molecule VLA-4
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424

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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/186,269A
? FILING DATE: 25-JAN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William L.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 15270-14
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-543-9600
? TELEFAX: 415-543-5043
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 119 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-561-521-10

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Query Match      78.1%; Score 407; DB 2; Length 119;
Best Local Similarity 78.6%; Pred. No. 8.7e-37;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Dd              1 QVOLLGSATEVKKPGASMKVSCMASGYPFTSYDISWYRQAPGGCLEMWGWISAYNGNTHY 60
                |||||:|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
            1 QVVLVGSGAEVKKRGASVKSCKRASGTTFTSYAMHWYRQAPOGLLEMGWINAGNKTKY 60

Oy              61 AOKFGGRVTMTTDSRTATYMELSLSDDTAVYYCAR 98
                :|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
            Dd          61 SOKFQRGVTTITRDTSASTAYMELSLSSEPTAVYYCAR 98


RESULT 11
US-09-438-954-41
; Sequence 41, Application US/09438954
; Patent No. 6458934
GENERAL INFORMATION:
APPLICANT: HONG, Hyo Jeong
APPLICANT: PARK, Sung Sup
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-Yul1
APPLICANT: YOON, Sung Kwan
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
FILE REFERENCE: 1303-124P
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Variable
OTHER INFORMATION: region of heavy chain of human antibody (M17750)
US-09-438-954-41

Query Match      78.1%; Score 407; DB 4; Length 119;
Best Local Similarity 78.6%; Pred. No. 8.7e-37;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Oy              1 QVOLLGSATEVKKPGASMKVSCMASGYPFTSYDISWYRQAPGGCLEMWGWISAYNGNTHY 60
                |||||:|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
            Dd          1 QVVLVGSGAEVKKRGASVKSCKRASGTTFTSYAMHWYRQAPOGLLEMGWINAGNKTKY 60

Oy              61 AOKFGGRVTMTTDSRTATYMELSLSDDTAVYYCAR 98
                :|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
            Dd          61 SOKFQRGVTTITRDTSASTAYMELSLSSEPTAVYYCAR 98

RESULT 12
PCT-US95-01219-10
```

```
Sequence 10, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-10

Query Match 78.1%; Score 407; DB 5; Length 119;
Best Local Similarity 78.6%; Pred. No. 8.7e-37;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLQSAIEVKKPKGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
DB 1 QVQLVQSGAEVKKPKGASVSKVSCASGYFTSYAMHWVRQAPGQRLIEWMGWIMAGNGNTKY 60
QY 61 AOKFGQGVTTMTDTSRRRAYMELRSLSRSDDTAVYYCAR 98
DB 61 SOKFGQGVTTTRDTSASTAYMELSLRSSEDTAVYYCAR 98

RESULT 13
US-09-025-769B-36
Sequence 36, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckethun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
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CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36

Query Match 77.9%; Score 406; DB 4; Length 120;
Best Local Similarity 78.6%; Pred. No. 1.1e-36;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLQSAIEVKKPKGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
DB 1 QVQLVQSGAEVKKPKGASVSKVSCASGYFTSYAMHWVRQAPGQRLIEWMGWIMAGNGNTKY 60
QY 61 AOKFGQGVTTMTDTSRRRAYMELRSLSRSDDTAVYYCAR 98
DB 61 AOKFGQGVTTTRDTSISTAYMELSLRSSEDTAVYYCAR 98

RESULT 14
US-09-025-769B-59
Sequence 59, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pluckethun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-59

Query Match 77.9%; Score 406; DB 4; Length 120;
Best Local Similarity 78.6%; Pred. No. 1.1e-36;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 1 QVOLLQSAIEYKKPGASKVKSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
Db 1 QVOLLQSAIEYKKPGASVYKSCASGYFTSYMEHWQAQPGGLEWVGWISAYNGNTHY 60
Qy 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCAR 98
Db 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCAR 98

RESULT 15
US-08-652-816A-19
Sequence 19, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-19

Query Match 77.8%; Score 405.5; DB 2; Length 120;
Best Local Similarity 80.4%; Pred. No. 1.3e-36;
Matches 78; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 1 QVOLLQSAIEYKKPGASKVKSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
Db 1 QVOLLQSAIEYKKPGASVYKSCASGYFTSYMEHWQAQPGGLEWVGWISAYNGNTHY 59
Qy 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCA 97
Db 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCA 96

Search completed: December 30, 2003, 11:05:32
Job time : 11.0346 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 / Search time 9.39399 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-28

Sequence: 1 QVQLQSGAEVRRKPGASVKV.....AYMELRLSRSDDTAVYYCAR 98

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	460	89.1	98	2	S26919 Ig heavy chain V r
2	457	88.6	129	2	S36260 Ig heavy chain V r
3	455	88.2	122	2	S36271 Ig heavy chain V r
4	454	88.0	124	2	S19665 Ig heavy chain V r
5	444	86.0	131	2	S21924 Ig heavy chain V r
6	443	85.9	160	2	PI0105 anti-PR2 erythrocy
7	424	82.2	111	2	S21925 Ig heavy chain V r
8	423	82.0	98	2	S26918 Ig heavy chain V r
9	420	81.4	136	2	S31600 Ig heavy chain V r
10	416	80.6	98	2	S26938 Ig heavy chain V r
11	416	80.6	117	2	S1680 Ig heavy chain V r
12	416	80.6	117	2	S18551 Ig heavy chain V r
13	415	80.6	135	2	S48530 anti-Sm antibody V
14	415	80.4	118	2	S36265 Ig heavy chain V r
15	413	80.0	127	2	S34014 Ig heavy chain V r
16	411	79.7	117	2	S18553 Ig heavy chain V r
17	408	79.1	98	2	S26912 Ig heavy chain V r
18	408	79.1	125	2	S68170 Ig heavy chain V r
19	408	79.1	129	2	S46392 Ig heavy chain V r
20	406	78.7	132	2	S31566 Ig heavy chain V r
21	403	78.1	104	2	S69899 Ig heavy chain V r
22	401	77.7	98	2	S26920 Ig heavy chain V r
23	401	77.7	123	2	D33548 Ig heavy chain V-1
24	399	77.3	148	2	S29257 Ig heavy chain pre
25	396	76.7	117	1	HYTHUC Ig heavy chain V r
26	396	76.7	171	1	S23623 Ig heavy chain V r
27	395	76.6	98	2	PH0871 Ig heavy chain V r
28	395	76.6	117	2	S18552 Ig heavy chain V r
29	394	76.4	110	2	PH1670 Ig heavy chain V r

30	393	76.2	142	2	A32483 Ig heavy chain V r
31	392	76.0	117	1	HYTHUC3 Ig heavy chain pre
32	390	75.0	116	2	S31667 Ig heavy chain V r
33	387	75.0	126	2	I44151 Ig heavy chain V r
34	386	74.6	114	2	PH1667 Ig heavy chain V r
35	386	74.6	118	2	PH1666 Ig heavy chain V r
36	385	74.6	98	2	S24680 Ig heavy chain V1
37	383	74.7	117	2	PR0371 Ig gamma chain pre
38	381	73.8	109	2	PH1668 Ig heavy chain V r
39	381	73.6	119	2	JN0295 Ig heavy chain V-D
40	381	73.6	135	2	B32274 Ig heavy chain pre
41	380	73.6	98	2	S26915 Ig heavy chain V r
42	380	73.6	116	2	S31698 Ig heavy chain pre
43	380	73.6	119	2	PH0959 Ig heavy chain V r
44	380	73.6	119	2	PH0961 Ig heavy chain V r
45	380	73.6	120	2	PH0962 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26919
Ig heavy chain V regi
C:Species: Homo sapie
C:Date: 22-Nov-1993 #
R:Accession: S26919
R:Tomlinson, I.M.; We
J. Mol. Biol. 227, 77
A>Title: The repetoi
A:Reference number: 5
A:Accession: S26919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOR
A:Cross-references: E
C:Superfamily: Immunoc
C:Keywords: heterotet
F:15-98/Domain: immun

Query Match
Best Local Similari
Matches 87; Cons

QY	1	QVQLQSGAEVRRKPGASVKV.....AYMELRLSRSDDTAVYYCAR 98	89.1%; Score 460; DB 2; Length 98; 88.8%; Pred. No. 1.5e-38; Active 4; Mismatches 7; Indels 0; Gaps 0;
DB	1	QVQLQSGAEVRRKPGASVKV.....AYMELRLSRSDDTAVYYCAR 98	
QY	61	AQKPGGR	AYMELRLSRSDDTAVYYCAR 98
DB	61	AQKPGGR	AYMELRLSRSDDTAVYYCAR 98

RESULT 2

S36260
Ig heavy chain V regi
C:Species: Homo sapie
C:Date: 03-Feb-1994 #
R:Accession: S36260
R:Griffiths, A.D.; Ma
EMBO J. 12, 725-734,
A>Title: Human anti-e
A:Reference number: S
A:Accession: S36260
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <GR
A:Cross-references: E
C:Superfamily: immunoc
C:Keywords: heterotet
F:15-98/Domain: immun

Query Match
Best Local Similari
Matches 87; Cons

Db 20 QVQLVSAEYVKKASVYKSCSKASGYFTSYGISMWRQAPGQGLEWMGMSISYNGDTNY 79
Oy 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 80 AQNLOGRVMTTDTSTSTAYMELSLRSDDTAVYYCAR 117

RESULT 7

S21925

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S21925

R:Friedman, D.F.

submitted to the EMBL Data Library, July 1991

A:Reference number: S21923

A:Accession: S21925

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 <FRI>

A:Cross-references: EMBL:X60503; NID:g33626; PIDN:CAA43023.1; PID:g33627

C:Genetics:

A:Insertions: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 82.2%; Score 424; DB 2; Length 111;
Best Local Similarity 88.0%; Pred. No. 6.2e-35;

Matches 81; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYGISMWRQAPGQGLEWMGMSISYNGDTY 60
Db 20 QVQLVSGAEYVKKASVYKSCSKASGYFTSYGISMWRQAPGQGLEWMGMSISYNGDTNY 79
Oy 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTA 92
Db 80 AOKLOGRVMTTDTSTSTAYMELSLRSDDTA 111

RESULT 8

S26918

Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26918

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 423; DB 2; Length 98;
Best Local Similarity 82.7%; Pred. No. 6.8e-35;

Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISYNGTDY 60
Db 1 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISYNGTGY 60
Oy 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98

RESULT 9

S31600
Ig heavy chain V region (DP-75) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993
C:Accession: S31600
R:Cuisinier, A.M.; Goujard, D.; Huez, G.; Virelizier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Reference number: S31600
A:Accession: S31600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <C>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 81.4%; Score 420; DB 2; Length 136;
Best Local Similarity 81.6%; Pred. No. 1.9e-34;

Matches 80; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISYNGTDY 60
Db 20 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISYNGTGY 79
Oy 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 80 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 117

RESULT 10

S26938

Ig heavy chain V region (DP-75) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26938

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26938

A:Accession: S26938

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1992

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 80.6%; Score 416; DB 2; Length 98;
Best Local Similarity 81.6%; Pred. No. 3.3e-34;

Matches 80; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISYNGTDY 60
Db 1 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISYNGTGY 60
Oy 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98
Db 61 AOKFOGRTVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98

RESULT 11

S31680

Ig heavy chain V region (DP-75) - human (man)

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31680

R:Cuisinier, A.M.; Goujard, D.; Huez, G.; Virelizier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanism that generate human immunoglobulin diversity operate from the

A:Reference number: S31585
A:Accession: S31680
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <CUI>
A:Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 416; DB 2; Length 117;
Best Local Similarity 81.6%; Pred. No. 4e-34;
Matches 80; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

OY 1 OVQLQSAAEVRKPGASVYVSCKASGYPTFSYDTSWVRQAQGCLGEMWGWSISGNTDY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 QVALVQSAGAEVKRKGASVKSCKASGYFTFSYVMHWVRQAQGCLGEMWGWINPNSGCTNY 79
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 61 AOKFOGRVTMTTDSRTATAYMELRSLSDDTAIVYYCAR 98
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 80 AOKFOGRVTMTTDSRTATAYMELRSLSDDTAIVYYCAR 117
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; F3:3625
R:Shin, B.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Seeda, E.; H
EMBO J. 10, 3641-3645, 1991
A>Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
J:ROlde, T.; Lu, E.W.; Huang, D.F.; Soto-Gill, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A>Title: Genetic analysis of self-associated immunoglobulin G rheumatoid factors from t
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 416; DB 2; Length 117;
Best Local Similarity 81.6%; Pred. NO. 4e-34;
Matches 80; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY 1 OVQLQSAAEVRKPGASVYVSCKASGYPTFSYDTSWVRQAQGCLGEMWGWSISGNTDY 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 20 QVALVQSAGAEVKRKGASVKSCKASGYFTFSYVMHWVRQAQGCLGEMWGWINPNSGCTNY 79
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 61 AOKFOGRVTMTTDSRTATAYMELRSLSDDTAIVYYCAR 98
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 80 AOKFOGRVTMTTDSRTATAYMELRSLSDDTAIVYYCAR 117
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999

Accession: S49530
R: Mahmoudi, M.; Edwa
submitted to the EMF
A: Description: Molec
A: Reference number:
A: Accession: S49530
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-135 <h
A: Cross-references:
C: Superfamily: Immun
F: 34-117/Domain: imm

Query Match
Best Local Similar
Matches 80; Cor

QY 1 QVOLL
Db 20 QVOLL
QY 61 AOKFO
Db 80 AOKFO

RESULT 14
S36265
IG heavy chain V re
C: Species: Homo sap
C: Date: 03-Feb-1994
C: Accession: S36265
R: Griffiths, A.D.; b
EMBO J. 12, 725-734,
A: Title: Human anti-
A: Reference number:
A: Accession: S36265
A: Status: preliminary
A: Molecule type: mAb
A: Residues: 1-118 <C
A: Cross-references:
C: Superfamily: Immun
C: Keywords: heterot
F: 15-98/Domain: immu

Query Match
Best Local Similar
Matches 79; Cor

QY 1 QVOLL
Db 1 QVOLL
QY 61 AOKFO
Db 61 AOKFO

RESULT 15
S34014
IG heavy chain V re
C: Species: Homo sap
C: Date: 02-Dec-1993
C: Accession: S34014
R: Mariette, X.; Tsai
Eur. J. Immunol. 23
A: Title: Nucleotid
A: Reference number:
A: Accession: S34014
A: Status: preliminary
A: Molecule type: mR
A: Residues: 1-127 <I
A: Cross-references:

J.; Cairns, E.; Bell, D.
ata Library, October 1994
Characterization of natural human anti-Sm autoantibodies.
797

L: Z46348; NID: g560839; PIDN: CA68467.1; PID: g560840
obulin V region; immunoglobulin homology
globulin homology <IMM>

80.6%; Score 416; DB 2; Length 135;
81.6%; Pred. No. 4.7e-34;
vative 5; Mismatches 13; Indels 0; Gaps 0;

EVRRKGSAYKVSCKASGYPTFTSDISWVRQAPGQGLEMMGMSISGNTDY 60
EVKKRGASAYKVSCKASGYFTGYVMMHVRQAPGQGLEMMGMINNSGNTY 79
WTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
MTRDTSISRTAYMELRSLSRSDDTAVYYCAR 117

(clone alpha-MUC1-1) - human (fragment)
(man)
quence_revision 03-Feb-1994 #text_change 23-Jul-1999

qvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
93
f antibodies with high specificity from phage display libraries
256; MUID: 93178448; PMID: 7679990

nucleic acid sequence not shown

L: Z18846; NID: g33121; PIDN: CAA79398.1; PID: g9339900
obulin V region; immunoglobulin homology
mer; immunoglobulin
lobulin homology <IMM>

80.4%; Score 415; DB 2; Length 118;
80.6%; Pred. No. 5.1e-34;
vative 7; Mismatches 12; Indels 0; Gaps 0;

EVRRKGSAYKVSCKASGYPTFTSDISWVRQAPGQGLEMMGMSISGNTDY 60
EVKKPGASAYKVSCKASGYFTGYVMMHVRQAPGQGLEMMGMINNSGNTY 60
WTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
MTRDTSISRTAYMELRSLSRSDDTAVYYCAR 98

1 - human
(man)
quence_revision 10-Nov-1995 #text_change 16-Aug-1996
10535
A.; Brouet, J.C.
6-851, 1993
quence analysis of the variable domains of four human monoclonal
1001; MUID: 93209281; PMID: 7681398

L: Z18321

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	80.0%;	Score 413;	DB 2;	Length 127;
-------------	--------	------------	-------	-------------

Beat Local Similarity 79.6%; Pred. No. 8.6e-34;
Matches 78; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Oy

1 QVQLLOSAAEYKPKGASIVKSCAASGYPTSYDLSWVRQAPGGGLEEMGMSTISYGNTDY 60
|||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db

1 QVQMVGSGAEYKKPGASIVKSCAASGYPTSVDINMVRQATGGGLEEMGMNPPSSCNTGY 60

61 A Q K F G R V T M T D T S R T A Y M E L R S L R S D D T A V Y Y C A R 98

Db 61 A Q K F K G R V T M T R N T S I S T A Y M E L S L R S E D T A V Y F C A R 98

```
Search completed: December 30, 2003, 11:03:14
Job time : 9.39399 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 5.25426 Seconds
(without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-28
Perfect score: 516
Sequence: 1 QVQLQSGAEVRRKPGASVKV.....AYMEIRSRSDTAIVYCAR 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	396	76.7	117	1	P01743 homo sapien
2	392	76.0	117	1	P23083 homo sapien
3	373	72.3	147	1	P01744 homo sapien
4	344	66.7	117	1	P01742 homo sapien
5	343	66.5	117	1	P06327 mus musculu
6	339	65.7	114	1	P01741 mus musculu
7	330	64.0	117	1	P01753 mus musculu
8	329	63.8	120	1	P01745 mus musculu
9	327	63.4	140	1	P01746 mus musculu
10	326	63.2	117	1	P01758 mus musculu
11	321	62.2	117	1	P01750 mus musculu
12	319	61.8	117	1	P01748 mus musculu
13	318	61.6	139	1	P01751 mus musculu
14	315	61.0	118	1	P06330 mus musculu
15	313	60.7	117	1	P01756 mus musculu
16	313	60.7	117	1	P01757 mus musculu
17	311	60.3	117	1	P01749 mus musculu
18	308	59.7	117	1	P01754 mus musculu
19	308	59.7	120	1	P06328 mus musculu
20	308	59.7	120	1	P06329 mus musculu
21	307	59.5	137	1	P01755 mus musculu
22	301	58.3	136	1	P01759 mus musculu
23	301	58.3	138	1	P03980 mus musculu
24	300	58.1	125	1	P06326 homo sapien
25	290	56.2	121	1	P06328 mus musculu
26	287.5	55.7	120	1	P06421 homo sapien
27	286	55.4	117	1	P01764 homo sapien
28	278	53.9	117	1	P18526 mus musculu
29	277	53.7	121	1	P01771 homo sapien
30	271	52.5	121	1	P01770 homo sapien
31	267	51.7	122	1	P01769 homo sapien
32	267	51.7	124	1	P01761 homo sapien
33	266	51.6	122	1	P01768 homo sapien

34	264	51.2	117	1	P19180 carassius a
35	262	50.8	114	1	P01763 homo sapien
36	261	50.6	119	1	P01777 homo sapien
37	261	50.6	124	1	P01760 homo sapien
38	260.5	50.5	116	1	P19181 carassius a
39	259	50.2	136	1	P01783 mus musculu
40	258.5	50.1	115	1	P01767 homo sapien
41	258	50.0	119	1	P01773 homo sapien
42	257	49.8	115	1	P01765 homo sapien
43	257	49.8	117	1	P01813 catman croc
44	257	49.8	117	1	P18525 mus musculu
45	255	49.4	122	1	P01762 homo sapien

ALIGNMENTS

```

RESULT 1
ID      HV1B_HUMAN      STANDARD;      PRT;      117 AA.
AC      P01743;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Ig heavy chain V-I region H33 precursor.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=83144028; PubMed=6298778;
RA      Reichart G., Ram D., Glazer L., Zakut R., Givol D.;
RT      "Evolutionary aspects of immunoglobulin heavy chain variable region
RT      (VH) gene subgroups.";
RL      Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@ebi.ac.uk).
CC
CC      -----
DR      EMBL; J00240; AAA52988.1; -.
DR      PIR; A02024; HVHUNG.
DR      HSSP; P01772; 2FB4.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding activity; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF0047; Ig; 1.
DR      SMART; SM00406; IgV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL      1
FT      CHAIN      19
FT      DOMAIN      20 117      IG HEAVY CHAIN V-I REGION H33.
FT      NON_TER      117      IG-LIKE.
SQ      SEQUENCE      117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
Query Match      76.7%; Score 396; DB 1; Length 117;
Best Local Similarity      Pred. No. 1e-38;
Matches 77; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
Qy      1 QVQLQSGAEVRRKPGASVKASGYPFTSYDYSWVRQAPGQGLRWGWSISYSGNTDY 60
Db      20 QVQLVQSGAEVRRKPGASVKASGYSYTFNSIYHWVRQAPGQGLRWGWSISYSGNTDY 79

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QY 61 AOKFOGRVTMTDTSRTAYMELRSDDTAVYYCAR 98
DB 80 AOKFOGRVTMTDTSRTAYMELRSDDTAVYYCAR 117

RESULT 2
HVLG_HUMAN STANDARD; PRT; 117 AA.
ID HVLG_HUMAN
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukushima S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL: X07448; - NOT_ANNOTATED_CDS.
DR PIR; S00476; HYHUS3.
DR HSSP; P01772; ZPB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 76.0%; Score 392; DB 1; Length 117;
Best Local Similarity 78.6%; Pred. No. 3e-38;
Matches 77; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRRKPGASVKYSCKASGYPTSYDISWVRQAPGGLEMMGWISISGNTDY 60
DB 20 QVOLLQSAAEVRRKPGASVKYSCKASGYPTSYDISWVRQAPGGLEMMGWISISGNTDY 79

RESULT 3
HVLG_HUMAN STANDARD; PRT; 147 AA.
ID HVLG_HUMAN
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=83065234; PubMed=6815656;
RA Kanten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.U.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RN SEQUENCE OF 20-147.
RA Benmich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal; Pyroglutamate carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD RES 20 20 PYROGLUTAMATE CARBOXYLIC ACID.
FT DISUFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 72.3%; Score 373; DB 1; Length 147;
Best Local Similarity 71.4%; Pred. No. 6e-36;
Matches 70; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRRKPGASVKYSCKASGYPTSYDISWVRQAPGGLEMMGWISISGNTDY 60
DB 20 QVOLLQSAAEVRRKPGASVKYSCKASGYPTSYDISWVRQAPGGLEMMGWISISGNTDY 79

RESULT 4
HVLG_HUMAN STANDARD; PRT; 117 AA.
ID HVLG_HUMAN
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.

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RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A.; Rutishauser U.; Gail W.E.; Gottlieb P.D.;
RA Maxdel M.J.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gail W.E.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90563; GIMHEU.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Fyrtrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 66.7%; Score 344; DB 1; Length 117;
Best Local Similarity 71.1%; Pred. No. 1e-32;
Matches 69; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVRRKSGASVSKVSCKASGYPFTSYDTSWVRQAPGQGLEWMGIMSTISGNTDY 60
DB 1 QVQLVQSGAEVRRKSGASVSKVSCKASGYPFTSYDTSWVRQAPGQGLEWMGIVPMGEPNY 60
QY 61 AOKFGQKRVTTTDSRTTAYMELSLRSDPTAVYYCA 97
DB 61 AOKFGQKRVTTTDSRTTAYMELSLRSDPTAVYYCA 97

RESULT 5
HV52_MOUSE STANDARD; PRT: 117 AA.
ID HV52_MOUSE STANDARD; PRT: 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578121;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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DR EMBL; M13787; AAA38499.1; -.
DR PIR; A02029; HYMSA1.
DR HSSP; P01810; 2PB3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC13865DFC9D CRC64;

Query Match 66.5%; Score 343; DB 1; Length 117;
Best Local Similarity 64.3%; Pred. No. 1.3e-32;
Matches 63; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVRRKSGASVSKVSCKASGYPFTSYDTSWVRQAPGQGLEWMGIMSTISGNTDY 60
DB 20 QVQLVQSGAEVRRKSGASVSKVSCKASGYPFTSYDTSWVRQAPGQGLEWMGIVPMGEPNY 79
QY 61 AOKFGQKRVTTTDSRTTAYMELSLRSDPTAVYYCA 98
DB 80 NEKFKGKATITADKSSSTAYMQLSLTSENSAVYFCAR 117

RESULT 6
HV00_MOUSE STANDARD; PRT: 114 AA.
ID HV00_MOUSE STANDARD; PRT: 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D.; Nisenzon A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGH1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02022; GIMSA1.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON TER 114 114

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SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A9F4BE CRC64;
 Query Match 65.7%; Score 339; DB 1; Length 114;
 Best Local Similarity 68.0%; Pred. No. 3.7e-32;
 Matches 66; Conservative 14; Mismatches 17; Indels 0; Gaps 0;
 QY 1 QVQLQSAAEVRRKPKASVYKSCASGYPTFSYDISWVRQAPGGLEMMGIMISYSGNTDY 60
 DB 1 EVQLQQSGAEIVKASSVYKSCATGYTFSYELTWVRQAPGGLEDDGYISSSAVYRY 60
 QY 61 AQKFGQVMTTDTSRRTAYMELRSLSRSDTAVYYCAR 97
 DB 61 AQKFGQVMTTDESTNTAYMELSSRSRSDTAVYYCAR 97
 RESULT 7
 HV09_MOUSE STANDARD; PRT; 117 AA.
 ID HV09_MOUSE
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 186-1 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RT Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR; D90809; HWS61.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;
 Query Match 64.0%; Score 330; DB 1; Length 117;
 Best Local Similarity 64.3%; Pred. No. 4.1e-31;
 Matches 63; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 QY 1 QVQLQSAAEVRRKPKASVYKSCASGYPTFSYDISWVRQAPGGLEMMGIMISYSGNTDY 60
 DB 20 QVQLQQPGAEIVKASVYKSCASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGCTKY 79
 QY 61 AQKFGQVMTTDTSRRTAYMELRSLSRSDTAVYYCAR 98
 DB 80 NEKFKSKATLTVDSSSTAYMQLSLTSEDSAVYYCAR 117
 RESULT 8
 HV03_MOUSE

ID HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 36-65.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83131846; PubMed=6186498;
 RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
 RA Marehah-Rotherstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenate
 RT idio type response of the strain A mouse.";
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 CC SEGMENT, JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 111 IG-LIKE.
 FT NON TER 120 120
 SQ SEQUENCE 120 AA; 13307 MW; F04E9A167B654AF CRC64;
 Query Match 63.8%; Score 329; DB 1; Length 120;
 Best Local Similarity 62.9%; Pred. No. 5.6e-31;
 Matches 61; Conservative 18; Mismatches 18; Indels 0; Gaps 0;
 QY 2 VQLQSAAEVRRKPKASVYKSCASGYPTFSYDISWVRQAPGGLEMMGIMISYSGNTDYA 61
 DB 1 VQLQSGAEIVKASVYKSCASGYTFTSYINWVKRPPGGLEWIGVINGNGYTKYN 60
 QY 62 OKFGQVMTTDTSRRTAYMELRSLSRSDTAVYYCAR 98
 DB 61 EKFKGKTLTVDKSSSTAYMQLSLTSEDSAVYYCAR 97
 RESULT 9
 HV02_MOUSE STANDARD; PRT; 140 AA.
 ID HV02_MOUSE
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 93G7 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=A/J;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 RT immunoglobulin heavy chain.";
 RL Science 216:309-311(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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DR EMBL; J00493; AAA8128.1; -
DR PIR; A94264; HVM5G7.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25AACBBE31DA5C8 CRC64;

Query Match 63.4%; Score 327; DB 1; Length 140;
Best Local Similarity 61.2%; Pred. No. 1.1e-30;
Matches 60; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Qy 1 QVOLLQSAAEVRKPKASVYKSCASGYPTSDISWVRAPOAGGLEMMGWISYSGNTDY 60
Db 20 EVQLQQSAELVKKASVYKSCASGYFTSTGIMVWVQRPQGLEWIGIYPPNGYIN 79

Qy 61 AQKFGKVTMTTDSRRATYMWELSLRSDPTAVYYCAR 98
Db 80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYYCAR 117

RESULT 10
HVI4_MOUSE
ID_HVI4_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Glivol D., Zakut R., Eitron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes."
RL Nature 292:426-430(1981).
CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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DR EMBL; J00488; AAA8519.1; -
DR PIR; A02041; HVM58A.
DR HSSP; P01810; 2PBJ.
DR MGP; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 63.2%; Score 326; DB 1; Length 117;
Best Local Similarity 61.2%; Pred. No. 1.2e-30;
Matches 60; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

Qy 1 QVOLLQSAAEVRKPKASVYKSCASGYPTSDISWVRAPOAGGLEMMGWISYSGNTDY 60
Db 20 EVQLQQSGPELVKPKASVYKSCASGYFTDYNNHVMVQSHGSKSLEWIGIYPPNGYIN 79

Qy 61 AQKFGKVTMTTDSRRATYMWELSLRSDPTAVYYCAR 98
Db 80 NQKFKSKATLTVDNSSSTAYMELSLTSEDSAVYYCAR 117

RESULT 11
HVI6_MOUSE
ID_HVI6_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -! MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
CC PIR: A02032; HVM502.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD51FCA8C CRC64;

Query Match 62.2%; Score 321; DB 1; Length 117;
Best Local Similarity 64.6%; Pred. No. 4.5e-30;
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 2 VOLLQSAAEVRKPKASVYKSCASGYPTSDISWVRAPOAGGLEMMGWISYSGNTDYA 61
Db 21 VQLQQSAELVKKASVYKSCASGYFTSYMMHVMVQRPQGLEWIGIRHPSDDTYNN 80

Qy 62 AQKFGKVTMTTDSRRATYMWELSLRSDPTAVYYCAR 97

RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J.3:517-523(1984).
DR PIR: A02040; MMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 61.0%; Score 315; DB 1; Length 118;
Best Local Similarity 60.2%; Pred. No. 2, 2e-29;
Matches 59; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSAEVRKPGASVVKSCASGYPTSYDISWVROAPQGLMWMGMSISYGNIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVQLQDSGPBELVKPGASVVKSCASGYFTFDYIMNMVKQSHKSLKMWIGDIPNNGTISY 60
QY 61 AOKFGRYVTMTTDSRRRTAYMELRLSRSDDTAVYYCAR 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NQKFKGKATLTVDKSSSTAYMELRLSLTSEDSAVYYCAR 98

RESULT 15

HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: CONTAINS 1 immunoglobulin-like domain.
DR PIR; A02039; MMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 60.7%; Score 313; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 3, 8e-29;

Matches 59; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 QVQLQSAEVRKPGASVVKSCASGYPTSYDISWVROAPQGLMWMGMSISYGNIDY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EVQLQDSGPBELVKPGASVVKSCASGYFTFDYIMNMVKQSHKSLKMWIGDIPNNGTISY 60
QY 61 AOKFGRYVTMTTDSRRRTAYMELRLSRSDDTAVYYCAR 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR 98
Search completed: December 30, 2003, 10:55:50
Job time : 5.25426 secs


```
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2001 (Tremblrel. 23, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR InterPro; IPR000005; HTHARC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
```

```
Query Match 73.3%; Score 378; DB 4; Length 614;
Best Local Similarity 72.4%; Pred. No. 2.3e-34;
Matches 71; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
```

```
Oy 1 QVOLLQSAAEVRKPGASVSKASGYPTSTYDISWVRQAPGGGLMMGMISISGNTDY 60
Db 20 QVOLLQSGAEVRKPGASVSKASGYPTSTYRILHWVRQAPGGGLMMGMHITFNGNTY 79
Oy 61 AQKFGQRLVTMTDTSRRRTAYMELRSLSRSDTAVYYCAR 98
Db 80 AQKFGQRLVTITRDRSMNTAYMELSLRSEDTAVYYCAR 117
```

```
RESULT 6
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SNC66, a Ig-like gene which is
RT down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A63ES CRC64;
```

```
Query Match 72.7%; Score 375; DB 4; Length 497;
Best Local Similarity 70.4%; Pred. No. 3.9e-34;
Matches 69; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
```

```
Oy 1 QVOLLQSAAEVRKPGASVSKASGYPTSTYDISWVRQAPGGGLMMGMISISGNTDY 60
Db 20 QVOLLQSGAEVRKPGASVSKASGYPTSTYRILHWVRQAPGGGLMMGMHITFNGNTY 79
```

```
Oy 61 AQKFGQRLVTMTDTSRRRTAYMELRSLSRSDTAVYYCAR 98
Db 80 AQKFGQRLTFSRDTSTINTAYMELSLRSDTAVYYCAR 117
```

```
RESULT 7
Q96Q50 PRELIMINARY; PRT; 159 AA.
AC Q96Q50;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
```

```
Query Match 72.3%; Score 373; DB 4; Length 159;
Best Local Similarity 72.4%; Pred. No. 1.6e-34;
Matches 71; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
```

```
Oy 1 QVOLLQSAAEVRKPGASVSKASGYPTSTYDISWVRQAPGGGLMMGMISISGNTDY 60
Db 20 QVOLLQSGAEVRKPGASVSKASGYPTSTYRILHWVRQAPGGGLMMGMHITFNGNTY 79
Oy 61 AQKFGQRLVTMTDTSRRRTAYMELRSLSRSDTAVYYCAR 98
Db 80 AQKFGQRLTMTDTSSTYVMDLSLSRSDTAVYYCAR 117
```

```
RESULT 8
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN (1)
RP SEQUENCE FROM N.A.
RA Song X.T., Peng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
```

DR PROSITE; PSS0835; IG LIKE; 1.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FA6AB CRC64;
Query Match 71.5%; Score 369; DB 5; Length 119;
Best Local Similarity 72.4%; Pred. No. 3.3e-34;
Matches 71; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
QY 1 QVQLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGQLEMGWISISGNTDY 60
DB 1 QVQLVESGAEVRKPGASVSKVSCKASGYPTFGYMMWVRQADGHGLEWIGYINPSRGYNY 60
QY 61 AOKFGQRYTMTDTSRRATVMEISSLRSDPTAVYYCAR 98
DB 61 NQKFKRVTMTTDSKFSATYMDLSLRSDASAVYYCAR 98
RESULT 9
Q9UL89 PRELIMINARY; PRT; 116 AA.
Q9UL89
AC Q9UL89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR HSSP; P01810; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;
Query Match 68.4%; Score 353; DB 4; Length 116;
Best Local Similarity 75.3%; Pred. No. 2.1e-32;
Matches 70; Conservative 7; Mismatches 16; Indels 0; Gaps 0;
QY 5 LOSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGQLEMGWISISGNTDYAOKF 64
DB 1 VOSGAEEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGQLEMGWISISGNTDYAOKF 60
QY 65 OGRVMTTDTSRRTAVMEISSLRSDPTAVYYCAR 97
DB 61 OGRVTTTADKSTSTAYMELSLRSEDPTAVYYCA 93
RESULT 10
Q925S3 PRELIMINARY; PRT; 147 AA.
Q925S3
AC Q925S3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice";
RL world J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse gene related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain";
RL Int. J. Radiat. Biol. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
Query Match 66.5%; Score 343; DB 11; Length 147;
Best Local Similarity 66.3%; Pred. No. 3.8e-31;
Matches 65; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
QY 1 QVQLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGQLEMGWISISGNTDY 60
DB 3 QVQLHSGEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGQLEMGWIFPGEGSTEX 62
QY 61 AOKFGQRYTMTDTSRRATVMEISSLRSDPTAVYYCAR 98
DB 63 NEKFKRATLSVDKSSSTAYMELTSLRSDASAVYYFCAR 100
RESULT 11
Q9Y298 PRELIMINARY; PRT; 150 AA.
Q9Y298
AC Q9Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.


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FT  NON TER      150      150
SQ  SEQUENCE     150 AA;  16031 MW;  563D164AB22802D5 CRC64;

Query Match
Best Local Similarity 66.3%; Score 342; DB 4; Length 150;
Best Local Similarity 69.1%; Pred. No. 5.1e-31;
Matches 67; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

OY  1 QVOLLQSAAEVRRKPGASVSKASGYPTSDISWVQAPQGLGEMMGWISYSGNTDY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  20 QVOLLQSGPELVKPGASVSKASGYPTSDISWVQAPQGLGEMMGWISYSGNTDY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY  61 AOKFGQVYMTTDTSRRTAYMELSLRSDDTAVYYCA 97
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  80 AREFGSVYMTADTSTDIAVMELSLRSDDTAVYYCA 116
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 12
O8VCX7  PRELIMINARY; PRT; 613 AA.
AC  O8VCX7;
DT  01-MAR-2002 (TREMBLrel. 20, Created)
DT  01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Hypothetical 67.9 kDa protein.
GN  IGH-6.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Salivary gland;
RA  Strausberg R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC018315; AAH18315.1; -.
DR  MGI; MGI:96448; Igh-6.
DR  InterPro; IPR007110; Igh-like.
DR  InterPro; IPR003006; IGH_MHC.
DR  InterPro; IPR003596; Igh_v.
DR  Pfam; PF00047; Igh_5.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IGH_LIKE; 5.
DR  PROSITE; PS00290; IGH_MHC; 3.
KW  Hypothetical protein.
SQ  SEQUENCE 613 AA;  67855 MW;  41A9384DD4C22862 CRC64;

Query Match
Best Local Similarity 65.7%; Score 339; DB 11; Length 613;
Matches 64; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

OY  1 QVOLLQSAAEVRRKPGASVSKASGYPTSDISWVQAPQGLGEMMGWISYSGNTDY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  20 QVOLLQSGPELVKPGASVSKASGYPTSDISWVQAPQGLGEMMGWISYSGNTDY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY  61 AOKFGQVYMTTDTSRRTAYMELSLRSDDTAVYYCA 98
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  80 NEKFKGKATFTADTSSNTAYMQLSLTSDSAVYYCAR 117
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
O91WT1  PRELIMINARY; PRT; 481 AA.
AC  O91WT1;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Hypothetical 52.1 kDa protein.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.

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RC  TISSUE=Colon;
RA  Strausberg R.;
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC013490; AAH13490.1; -.
DR  InterPro; IPR007110; Igh-like.
DR  InterPro; IPR003006; IGH_MHC.
DR  InterPro; IPR003596; Igh_v.
DR  Pfam; PF00047; Igh_4.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IGH_LIKE; 4.
DR  PROSITE; PS00290; IGH_MHC; 2.
KW  Hypothetical protein.
SQ  SEQUENCE 481 AA;  52105 MW;  97DF68D159463F65 CRC64;

Query Match
Best Local Similarity 65.5%; Score 338; DB 11; Length 481;
Matches 64; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

OY  1 QVOLLQSAAEVRRKPGASVSKASGYPTSDISWVQAPQGLGEMMGWISYSGNTDY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  20 QVOLLQSGPELVKPGASVSKASGYPTSDISWVQAPQGLGEMMGWISYSGNTDY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY  61 AOKFGQVYMTTDTSRRTAYMELSLRSDDTAVYYCA 98
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  80 NEKFKGKATFTADTSSNTAYMQLSLTSDSAVYYCFCTR 117
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
Q9DBL4  PRELIMINARY; PRT; 473 AA.
AC  Q9DBL4;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  1810060099rik protein.
DE  IGH-1 OR 1810060009rik.
GN  IGH-1 OR 1810060009rik.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Pancreas;
RX  MEDLINE=21085660; Pubmed=11217851;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA  Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Guerinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Salamito N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
DR  EMBL; AK007918; BAB25349.1; -.
DR  HSSP; P01842; 7FAB.
DR  MGI; MGI:96443; Igh-1.
DR  InterPro; IPR007110; Igh-like.
DR  InterPro; IPR003006; IGH_MHC.
DR  InterPro; IPR003596; Igh_v.
DR  Pfam; PF00047; Igh_4.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IGH_LIKE; 4.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 31.5256 Seconds
(without alignment)
493.415 Million cell updates/sec

Title: US-09-674-752-28
Perfect score: 516
Sequence: 1 QVQLQSGAEVRKPGASVKV.....AYWELESLRSDTAIVYCAR 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504	97.7	98	21	AA50955 Human anti-factor
2	500	96.9	132	21	AA50953 Human anti-factor
3	491	95.2	132	21	AA50950 Human anti-factor
4	471	91.3	98	21	AA50954 Human anti-factor
5	467	90.5	247	23	ABP45105 Human Blys binding
6	467	90.5	250	23	ABP45549 Human Blys binding
7	464	89.9	250	21	ABP45584 Human anti-factor
8	460	89.1	98	21	AA50952 Human anti-factor
9	460	89.1	98	23	ABG91862 Human antibody fra

10	460	89.1	98	23	ABG78171 Human Fv molecule
11	460	89.1	104	22	ABG55895 Human liver peptid
12	460	89.1	104	22	ABP40538 Peptide #8044 enco
13	460	89.1	117	16	ABP66311 Human immunoglobul
14	460	89.1	248	23	ABP45461 Human Blys binding
15	460	89.1	251	23	ABP45551 Human Blys binding
16	460	89.1	251	23	ABP45861 Human Blys binding
17	460	89.1	251	23	ABP45910 Human Blys binding
18	460	89.1	255	23	ABP45179 Human Blys binding
19	460	89.1	259	23	ABP45345 Human Blys binding
20	458	88.8	251	23	ABP45727 Human Blys binding
21	457	88.6	247	23	ABP45862 Human Blys binding
22	457	88.6	249	23	ABP45414 Human Blys binding
23	457	88.6	250	23	ABP45550 Human Blys binding
24	457	88.6	251	23	ABP45582 Human Blys binding
25	457	88.6	251	23	ABP45867 Human Blys binding
26	456	88.4	248	23	ABP45860 Human Blys binding
27	456	88.4	251	23	ABP45575 Human Blys binding
28	456	88.4	251	23	ABP45859 Human Blys binding
29	455	88.2	248	23	ABP45767 Human Blys binding
30	455	88.2	257	23	ABP45568 Human Blys binding
31	454	88.0	251	23	ABP45544 Human Blys binding
32	454	88.0	254	23	ABP45394 Human Blys binding
33	453	87.8	253	23	ABP45953 Human Blys binding
34	452	87.6	248	23	ABP45866 Human Blys binding
35	451.5	87.5	246	23	ABP45181 Human Blys binding
36	451	87.4	98	21	AA50951 Human anti-factor
37	451	87.4	247	23	ABP45715 Human Blys binding
38	451	87.4	257	23	ABP45599 Human Blys binding
39	451	87.4	259	23	ABP44962 Human Blys binding
40	450	87.2	251	23	ABP44919 Human Blys binding
41	450	87.2	251	23	ABP45725 Human Blys binding
42	450	87.2	251	23	ABP45858 Human Blys binding
43	449	87.0	121	22	AAU02549 Anti-adipocyte mon
44	449	87.0	253	23	ABP45625 Human Blys binding
45	449	87.0	259	23	ABP45441 Human Blys binding

ALIGNMENTS

RESULT 1
AA50955
ID AA50955 standard; Protein: 98 AA.
XX
AC AA50955;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH protein VH EL-25.
XX
XX Human; heavy chain; antibody; factor VIII; hemostatic;
KW hemophilia A; VH protein.
XX
OS Homo sapiens.
XX
PN W09958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SAND-) STICHTING SANDUIN BLOEDVOORZIEENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX WPI: 2000-053102/04.
XX
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -

XX Example 4; Fig 4B; 61pp; English.

PS This invention describes a novel polynucleotide (1) (and complements and

CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

CC coding for a human antibody with factor VIII specificity which has

CC hemostatic activity. (1) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents the human

CC anti-factor VIII antibody VH EL-25 protein which is used in the method

CC of the invention.

XX Sequence 98 AA;

SQ

Query Match 97.7%; Score 504; DB 21; Length 98;

Best Local Similarity 98.0%; Pred. No. 8,6e-43;

Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCASGYPTFSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

DB 1 QVQLQSAAEVRKPGASVKVSCASGYPTFSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

OY 61 AQKFGGRVTMTTDSRTATMELRSLSRSDPTAVYYCAR 98

DB 61 AQKFGGRVTMTTDSRTATMELRSLSRSDPTAVYYCAR 98

RESULT 2

AA50953

ID AA50953 standard; Protein; 132 AA.

XX

AC AA50953;

XX

DT 23-MAR-2000 (first entry)

XX

DE Human anti-factor VIII antibody VH protein VH IT-2.

XX

KM Human; heavy chain; antibody; factor VIII; hemostatic;

XX

OS Homo sapiens.

OS

PN MO958680-A2.

PN

PD 18-NOV-1999.

PD

PF 07-MAY-1999; 99MO-NL00285.

PF

XX

PR 08-MAY-1998; 98EP-0201543.

PR

XX

PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;

PI

DR WPI; 2000-053102/04.

DR

XX

PT New polynucleotide, polypeptide and antibody useful for diagnosing the

PT presence of neutralizing antibodies against factor VIII and for

PT treatment of hemophilia A patients with these antibodies -

PT

XX

PS Example 4; Fig 4B; 61pp; English.

XX

CC This invention describes a novel polynucleotide (1) (and complements and

CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

CC coding for a human antibody with factor VIII specificity which has

CC hemostatic activity. (1) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents the human

CC anti-factor VIII antibody VH IT-2 protein which is used in the method

CC of the invention.

XX

SQ Sequence 132 AA;

Query Match 96.9%; Score 500; DB 21; Length 132;

Best Local Similarity 95.9%; Pred. No. 3e-42;

Matches 94; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCASGYPTFSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

DB 1 QVQLQSAAEVRKPGASVKVSCASGYPTFSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

OY 61 AQKFGGRVTMTTDSRTATMELRSLSRSDPTAVYYCAR 98

DB 61 AQKFGGRVTMTTDSRTATMELRSLSRSDPTAVYYCAR 98

RESULT 3

AA50950

ID AA50950 standard; Protein; 132 AA.

XX

AC AA50950;

XX

DT 23-MAR-2000 (first entry)

XX

DE Human anti-factor VIII antibody VH clone IT-2 encoded protein.

XX

KM Human; heavy chain; antibody; factor VIII; hemostatic;

XX

KM hemophilia A; VH gene.

XX

OS Homo sapiens.

OS

PN MO958680-A2.

PN

PD 18-NOV-1999.

PD

PF 07-MAY-1999; 99MO-NL00285.

PF

XX

PR 08-MAY-1998; 98EP-0201543.

PR

XX

PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;

PI

DR WPI; 2000-053102/04.

DR

XX

PT New polynucleotide, polypeptide and antibody useful for diagnosing the

PT presence of neutralizing antibodies against factor VIII and for

PT treatment of hemophilia A patients with these antibodies -

PT

XX

PS Example 4; Fig 4A; 61pp; English.

XX

CC This invention describes a novel polynucleotide (1) (and complements and

CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

CC coding for a human antibody with factor VIII specificity which has

CC hemostatic activity. (1) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents the human

CC anti-factor VIII antibody clone IT-2 protein which is used in the method

CC of the invention.

XX

SQ Sequence 132 AA;

Query Match 95.2%; Score 491; DB 21; Length 132;

Best Local Similarity 94.9%; Pred. No. 2,3e-41;

Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCASGYPTFSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

DB 1 QVQLQSAAEVRKPGASVKVSCASGYPTFSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

```

QY 61 AAKFGGRVTMTTDSRRATAYMELSLRSDDTAAYYCAR 98
   |||||||
DB 61 AAKFGGRVTMTTDSRRATAYMELSLRSDDTAAYYCAR 98

RESULT 4
AAY50954
XX AAY50954 standard; Protein; 98 AA.
AC AAY50954;
XX
XX 23-MAR-2000 (first entry)
XX
XX Human anti-factor VIII antibody VH protein VH EL-5.
DE
XX
XX Human, heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; VH protein.
XX
XX Homo sapiens.
OS
XX MO9958680-A2.
PN
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-NL00285.
PF
XX
XX 08-MAY-1998; 98EP-0201543.
PR
XX
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
PA
XX
XX Voorberg JJ, Van Den Brink EN, Turehout EAM;
PI
XX WPI; 2000-053102/04.
DR
XX
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
XX Example 4; Fig 4B; 61pp; English.
XX
XX This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody VH EL-5 protein which is used in the method
CC of the invention.
XX
XX Sequence 98 AA;
SQ

Query Match 91.3%; Score 471; DB 21; Length 98;
Best Local Similarity 89.8%; Pred. No. 1.7e-39;
Matches 88; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```

```

XX
DE Human Blys binding scFv seq ID 116.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineutritic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX MO200202641-A1.
PN
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US19110.
PP
XX
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX WPI; 2002-114799/15.
DR
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1; Page 1734-1735; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineutritic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
XX Sequence 247 AA;
SQ

Query Match 90.5%; Score 467; DB 23; Length 247;
Best Local Similarity 90.8%; Pred. No. 1.1e-38;
Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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AC ABP45549;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1560.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
XX
PR 17-OCT-2000; 2000US-240816P.
XX
PR 16-MAR-2001; 2001US-276248P.
XX
PR 21-MAR-2001; 2001US-277379P.
XX
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2264-2265; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 250 AA;
XX
Query Match 90.5%; Score 467; DB 23; Length 250;
Best Local Similarity 90.8%; Pred. No. 1,1e-38;
Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 OVOLLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGGGLEMMGWISYSGNTDY 60
DB 1 OVOLLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGGGLEMMGWISYSGNTNY 60
QY 61 AOKFGQGVTTTDSRTATYMELRSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTATYMELRSLRSDDTAVYYCAR 98
RESULT 7

ABP45584
ID ABP45584 standard; Protein; 250 AA.
XX
AC ABP45584;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1595.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
XX
PR 17-OCT-2000; 2000US-240816P.
XX
PR 16-MAR-2001; 2001US-276248P.
XX
PR 21-MAR-2001; 2001US-277379P.
XX
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2306-2307; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 250 AA;
XX
Query Match 89.9%; Score 464; DB 23; Length 250;
Best Local Similarity 89.8%; Pred. No. 2.2e-38;
Matches 88; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 OVOLLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGGGLEMMGWISYSGNTDY 60
DB 1 OVOLLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGGGLEMMGWISYSGNTNY 60
QY 61 AOKFGQGVTTTDSRTATYMELRSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTATYMELRSLRSDDTAVYYCAR 98

```
RESULT 8
AA50952
ID AA50952 standard; Protein; 98 AA.
XX
XX AA50952;
XX
XX 23-MAR-2000 (first entry)
XX
XX Human anti-factor VIII antibody VH clone DP-14 protein #2.
XX
XX Human; heavy chain; antibody; factor VIII; hemostatic;
XX
XX hemophilia A; VH gene.
XX
XX Homo sapiens.
XX
XX MO9958680-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-NL00285.
XX
XX 08-MAY-1998; 98EP-0201543.
XX
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
XX Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX
XX WPI; 2000-053102/04.
XX
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
XX
XX presence of neutralizing antibodies against factor VIII and for
XX
XX treatment of hemophilia A patients with these antibodies -
XX
XX Example 4; Fig 4B; 61pp; English.
XX
XX This invention describes a novel polynucleotide (1) (and complements and
XX
XX hybridizable polynucleotides) comprising a contiguous nucleotide sequence
XX
XX coding for a human antibody with factor VIII specificity which has
XX
XX hemostatic activity. (1) is useful a primer or probe for detecting the
XX
XX presence of inhibitory antibodies directed against factor VIII. The
XX
XX polypeptides of the invention and the antibodies generated from them
XX
XX are useful in compositions for neutralizing factor VIII inhibiting
XX
XX antibodies in hemophilia A patients. This sequence represents the human
XX
XX anti-factor VIII antibody clone DP-14 protein which is used in the method
XX
XX of the invention.
XX
XX Sequence 98 AA;
XX
XX Query Match 89.1%; Score 460; DB 21; Length 98;
XX
XX Best Local Similarity 88.8%; Pred. No. 2.1e-38;
XX
XX Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX
XX
XX 1 QVOLLQSAAEVRKPKASVYKSCASGYPTSYDISYRWQAQGGLEMMGWISYSGNTDY 60
XX
XX 1 QVOLLQSAAEVRKPKASVYKSCASGYPTSYDISYRWQAQGGLEMMGWISYNGNTNY 60
XX
XX 61 AQKFGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCAR 98
XX
XX 61 AQKFGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCAR 98
XX
XX Db
XX
XX RESULT 9
XX
XX ABG91862
XX
XX ID ABG91862 standard; Protein; 98 AA.
XX
XX
XX AC ABG91862;
XX
XX
XX 04-DEC-2002 (first entry)
XX
XX
XX Human antibody fragment #46.
XX
XX
```

```
XX
XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX
XX metastasis; hypervariable region; autoimmune disease; thrombosis;
XX
XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX
XX myocardial infarction; retinopathic disease; abnormal platelet function;
XX
XX sulphated tyrosine-dependent protein-protein interaction.
XX
XX Homo sapiens.
XX
XX WO200253700-A2.
XX
XX 11-JUL-2002.
XX
XX 31-DEC-2001; 2001WO-US49442.
XX
XX 29-DEC-2000; 2000US-258948P.
XX
XX 29-DEC-2000; 2000US-0751181.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
XX
XX Lazarovits J, Hagai Y, Plakein D, Vogel T, Nimrod A, Mar-Haim H;
XX
XX Szantonon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
XX WPI; 2002-674776/72.
XX
XX
XX Novel isolated epitope present on cancer cells and important in
XX
XX physiological phenomena such as cell rolling, metastasis and
XX
XX inflammation, for treating autoimmune, inflammatory or cardiovascular
XX
XX diseases, and cancer -
XX
XX Disclosure; Page 246-247; 310pp; English.
XX
XX
XX The invention relates to an isolated epitope present on cancer cells and
XX
XX important in physiological phenomena such as cell rolling, metastasis and
XX
XX inflammation, where the epitope is capable of being bound by an antibody,
XX
XX its antigen-binding fragment or its complex comprising at least one
XX
XX antibody or its binding fragment having a first hypervariable region. The
XX
XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
XX
XX disease, thrombosis, restenosis, metastasis, growth and/or replication of
XX
XX tumour or leukaemia cells, increase in number of tumour or leukaemia
XX
XX cells in a patient, cell-cell, cell-matrix, platelet-matrix,
XX
XX platelet-platelet and/or cell-platelet adhesion or aggregation, for
XX
XX increasing mortality of tumour or leukaemia cells, for increasing the
XX
XX susceptibility of diseased cells to damage by anti-disease, anti-cancer
XX
XX or anti-leukaemia agents, or for decreasing the number of tumour or
XX
XX leukaemia cells in a patient, or in the manufacture of a medicament for
XX
XX the above mentioned purposes. The epitopes are useful for diagnosing and
XX
XX treating diseases such as cancer, leukaemia, autoimmune diseases,
XX
XX inflammatory diseases, cardiovascular diseases such as myocardial
XX
XX infarction, retinopathic diseases and other diseases mediated by abnormal
XX
XX platelet function and diseases caused by sulphated tyrosine-dependent
XX
XX protein-protein interactions. This sequence represents a human antibody
XX
XX fragment of the invention.
XX
XX Sequence 98 AA;
XX
XX Query Match 89.1%; Score 460; DB 23; Length 98;
XX
XX Best Local Similarity 88.8%; Pred. No. 2.1e-38;
XX
XX Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX
XX
XX 1 QVOLLQSAAEVRKPKASVYKSCASGYPTSYDISYRWQAQGGLEMMGWISYSGNTDY 60
XX
XX 1 QVOLLQSAAEVRKPKASVYKSCASGYPTSYDISYRWQAQGGLEMMGWISYNGNTNY 60
XX
XX 61 AQKFGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCAR 98
XX
XX 61 AQKFGQRTVMTTDTSTSTAYMELSLRSDDTAVYYCAR 98
XX
XX Db
XX
XX RESULT 10
XX
XX ABG78171
XX
XX ID ABG78171 standard; Protein; 98 AA.
XX
XX
XX AC ABG78171;
XX
XX
```

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XX DT 15-NOV-2002 (first entry)
XX XX
XX DE Human Fv molecule hypervariable region related peptide #46.
XX XX
XX DE Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX KM disulfide Fv; dsFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX OS Homo sapiens.
XX PN WO200259264-A2.
XX XX
XX PD 01-AUG-2002.
XX XX
XX PF 31-DEC-2001; 2001WO-US94440.
XX PR 29-DEC-2000; 2000US-0751181.
XX XX
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX XX
XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
XX PI Plaksin D, Peretz T;
XX XX
XX DR WPI; 2002-619166/66.
XX XX
XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX PT or fragment, or construct of fragment with enhanced binding
XX PT characteristics so as to selectively bind target cell in favour of other
XX PT cells -
XX XX
XX PS Claim 13; Page 169; 232pp; English.
XX XX
XX CC The invention relates to a peptide or polypeptide comprising an Fv
XX CC molecule, a construct or fragments or a construct of a fragment with
XX CC enhanced binding characteristics which selectively and/or specifically
XX CC binds to a target cell in favour of other cells, where binding is
XX CC primarily determined by a first hypervariable region and Fv is a single
XX CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX CC association with or attached, coupled, combined, linked or fused to a
XX CC pharmaceutical agent, is useful in the manufacture of a medicament, where
XX CC the medicament has activity against a diseased cell, preferably a cancer
XX CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
XX CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
XX CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
XX CC composition for use in inhibiting the growth of a diseased or cancer
XX CC cell. This sequence represents a human Fv molecule hypervariable region
XX CC related peptide of the invention.
XX XX
XX SQ Sequence 98 AA;
XX XX
XX Query Match 89.1%; Score 460; DB 23; Length 98;
XX Best Local Similarity 88.8%; Pred. No. 2.1e-38;
XX Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX XX
XX QY 1 QVQLLOSAAEVRKKGASVSKASGYPTFTSYDTSWVRQAPGQGLEWMGMSISYSGTDY 60
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 QVQLVQSGAEVKKPKGASVSKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGTNY 60
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX QY 61 AOKFGQRYMTTDTSTRTAYMELRSRSDTAAYYCAR 98
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 AOKLQGRVMTTDTSTRTAYMELRSRSDTAAYYCAR 98
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 61 AOKLQGRVMTTDTSTRTAYMELRSRSDTAAYYCAR 98
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX XX
XX RESULT 11
XX ID ABB55895
XX AC ABB55895 standard; Peptide; 104 AA.
XX XX
XX AC ABB55895;
XX XX
XX DT 25-FEB-2003 (first entry)
XX XX
XX KM Human liver peptide, SEQ ID NO 34543.
XX XX

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XX KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KM hypercholesterolemia; coronary heart disease.
XX XX
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00664.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488898/53.
XX XX
XX DR WPI; 2001-488898/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analysing gene expression in human adult liver -
XX PT Claim 27; SEQ ID NO 34543; 658pp; English.
XX XX
XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult
XX CC liver. (I) may be used for predicting, measuring and displaying gene
XX CC expression in samples derived from human adult liver. The genes
XX CC identified may be involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolemia which
XX CC is associated with coronary heart disease. ABB47348-ABB59930 represent
XX CC human liver single exon encoded peptides of the invention.
XX CC Note: The sequence information for this patent does not appear in the
XX CC printed specification but was obtained in electronic format directly
XX CC from WIPO at ffp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 104 AA;
XX XX
XX Query Match 89.1%; Score 460; DB 22; Length 104;
XX Best Local Similarity 88.8%; Pred. No. 2.2e-38;
XX Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX XX
XX QY 1 QVQLLOSAAEVRKKGASVSKASGYPTFTSYDTSWVRQAPGQGLEWMGMSISYSGTDY 60
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 4 QVQLVQSGAEVKKPKGASVSKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGTNY 63
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX QY 61 AOKFGQRYMTTDTSTRTAYMELRSRSDTAAYYCAR 98
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 64 AOKLQGRVMTTDTSTRTAYMELRSRSDTAAYYCAR 101
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX DB 64 AOKLQGRVMTTDTSTRTAYMELRSRSDTAAYYCAR 101
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX XX
XX RESULT 12
XX ID ABB40538
XX AC ABB40538 standard; Peptide; 104 AA.
XX XX
XX AC ABB40538;
XX XX
XX DT 04-FEB-2002 (first entry)
XX XX
XX DE Peptide #8044 encoded by human foetal liver single exon probe.
XX KM Human; foetal liver; gene expression; single exon nucleic acid probe.
XX XX

```


XX	10-MAY-1993;	93WO-JP00603.
PR	(NISR) JAPAN TOBACCO INC.	
PA	Honjo T, Matsuda F;	
PI	WPI; 1995-006791/01.	
DR	N-PSDB; AAQ78956.	
XX	DNA fragment comprising human immunoglobulin Vh genes - for the	
PT	production of human immunoglobulin in mammalian hosts	
PS	Claim 27; Page 54-55; 130pp; Japanese.	
XX	Protein sequences (AAR6295-51) are novel human immunoglobulin heavy	
CC	chain sequences encoded by novel isolated genes. The genes	
CC	(AAQ7939-79902) were isolated and cloned from a series of cosmid	
CC	constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M31, by PCR	
CC	amplification using primers AAQ78917-38. The genes are subdivided into 5	
CC	families of Vh genes. The fragments cover a region of 800 kb. The DNA	
CC	fragments were isolated from high molecular weight DNA from human	
CC	placenta. The DNA was partially digested with TaqI restriction enzyme.	
CC	The fragments were separated by gel electrophoresis and 35-45 Kb fractions	
CC	were collected. The fragments were ligated with ClaI-digested cosmid	
CC	vector pDB81. The ligation products were in vitro packed and infected	
CC	into E.coli 490A. The fragments were then subcloned by colony	
CC	hybridisation. The Vh genes and the DNA fragments encoding them are	
CC	useful in producing human immunoglobulin in mammalian hosts.	
CC	(Updated on 25-MAR-2003 to correct FN field.)	
XX		
SQ	Sequence	117 AA;
Query Match	89.1%; Score 460; DB 16; Length 117;	
Best Local Similarity	88.8%; Pred. No. 2.5e-38;	
Matches	87; Conservative 4; Mismatches 7; Indels 0; Gaps 0	
QY	1 QVQLQSGAEVRKPGASVKVSCKASGYPFTSYDYSISWYQAQPGQGLMMGMISVSGNTDY 60	
	20 QVQLVSGAEVKRKGASVKVSCKASGVTFTSYDYSISWYQAQPGQGLMMGMISVSGNTDY 79	
QY	61 AQRFGQGVMTTDTSRRTAYMELSLNSDDPTAVYYCAR 98	
	80 AQRKQGVMTTDTSRRTAYMELSLNSDDPTAVYYCAR 117	
Db	80 AQRKQGVMTTDTSRRTAYMELSLNSDDPTAVYYCAR 117	
RESULT 14		
ABP45461	ID	ABP45461 standard; Protein; 248 AA.
XX	ABP45461;	
AC	ABP45461;	
XX	19-AUG-2002 (first entry)	
DT	Human Bly's binding scFv SEQ ID 1472.	
XX	Human Bly's binding scFv SEQ ID 1472.	
XX	Bly's B lymphocyte stimulator; TNF superfamily; human; cytostatic;	
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;	
KM	immunosuppressive; immunomodulatory; antineoplastic;	
KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;	
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.	
XX		
OS	Homo sapiens.	
XX	WO200202641-A1.	
PN	10-JAN-2002.	
PD	15-JUN-2001; 2001WO-US19110.	
PF	16-JUN-2000; 2000US-212210P.	
XX	17-OCT-2000; 2000US-240816P.	
RR		

TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-324

Query Match 89.1%; Score 460; DB 12; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLQSAAEVRRKPGASVKVSCKASGYPTSYDISWVRQAPGQGLEWMGMSISYSGNTDY 60
Db 1 QVQLVSGAEVKKRPGASVKVSCKASGYPTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

Qy 61 AOKFQGRVTMTTDTTSRTAYMELRSLSRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

RESULT 6
US-10-041-860-326

Sequence 326, Application US/10041860
Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvahan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FaastSeq for Windows Version 4.0

SEQ ID NO 326

LENGTH: 98

TYPE: PRT

ORGANISM: homo sapiens

US-10-041-860-326

Query Match 89.1%; Score 460; DB 12; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLQSAAEVRRKPGASVKVSCKASGYPTSYDISWVRQAPGQGLEWMGMSISYSGNTDY 60
Db 1 QVQLVSGAEVKKRPGASVKVSCKASGYPTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

Qy 61 AOKFQGRVTMTTDTTSRTAYMELRSLSRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

RESULT 7
US-10-041-860-355

Sequence 355, Application US/10041860
Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvahan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 355
LENGTH: 98
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-355

Query Match 89.1%; Score 460; DB 12; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLQSAAEVRRKPGASVKVSCKASGYPTSYDISWVRQAPGQGLEWMGMSISYSGNTDY 60
Db 1 QVQLVSGAEVKKRPGASVKVSCKASGYPTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

Qy 61 AOKFQGRVTMTTDTTSRTAYMELRSLSRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

RESULT 8
US-10-041-860-356

Sequence 356, Application US/10041860
Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvahan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FaastSeq for Windows Version 4.0

SEQ ID NO 356

LENGTH: 98

TYPE: PRT

ORGANISM: homo sapiens

US-10-041-860-356

Query Match 89.1%; Score 460; DB 12; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLQSAAEVRRKPGASVKVSCKASGYPTSYDISWVRQAPGQGLEWMGMSISYSGNTDY 60
Db 1 QVQLVSGAEVKKRPGASVKVSCKASGYPTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

Qy 61 AOKFQGRVTMTTDTTSRTAYMELRSLSRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

RESULT 9
US-10-308-817-44

Sequence 44, Application US/10308817
Publication No. US20030219861A1

GENERAL INFORMATION:
APPLICANT: Rocher, Russell

APPLICANT: Wu, Dayang

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 1087-37

CURRENT APPLICATION NUMBER: US/10/308,817

CURRENT FILING DATE: 2002-12-03

NUMBER OF SEQ ID NOS: 195

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-44

Query Match      89.1%; Score 460; DB 12; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 OVQLQSAAEVRRKPGASVSKASGYPTSYDISWVQAPQGLQEMMGWISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLVQSAAEVRRKPGASVSKASGYPTSYDISWVQAPQGLQEMMGWISAYNGNTNY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 AOKFGQRYVTMTTDTSTRRTAYMELRLSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-194-975-4
; Sequence 4, Application US/10194975
; Publication No. US200300396499A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-4

Query Match      89.1%; Score 460; DB 15; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 OVQLQSAAEVRRKPGASVSKASGYPTSYDISWVQAPQGLQEMMGWISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLVQSAAEVRRKPGASVSKASGYPTSYDISWVQAPQGLQEMMGWISAYNGNTNY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 AOKFGQRYVTMTTDTSTRRTAYMELRLSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-864-761-47285
; Sequence 47285, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
```

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47285
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALU8 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW403728.1, EVALU8 4.00e-45
US-09-864-761-47285

Query Match      89.1%; Score 460; DB 9; Length 104;
Best Local Similarity 88.8%; Pred. No. 3.8e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 OVQLQSAAEVRRKPGASVSKASGYPTSYDISWVQAPQGLQEMMGWISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 OVQLVQSAAEVRRKPGASVSKASGYPTSYDISWVQAPQGLQEMMGWISAYNGNTNY 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 AOKFGQRYVTMTTDTSTRRTAYMELRLSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 AOKLQGRVTMTTDTSTSTAYMELRLSLRSDDTAVYYCAR 101
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-041-860-206
; Sequence 206, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvahan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binayam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USBS
; FILE REFERENCE: ABGENIX.051A
```

```

; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 117
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-206

Query Match      89.1%; Score 460; DB 12; Length 117;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QVQLQSAAEVRKPKGASVYVSCKASGYPTSYDISMWRQAPQGLGEMMGWISYSGNTDY 60
Db 1 QVQLVQSGAEVKKPKASVYVSCKASGYFTSYGISMWRQAPQGLGEMMGWISAYNGNTNY 60

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 13
US-10-041-860-42
; Sequence 42, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binayad
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-42

Query Match      89.1%; Score 460; DB 12; Length 125;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QVQLQSAAEVRKPKGASVYVSCKASGYPTSYDISMWRQAPQGLGEMMGWISYSGNTDY 60
Db 1 QVQLVQSGAEVKKPKASVYVSCKASGYFTSYGISMWRQAPQGLGEMMGWISAYNGNTNY 60

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 14
US-10-041-860-207
; Sequence 207, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
```

```

; APPLICANT: Weber, Richa
; APPLICANT: Bezaheh, Bin
; TITLE OF INVENTION: ANTI
; TITLE OF INVENTION: THE
; FILE REFERENCE: ABGENIX.
; CURRENT APPLICATION NUMB
; CURRENT FILING DATE: 20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 207
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-207

Query Match      8 %; Score 460; DB 12; Length 125;
Best Local Similarity 8 %; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QVQLQSAAEVRKPKASVYVSCKASGYPTSYDISMWRQAPQGLGEMMGWISYSGNTDY 60
Db 1 QVQLVQSGAEVKKPKASVYVSCKASGYFTSYGISMWRQAPQGLGEMMGWISAYNGNTNY 60

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 15
US-10-269-805-45
; Sequence 45, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPEPTIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-45

Query Match      89.1%; Score 460; DB 15; Length 125;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QVQLQSAAEVRKPKGASVYVSCKASGYPTSYDISMWRQAPQGLGEMMGWISYSGNTDY 60
Db 1 QVQLVQSGAEVKKPKASVYVSCKASGYFTSYGISMWRQAPQGLGEMMGWISAYNGNTNY 60

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
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Search completed: December 30, 2003, 11:45:23
Job time : 22.0171 secs


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-45

Query Match      82.5%; Score 425.5; DB 2; Length 129;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVOLLQSAAEVRKPGASVSKASCASGYPTFSYDISWVRQAPGQGLEMMGNISY-SGNTD 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLVQSGAEVKKRGASVSKASCASGYTFTSYAISWVRQAPGQGLEMMGNINYGNDTN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YAAKFGQGVYTTTDSRTATMELRSLRSDDTAVYYCAR 98
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAAKFGQGVYTTTADTSTSTAYMELSLRSEDTAVYYCAR 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-08-525-539A-77
; Sequence 77, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-77

Query Match      82.5%; Score 425.5; DB 4; Length 129;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVOLLQSAAEVRKPGASVSKASCASGYPTFSYDISWVRQAPGQGLEMMGNISY-SGNTD 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLVQSGAEVKKRGASVSKASCASGYTFTSYAISWVRQAPGQGLEMMGNINYGNDTN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YAAKFGQGVYTTTDSRTATMELRSLRSDDTAVYYCAR 98
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAAKFGQGVYTTTADTSTSTAYMELSLRSEDTAVYYCAR 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 8
PCT-US95-01219-45
; Sequence 45, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-45

Query Match      82.5%; Score 425.5; DB 5; Length 129;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVOLLQSAAEVRKPGASVSKASCASGYPTFSYDISWVRQAPGQGLEMMGNISY-SGNTD 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLVQSGAEVKKRGASVSKASCASGYTFTSYAISWVRQAPGQGLEMMGNINYGNDTN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YAAKFGQGVYTTTDSRTATMELRSLRSDDTAVYYCAR 98
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAAKFGQGVYTTTADTSTSTAYMELSLRSEDTAVYYCAR 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Taseku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
```

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-96

Query Match 82.0%; Score 423; DB 3; Length 117;
Best Local Similarity 82.7%; Pred. No. 1e-37;
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCKASGYPTSDISWVROAPGQGLEWMGNIISYSGNTDY 60
DB 20 QVQLVSGAEVKKRPGASVKVSKASGYPTSDISWVROAPGQGLEWMGMNINPSGNTGY 79

QY 61 AAKFGGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 98
DB 80 AAKFGGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 117

RESULT 10
US-09-025-769B-36
Sequence 36, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, VIC
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36

Query Match 81.6%; Score 421; DB 4; Length 120;
Best Local Similarity 82.7%; Pred. No. 1.7e-37;
Matches 81; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCKASGYPTSDISWVROAPGQGLEWMGNIISYSGNTDY 60
DB 1 QVQLVSGAEVKKRPGASVKVSKASGYPTSDISWVROAPGQGLEWMGMNINPSGNTGY 60

QY 61 AAKFGGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 98
DB 61 AAKFGGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 98

RESULT 11
US-09-025-769B-59
Sequence 59, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, VIC
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids

MEDIUM TYPE: Diskette

```

1  COMPUTER: IBM Compatible
2  OPERATING SYSTEM: Windows95
3  SOFTWARE: FastSEO for Windows Version 2.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/545.809A
6  FILING DATE: 27-MAR-1996
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: PCT/JP93/00603
9  FILING DATE: 10-MAY-1993
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Freeman, John W.
12 REGISTRATION NUMBER: 29,066
13 REFERENCE/DOCKET NUMBER: 06501/004001
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 617-542-5070
16 TELEFAX: 617-542-8906
17
18 TELEX: 200154
19
20 INFORMATION FOR SEQ ID NO: 90:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 117 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25
26 MOLECULE TYPE: protein
27
28 US-08-545-809A-90

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Query Match	80.6%;	Score 416;	DB 3;	Length 117;
Best Local Similarity	81.6%;	Pred. No. 5.7e-37;		
Matches 80; Conservative	5;	Mismatches 13;	Indels 0;	Gaps 0;

[illegible]

RESULT 15
US-08-561

: Sequence 10, Application US/08561521
: Patent No. 5840299

; GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocytes

TITLE OF INVENTION: Adhesion molecule VLA-4

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: 4

ADDRESS: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California
COUNTRY: USA

COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DataTrin Release #1.0 Version #1.00

```

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/561,521

FILING DATE:

CLASSIFICATION: 424
;
; DTIC ADDITIONAL DATA

APPLIICATION NUMBER: IIS/08/186 269A

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15370-14

```

: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 415-543-9600
:
: TELEFAX: 415-543-5043
:
: INFORMATION FOR SEQ ID NO: 10:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 119 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
US-08-561-521-10

```

Query Match	79.7%;	Score 411;	DB 2;	Length 119;
Best Local Similarity	79.6%;	Pred. NO. 2e-36;		
Matches 78;	Conservative 8;	Mismatches 12;	Indels 0;	Gaps 0;

Oy	1	QVOLLGSAAEVRKKGASAVKVKSCAKSGVPPTSDYDLSMWRQAQGCGGLEMMGWISITSGNDY	60
		: : :	
Db	1	QVQLVDSGAELFKRKGASAVKVKSCAKSGYTFTFSYAMHWNRQAAGQGLLEMMGWIMNAGNGTKY	60
Oy	61	AQKFGCVMTTDTTSRRRTAYWELSLASDDPDAVVYCCAR	98
		: : : :	
Db	61	SQRFGSVLTTRDTSSASTAWELSLASESDPAVVYCCAR	98

Search completed: December 30, 2003, 11:05:32
Job time : 10.0346 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 / Search time 2.013 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-29

Sequence: 1 OQNGWYEGPLLEPRPDALDI 21

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.76:*
2: pir3:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	43.3	1000	2 JE0110	mitotic control pr
2	51	42.5	435	2 A49171	translation elonga
3	50	41.7	164	2 T37174	protein-tyrosine-p
4	50	41.7	205	2 S26854	microfilarial sheat
5	50	41.7	403	2 H72634	proline-rich sheat
6	49	40.8	205	2 A40525	probable pyruvate
7	49	40.8	363	2 AG0189	translation elonga
8	49	40.8	435	2 S43507	translation elonga
9	49	40.8	435	2 H90162	hypothetical prote
10	48.5	40.4	75	2 G95891	hypothetical prote
11	48	40.0	354	2 T12741	hypothetical prote
12	48	40.0	435	1 EFUC1A	translation elonga
13	47	39.2	362	1 B64793	glycerol dehydroge
14	47	39.2	362	2 F90708	probable oxidoredu
15	47	39.2	362	2 B85559	probable oxidoredu
16	47	39.2	362	2 AD0576	hypothetical prote
17	46	38.3	366	2 P44247	hypothetical prote
18	46	38.3	423	2 A88339	sugar binding prote
19	46	38.3	423	2 A12943	hypothetical prote
20	46	38.3	524	2 S47143	A mating type prot
21	46	38.3	579	2 S47327	conserved hypotnet
22	46	38.3	647	2 T43952	hypothetical prote
23	46	38.3	759	2 T44142	DR1 protein (import
24	46	38.3	825	2 T23612	hypothetical prote
25	46	38.3	1062	2 T64444	hypothetical prote
26	45.5	37.9	1327	2 B90674	Aida-1 adhesin-lik
27	45.5	37.9	1349	2 B85524	probable beta-bar
28	45.5	37.9	2425	2 D69426	surface layer prot
29	45	37.5	213	2 B85066	hypothetical prote

30	45	37.5	255	2 A12578	conserved hypotnet
31	45	37.5	255	2 H97360	hypothetical prote
32	45	37.5	302	2 J01878	hypothetical 33.4X
33	45	37.5	376	2 G95949	probable oligopept
34	45	37.5	383	2 B87579	hypothetical prote
35	45	37.5	395	2 T43892	translation elonga
36	45	37.5	555	2 T45351	ferredoxin (import
37	45	37.5	1175	2 D85089	hypothetical prote
38	45	37.5	1472	2 A84470	hypothetical prote
39	45	37.5	1756	2 T02599	hypothetical prote
40	44.5	37.1	76	2 C71852	ribosomal protein
41	44.5	37.1	76	2 G64663	ribosomal protein
42	44.5	37.1	275	2 B49394	translation elonga
43	44.5	37.1	644	2 AD3471	adenyl-yl-sulfate x
44	44	36.7	147	2 H71016	hypothetical prote
45	44	36.7	239	2 T16159	hypothetical prote

ALIGNMENTS

RESULT 1

JE0110 mitotic control protein dis3 homolog - human

C/Species: Homo sapiens (man)

C/Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 02-Nov-2001

C/Accession: JE0110; T12542

R/Shiom, T.; Fukushima, K.; Suzuki, N.; Nakashima, N.; Noguchi, E.; Nishimoto, T.

U. Biochem. 123, 883-890, 1998

A/Title: Human Dis3p, which binds to either GTP- or GDP-Ran, complements Saccharomyces

A/Reference number: JE0110; MUID:98230695; PMID:9562621

A/Accession: JE0110

A/Molecule type: mRNA

A/Residues: 1-1000 <SH1>

R/Wambolt, R.; Heubner, D.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A/Reference number: Z17524

A/Accession: T12542

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 369-593, 'K', 595-1000 <WAM>

A/Cross-reference: EMBL:AL080158

A/Experimental source: adult testis; clone DKFZp434L194

C/Comment: This protein enhances a temperature-sensitive mutant RCC1-stimulated nucleot

C/Genetic: A/Note: DKFZp434L194.1

C/Superfamily: mitotic control protein dis3

Query Match 43.3%; Score 52; DB 2; Length 1000;
Best Local Similarity 69.2%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GQWYEGPLLEPRP 16

Db 40 GQWYEGPLLEPRP 52

RESULT 2

A49171 translation elongation factor eEF-1 alpha chain - Tetrahymena pyriformis

C/Species: Tetrahymena pyriformis

C/Date: 21-Jan-1994 #sequence_revision 15-Oct-1994 #text_change 02-Feb-2001

C/Accession: A49171; B49171

R/Kuraawa, Y.; Numata, O.; Katoh, M.; Hirano, H.; Chiba, J.; Watanabe, Y.

Exp. Cell Res. 203, 251-258, 1992

A/Title: Identification of Tetrahymena 14-nm filament-associated protein as elongation

A/Reference number: A49171; MUID:93049915; PMID:1385189

A/Accession: A49171

A/Molecule type: mRNA

A/Residues: 1-435 <KUR>

A/Cross-reference: GB:D11083; NID:9217407; PIDN:BA01856.1; PID:9217408

A/Note: sequence extracted from NCBI backbone (NCBI:117509, NCBI:117510)

A:Accession: B49171
 A:Molecule type: protein
 A:Residues: 2-21 <KU2>
 C:Genetics:
 A:Genetic code: SGCS
 C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
 C:Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
 F:2-435/Product: translation elongation factor eEF-1 alpha chain #status experimental <E
 F:9-157/Domains: translation elongation factor Tu homology <STU>
 F:15-22/Region: nucleotide-binding motif A (P-loop)
 F:95-98/Region: GTP binding #status predicted
 F:154-157/Region: GTP binding #status predicted

Query Match 42.5%; Score 51; DB 2; Length 435;
 Best Local Similarity 50.0%; Pred. No. 6.1;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 NGCWYEGPLLEPPDALD 20
 DB 208 NAWYKGPILVEALDALE 225

RESULT 3
 T37174
 protein-tyrosine-phosphatase, low molecular weight - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C:Accession: T37174
 R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: 221598
 A:Accession: T37174
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-164 <SEE>
 A:Cross-references: EMBL:AL096823; PIDN:CA846959.1; GSPDB:GN00070; SCQDB:SCQ11.04c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: ptpA; SCQDB:SCQ11.04c
 C:Superfamily: protein-tyrosine-phosphatase, low molecular weight

Query Match 41.7%; Score 50; DB 2; Length 164;
 Best Local Similarity 50.0%; Pred. No. 2.9;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCMWYEGPLLEPPDAL 19
 DB 44 GCMWEGADPRTRAV 59

RESULT 4
 S26854
 microfilarial sheath protein, major component - nematode (Brugia pahangi)
 C:Species: Brugia pahangi
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
 C:Accession: S26854
 R:Seilkirk, M.
 submitted to the EMBL Data Library, February 1991
 A:Reference number: S26854
 A:Accession: S26854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <SEL>
 A:Cross-references: EMBL:X58063; NID:G5951; PID:G5952
 C:Genetics:
 A:Introns: 123/2

Query Match 41.7%; Score 50; DB 2; Length 205;
 Best Local Similarity 52.9%; Pred. No. 3.7;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDA 18

DB 162 QTRGWTGPRLTPKPTA 178

RESULT 5
 H72634
 probable pyruvate formate lyase activating protein APE1535 - Aeropyrum pernix (strain
 C:Species: Aeropyrum pernix
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: H72634
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak
 awa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
 DNA Res. 6, 83-101, 1999
 A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: H72634
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-403 <KAW>
 A:Cross-references: DDBJ:AP000061; NID:G5104821; PIDN:BAA80534.1; PID:dl044320; PID:G5
 A:Experimental source: strain KI
 C:Genetics:
 A:Gene: APE1535

Query Match 41.7%; Score 50; DB 2; Length 403;
 Best Local Similarity 40.0%; Pred. No. 7.9;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDALDI 21
 DB 108 REGGYEGDIXDARPELMDV 127

RESULT 6
 A40525
 proline-rich sheath protein ME22 precursor - nematode (Brugia pahangi)
 C:Species: Brugia pahangi
 C>Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 27-Jan-1995
 C:Accession: A40525; S18744
 R:Seilkirk, M.E.; Yazdandbaksh, M.; Freedman, D.; Blaxter, M.L.; Cookson, E.; Jenkins,
 J. Biol. Chem. 266, 11002-11008, 1991
 A>Title: A proline-rich structural protein of the surface sheath of larval Brugia flla
 A:Reference number: A40525; MUID:91250404; PMID:1170216
 A:Accession: A40525
 A:Status: preliminary
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <SEL>
 A:Cross-references: GB:X58063
 A>Note: the authors translated the codon GCA for residue 23 as Arg, CTG for residue 14

Query Match 40.8%; Score 49; DB 2; Length 205;
 Best Local Similarity 52.9%; Pred. No. 5.2;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDA 18
 DB 162 QTRGWTGPRLTPKPTA 178

RESULT 7
 AG0189
 probable dehydrogenase YPO1556 (imported) - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AG0189
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.
 deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
 Nature 413, 523-527, 2001
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AG0189
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-363 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC90378.1; PID:G15979597; GSPDB:GN00175
C:Genetics:
A:Gene: YPO556
C:Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

Query Match 40.8%; Score 49; DB 2; Length 363;
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 6 WYEGPLLEPPDALDI 21
DB 178 WYEAVALSPQPERTSL 193

RESULT 8
S43507
translation elongation factor EF-1 alpha chain - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Feb-2001
C:Accession: S43507; S33719; S37631; T11747
R:Arcari, P.; Gallo, M.; Iannicello, G.; Russo, A.D.; Bocchini, V.
Biochim. Biophys. Acta 1217, 333-337, 1994
A:Title: The nucleotide sequence of the gene coding for the elongation factor 1-alpha in Sulfolobus solfataricus.
A:Reference number: S43507; MUID:94198299; PMID:8148382
A:Accession: S43507
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <ARC>
A:Cross-references: EMBL:X70701; NID:G395380; PIDN:CAA50033.1; PID:G395381
R:Arcari, P.; Gallo, M.; Iannicello, G.; dello Russo, A.; Bocchini, V.
Nucleic Acids Res. 21, 1666, 1993
A:Title: Primary structure of the elongation factor 1-alpha in Sulfolobus solfataricus.
A:Reference number: S33718; MUID:93241951; PMID:8369039
A:Accession: S33719
A:Molecule type: DNA
A:Residues: 1-13, 'Q', 15-435 <ARC>
A:Cross-references: EMBL:X70701
A:Note: this sequence has been revised in reference S37631
R:Arcari, P.; Gallo, M.; Iannicello, G.; dello Russo, A.; Bocchini, V.
Nucleic Acids Res. 21, 3920, 1993
A:Reference number: S37631
A:Contents: erratum
A:Accession: S37631
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'H', 2-13, 'Q', 15-435 <ARC>
A:Note: this is a revision to the sequence from reference S33718
R:Iannicello, G.; Gallo, M.; Arcari, P.; Bocchini, V.
Biochem. Mol. Biol. Int. 33, 927-937, 1994
A:Title: Organization of a Sulfolobus solfataricus gene cluster homologous to the Escherichia coli lac operon.
A:Reference number: Z17331; MUID:95078778; PMID:7527264
A:Accession: T11747
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residue type: DNA
A:Residues: 1-435 <IAN>
A:Cross-references: EMBL:X76767; NID:G510206; PID:G510209
A:Experimental source: ATCC 49255 / MT-4
C:Genetics:
A:Gene: EF-1a; aEF-1a1pha
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C:Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F:7-155/Domain: translation elongation factor Tu homology <ETU>
F:113-20/Region: nucleotide-binding motif A (P-loop)
F:155-155/Region: GTP-binding NKXD motif

Query Match 40.8%; Score 49; DB 2; Length 435;
Best Local Similarity 45.0%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 2 QNGMYEGPLLEPPDALDI 21
DB 205 ENMKWNGPPLLEVLDQLEL 224

RESULT 9
H90162
hypothetical protein tuf-1 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: H90162
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Char
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Tni-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Seneen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <KUR>
A:Cross-references: GB:AE006641; NID:G13813351; PIDN:AAK40559.1; GSPDB:GN00155
C:Genetics:
A:Gene: tuf-1

Query Match 40.8%; Score 49; DB 2; Length 435;
Best Local Similarity 45.0%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 2 QNGMYEGPLLEPPDALDI 21
DB 205 ENMKWNGPPLLEVLDQLEL 224

RESULT 10
G95891
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: G95891
R:Finan, T.M.; Weidner, S.; Wong, K.; Bhurmesler, J.; Chain, P.; Vorholter, F.J.; Herm
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing en
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95891
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC48799.1; PID:G15140272; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Klee, E.; Komp, C.; Leilaure
hebulic, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, J
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMD20413
A:Gene: plasmid

Query Match 40.4%; Score 48.5; DB 2; Length 75;
Best Local Similarity 61.1%; Pred. No. 2;
Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
QY 2 QNGMYEG-PLLEPPDA 18
DB 42 RSGSGRNGPPLPLSPRDA 59

RESULT 11
T12741
hypothetical protein 25 - Methanobacterium phage psiM2
C:Species: Methanobacterium phage psiM2

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 05-May-2000
 C/Accession: T12741
 R/Pfifter, P.; Wasserrfallen, A.; Stettler, R.; Leisinger, T.
 Submitted to the EMBL Data Library, May 1998
 A/Description: Archaeophages PsiM2 complete genomic DNA.
 A/Reference number: 217578
 A/Accession: T12741
 A/Status: translated from GB/EMBL/DBD
 A/Molecule type: DNA
 A/Residues: 1-354 <PFI>
 A/Cross-references: EMBL:AF065411; NID:g3249585; PID:g3249610; PIDN:AAC27064.1
 A/Experimental source: host Methanobacterium thermoautotrophicum strain Marburg
 C/Superfamily: Methanobacterium phage psiM2 hypothetical protein 25

Query Match 40.0%; Score 48; DB 2; Length 354;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 QONGWYEPPLER 14
 DB 8 QENRGWYVPKDP 21

RESULT 12
 EFU01A
 translation elongation factor aEF-1 alpha chain - Sulfolobus acidocaldarius
 C/Species: Sulfolobus acidocaldarius
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 19-Jan-2001
 C/Accession: S12818
 R/Auer, J.
 submitted to the EMBL Data Library, March 1990
 A/Reference number: S12817
 A/Accession: S12818
 A/Molecule type: DNA
 A/Residues: 1-435 <AUE>
 A/Cross-references: EMBL:X52382; NID:g46562; PIDN:CAA3608.1; PID:g46564
 C/Genetics:
 A/Gene: EF-1a
 C/Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
 C/Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
 F;7-155/Domain: translation elongation factor Tu homology <ETU>
 F;13-20/Region: nucleotide-binding motif A (P-loop)
 F;152-155/Region: GTP-binding NKXD motif

Query Match 40.0%; Score 48; DB 1; Length 435;
 Best Local Similarity 56.2%; Pred. No. 17;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDADI 21
 DB 209 WYNGPTLEELDQLEI 224

RESULT 13
 E64793
 glycerol dehydrogenase (EC 1.1.1.6) ybDh - Escherichia coli (strain K-12)
 C/Species: Escherichia coli
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
 A/Accession: E64793
 R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A/Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: E64793
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-362 <BLAT>
 A/Cross-references: GB:AE000165; GB:U00096; NID:g1786808; PIDN:AACT3700.1; PID:g1786815;
 A/Experimental source: strain K-12, substrain MG1655
 C/Genetics:
 A/Gene: ybDh
 C/Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

C/Keywords: oxidoreductase; transmembrane protein
 F;9-354/Domain: lactaldehyde reductase homology <LAR>
 F;109-125/Domain: transmembrane #status predicted <TM>

Query Match 39.2%; Score 47; DB 1; Length 362;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDADI 21
 DB 178 WYEAVALAQPETPL 193

RESULT 14

P90708
 probable oxidoreductase EC0638 [imported] - Escherichia coli (strain O157:H7, substra
 C/Species: Escherichia coli
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C/Accession: P90708
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
 gaeswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge
 A/Reference number: A99629; MUID:21156231; PMID:11258796
 A/Accession: P90708
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-362 <HAY>
 A/Cross-references: GB:BA000007; PIDN:BAB34061.1; PID:g13360096; GSPDB:GN00154
 A/Experimental source: strain O157:H7, substrain RIMD 0509952
 C/Genetics:
 A/Gene: EC0638
 C/Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

Query Match 39.2%; Score 47; DB 2; Length 362;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDADI 21
 DB 178 WYEAVALAQPETPL 193

RESULT 15

B85559
 probable oxidoreductase ybDh [imported] - Escherichia coli (strain O157:H7, substrain
 C/Species: Escherichia coli
 C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C/Accession: B85559
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 ller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallante, E.; Potamousle, K.; Apodec
 Nature 409, 529-533, 2001
 A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A/Reference number: A85480; MUID:21074935; PMID:11206551
 A/Accession: B85559
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-362 <STO>
 A/Cross-references: GB:AE005174; NID:g12513492; PIDN:ANG54934.1; GSPDB:GN00145; UMGP:
 A/Experimental source: strain O157:H7, substrain EDL933
 C/Genetics:
 A/Gene: ybDh
 C/Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

Query Match 39.2%; Score 47; DB 2; Length 362;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDADI 21
 DB 178 WYEAVALAQPETPL 193

Tue Dec 30 11:49:04 2003

us-09-674-752-29.rpr

Page 5

Search completed: December 30, 2003, 11:03:16
Job time : 4.013 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 1.12391 Seconds
(without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120
Sequence: 1 QQNGWEGPPLLEPRDALDI 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	43.3	928	1 RR44_HUMAN	Q9211 homo sapien
2	51	42.5	435	1 EF1A_TETPY	Q04634 tetrahymena
3	50	41.7	164	1 PTPA_STRCO	P53433 streptomyces
4	50	41.7	348	1 DDL_ENTFA	Q47758 enterococcu
5	50	41.7	435	1 EF1A_SULTO	Q97651 sulfolobus
6	49	40.8	435	1 EF1A_SULSO	P35021 sulfolobus
7	48	40.0	435	1 EF1A_SULAC	P17196 sulfolobus
8	47	39.2	362	1 YBDH_ECOLI	P45579 escherichia
9	46	38.3	449	1 EF1C_PORPU	P50256 porphyra pu
10	45	37.5	555	1 FPRB_MYCLE	Q33064 mycobacteri
11	44.5	37.1	76	1 RS16_HELPU	Q9263 helicobacte
12	44.5	37.1	76	1 RS16_HELPU	P56023 helicobacte
13	44	36.7	128	1 Y14D_BPT4	P39507 bacteriopho
14	44	36.7	128	1 Y14D_BPT6	Q38169 bacteriopho
15	44	36.7	358	1 DDL_ENTHR	Q47827 enterococcu
16	44	36.7	414	1 YB8C_BACSU	P40407 bacillus su
17	44	36.7	476	1 CYSN_VIBPA	O87899 vibrio para
18	43.5	36.2	208	1 NQ8R_HABIN	P43558 haemophilus
19	43	35.8	74	1 COLE_ZOPAT	P80032 zophobas at
20	43	35.8	167	1 NUOE_RICCN	Q92102 rickettsia
21	43	35.8	383	1 YJIM_YEAST	P39384 escherichia
22	43	35.8	435	1 GAL8_YEAST	P04387 saccharomyc
23	43	35.8	438	1 EF1A_DESMO	P41203 desulfuroco
24	43	35.8	862	1 SMAD_HUMAN	Q92854 homo sapien
25	42.5	35.4	396	1 EF1A_GIALA	Q08046 giardia lam
26	42.5	35.4	398	1 HEMT_ECOLI	P09128 escherichia
27	42.5	35.4	541	1 MYRO_ARATH	P37702 arabidopsis
28	42.5	35.4	1290	1 PIGI_RAT	P10686 rattus norv
29	42.5	35.4	88	1 YDHA_SCHPO	Q92349 schizosacch
30	42	35.0	88	1 ECLH_MANSE	P11919 manuca sex
31	42	35.0	172	1 BFLI_MOUSE	Q07440 mus musculu
32	42	35.0	246	1 NUKC_ORYSA	P12159 oryza sativ
33	42	35.0	324	1 B3G2_MOUSE	P59270 mus musculu

34	42	35.0	324	1 B3G2_RAT	Q92137 rattus norv
35	42	35.0	419	1 GLPB_ECOLI	P13033 escherichia
36	42	35.0	420	1 EF1A_HALMA	P16018 halocaula
37	42	35.0	457	1 GAL8_KLULA	Q06433 kluyveromyc
38	42	35.0	530	1 FUSA_BURCE	P24126 burkholderi
39	42	35.0	814	1 FADE_ECO57	O87122 escherichia
40	42	35.0	814	1 FADE_ECOLI	Q47146 escherichia
41	42	35.0	814	1 FADE_SALTI	O82937 salmonella
42	42	35.0	824	1 JIP2_HUMAN	Q82137 homo sapien
43	42	35.0	888	1 YGB4_YEAST	P25339 saccharomyc
44	42	35.0	888	1 YGB4_YEAST	P25339 saccharomyc
45	42	35.0	1550	1 GLTB_SYNY3	P55037 bynechocycet

ALIGNMENTS

RESULT 1
RR44_HUMAN STANDARD; PRT; 928 AA.
ID RR44_HUMAN
AC Q9Y2L1; Q8WM12; Q9UG36;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA
processing protein 44) (Dis3 protein homolog).
GN DIS3 OR RRP44 OR KIAA1008.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=98230695; PubMed=9562621;
RA Shiomi T., Fukushima K., Suzuki N., Nakashima N., Noguchi E.,
RT Nishimoto T.,
RT "Human dis3, which binds to either GTP- or GDP-Ran, complements
RT Saccharomyces cerevisiae dis3.";
RL J. Biochem. 123:883-890(1998).
RN (2)
RP ERRATUM.
RA Shiomi T., Fukushima K., Suzuki N., Nakashima N., Noguchi E.,
RT Nishimoto T.,
RL J. Biochem. 124:250-250(1998).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirogawa M.,
RT Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
RN (4)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Peripheral blood leukocytes;
RX MEDLINE=21932550; PubMed=11935316;
RA Rozenblum E., Valteristo P., Sandberg T., Bergthorsson J.T.,
RT Syrjakoski K., Weaver D., Haraldsson K., Johannsdottir H.K.,
RA Vehneman P., Migan S., Golberger N., Robbins C., Pak E., Dutra A.,
RA Gillander E., Stephan A., Bailey-Wilson J., Joo S.-H.H., Kalnu T.,
RA Aarason A., Barkardottir R.B., Nevallinna H., Borg A.,
RA Kallioniemi O.-P.,
RT "A genomic map of a 6-Mb region at 19q21-q22 implicated in cancer
RT development: identification and characterization of candidate genes.";
RL Hum. Genet. 110:111-121(2002).
RN (5)
RP SEQUENCE OF 297-928 FROM N.A.
RC TISSUE=Testis;
RA Wambutt R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.,
RL Sambrook (Jun-1999) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: COMPONENT OF THE EXOSOME 3->5 EXORIBONUCLEASE COMPLEX.

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RT      "Complete genome sequence of an aerobic thermophilic
RT      Crenarchaeon, Sulfolobus tokodaii strain7."
RL      DNA Res. 8:123-140(2001).
CC      -1- FUNCTION: This protein promotes the GTP-dependent binding of
CC      aminoacyl-tRNA to the A-site of ribosomes during protein
CC      biosynthesis.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC      EF-TU/EF-1A SUBFAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: AP000982; BAB65236.1; -.
DR      HAMAP: MF_00118; -.
DR      InterPro: IPR004539; EFL_alpha.
DR      InterPro: IPR000795; EFT_GTPbind.
DR      InterPro: IPR004160; EFTU_Cterm.
DR      InterPro: IPR004161; EFTU_D2.
DR      Pfam: PF00009; GTP_EFTU; 1.
DR      Pfam: PF03143; GTP_EFTU_D2; 1.
DR      TIGRfam: TIGR00483; EF-1_alpha; 1.
DR      PROSITE: PS00301; EFACOR_GTP; 1.
KW      Elongation factor; Protein biosynthesis; GTP-binding;
KM      Complete proteome.
FT      NP_BIND 13 20 GTP (BY SIMILARITY).
FT      NP_BIND 90 94 GTP (BY SIMILARITY).
FT      NP_BIND 152 155 GTP (BY SIMILARITY).
SQ      SEQUENCE 435 AA; 48331 MW; D4071B81BD73D60 CRC64;

Query Match          41.7%; Score 50; DB 1; Length 435;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      2 QNGGWYEGPLEPRDALDI 21
Db      205 ENMKWYTGPLEEYDLQLEI 224

RESULT 6
EF1A_SULSO          STANDARD; PRT; 435 AA.
ID      EF1A_SULSO
AC      P35021;
DT      01-FEB-1994 (Rel. 28, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu).
GN      TUF OR TEFI OR SSO0216.
OS      Sulfolobus solfataricus.
OC      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC      Sulfolobus.
OX      NCBI_TaxID=2287;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX      MEDLINE=93241951; PubMed=8369039;
RA      Arcati P., Gallo M., Iannicelli G., Dello Russo A., Bocchini V.,
RT      "Primary structure of the elongation factor 1 alpha in Sulfolobus
RT      solfataricus."
RL      Nucleic Acids Res. 21:1666-1666(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX      MEDLINE=94198299; PubMed=8148382;
RA      Arcati P., Gallo M., Iannicelli G., Dello Russo A., Bocchini V.,
RT      "The nucleotide sequence of the gene coding for the elongation factor
RT      1 alpha in Sulfolobus solfataricus. Homology of the product with

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RT      related proteins."
RL      Biochim. Biophys. Acta 1217:333-337(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MT-3;
RA      Arcati P., Masullo M., Bocchini V.;
RT      "The nucleotide sequence of the gene encoding the elongation factor 1
RT      alpha from the archaeon Sulfolobus solfataricus isolate MT3."
RL      Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 35092 / DSM 1617 / P2;
RX      MEDLINE=21332296; PubMed=11427726;
RA      She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA      Aweyer M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
RA      De Moors A., Eraso G., Fletcher C., Gordon P.M.K.,
RA      Helkamp-de Jong I., Jellies A.C., Kozera C.J., Medina N., Peng X.,
RA      Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA      Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA      Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT      "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC      -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC      AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC      BIOSYNTHESIS.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC      EF-TU/EF-1A SUBFAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X70701; CAA50033.1; -.
DR      EMBL: X76767; CAA54162.1; -.
DR      EMBL: AJ312397; CAC42886.1; -.
DR      EMBL: AB006658; AAK40559.1; -.
DR      PIR: H90162; H90162.
DR      PIR: S43507; S43507.
DR      PDB: 1UNY; 23-JAN-02.
DR      HAMAP: MF_00118; -.
DR      InterPro: IPR004539; EFL_alpha.
DR      InterPro: IPR000795; EFT_GTPbind.
DR      InterPro: IPR004160; EFTU_Cterm.
DR      InterPro: IPR004161; EFTU_D2.
DR      Pfam: PF00009; GTP_EFTU; 1.
DR      Pfam: PF03144; GTP_EFTU_D2; 1.
DR      Pfam: PF03143; GTP_EFTU_D3; 1.
DR      PRINTS: PR00315; ELONGATNFCF.
DR      TIGRfam: TIGR00483; EF-1_alpha; 1.
DR      PROSITE: PS00301; EFACOR_GTP; 1.
KW      Elongation factor; Protein biosynthesis; GTP-binding;
KM      Complete proteome; 3D-structure.
FT      NP_BIND 13 20 GTP (BY SIMILARITY).
FT      NP_BIND 90 94 GTP (BY SIMILARITY).
FT      NP_BIND 152 155 GTP (BY SIMILARITY).
FT      VARIANT 196 196 A -> S (IN STRAINS MT-3 AND MT-4).
FT      VARIANT 203 203 R -> K (IN STRAINS MT-3 AND MT-4).
FT      VARIANT 347 347 I -> L (IN STRAINS MT-3 AND MT-4).
FT      CONFLICT 14 14 H -> Q (IN REF. 1).
FT      CONFLICT 240 240 V -> R (IN REF. 1 AND 2).
SQ      SEQUENCE 435 AA; 48489 MW; 222B540A31768A59 CRC64;

Query Match          40.8%; Score 49; DB 1; Length 435;
Best Local Similarity 45.0%; Pred. No. 6.3;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY      2 QNGGWYEGPLEPRDALDI 21

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Db 205 ENMKWNGPTLEBYDQLEI 224

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RESULT 7
EF1A_SULAC STANDARD; PRT; 435 AA.
ID EF1A_SULAC
AC P1156;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu).
GN Sulfobolus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfobolales; Sulfobocaceae;
OC Sulfobolus.
OX NCBI_TaxID=2285;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RA Auer J., Spicker G., Neyerhofer L., Puhler G., Boeck A.;
RT "Organisation and nucleotide sequence of a gene cluster comprising the
RT translation elongation factor 1-alpha from the extreme thermophilic
RT archaeobacterium Sulfobolus acidocaldarius: phylogenetic
RT implications.";
RL Syst. Appl. Microbiol. 14:14-22(1991).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
CC -----
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CC -----
DR EMBL; X52382; CAA36608.1; -.
DR PIR; S12818; EFUC1A.
DR HSSP; P07157; IAIIP.
DR HAMAP; MF_00118; 1.
DR InterPro; IPR004539; EF1_alpha.
DR InterPro; IPR000795; EF_Gtpbind.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PRO0315; ELONGATNCT.
DR TIGRFS; TIGR00483; EF-1_alpha; 1.
DR PROSITE; PS00301; EFATOR_GTP; 1.
DR Elongation factor; Protein biosynthesis; GTP-binding.
FT NP_BIND 13 20 GTP (BY SIMILARITY).
FT NP_BIND 90 94 GTP (BY SIMILARITY).
FT NP_BIND 152 155 GTP (BY SIMILARITY).
SQ SEQUENCE 435 AA; 48200 MW; A012AF564624803F CRC64;
Query Match 40.0%; Score 48; DB 1; Length 435;
Best Local Similarity 56.2%; Pred. No. 8.9;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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RESULT 8
 YBDH_ECOLI STANDARD; PRT; 362 AA.
 AC P45579; P77632;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase YbdH (EC 1.1.-.-).
GN YBDH OR B0599.
OC Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Bregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federapfel N., Hyman R., Kaiman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Maeda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horinouchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE OF 282-362 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91162636; PubMed=1848300;
RA Schultz J.E., Martin A.;
RT "Molecular and functional characterization of a carbon starvation
RT gene of Escherichia coli.";
RL J. Mol. Biol. 218:129-140(1991).
RN [5]
RP IDENTIFICATION.
RX MEDLINE=96032851; PubMed=7567469;
RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
RA Danchin A.;
RT "Detection of new genes in a bacterial genome using Markov models for
RT three gene classes.";
RL Nucleic Acids Res. 23:3554-3562(1995).
CC -1- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY. STRONG, TO BACTERIAL GLYCEROL DEHYDROGENASE.
CC -----
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CC -----
DR EMBL; AB000165; AAC73700.1; -.
DR EMBL; U82598; AAB40800.1; -.
DR EMBL; D90701; BAA35229.1; -.
DR EMBL; X52904; -; NOT_ANNOTATED_CDS.
DR PIR; E64793; E64793.
DR EcoGene; EG12692; YbdH.
DR InterPro; IPR001670; Fe-ADH.

```

DR Pfam: PF00465; Fe-ADH; 1.
 DR PROSITE: PS00913; ADH_IRON_1; 1.
 DR PROSITE: PS00060; ADH_IRON_2; FALSE_NEG.
 DR Hypothetical protein; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 362 AA; 39091 MW; C28BBB4F8F247AE2 CRC64;

Query Match 39.2%; Score 47; DB 1; Length 362;
 Best Local Similarity 43.8%; Pred. No. 10;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 6 WYEGPLLEPPDALDI 21
 178 WYEAVALPQPETPL 193

RESULT 9
 EFIC_PORPU STANDARD; PRT; 449 AA.
 AC P50256;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Elongation factor 1-alpha C (EF-1-alpha).
 GN TEF-C.
 OS Porphyra purpurea.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TaxID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RX MEDLINE=96309386; PubMed=8704161;
 RA Liu Q.Y., Baldauf S.L., Reich M.E.;
 RT "Elongation factor 1 alpha genes of the red alga Porphyra purpurea
 include a novel, developmentally specialized variant.";
 RL Plant Mol. Biol. 31:77-85(1996).
 CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
 AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
 BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN BOTH SPOROPHYTE AND GAMETOPHYTE
 PHASES OF THE LIFE CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-TU/EF-1A SUBFAMILY.

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 CC EMBL: U08844; AAA61793.1; -.
 DR HSSP: P07157; IAIIP.
 DR InterPro: IPR004539; EFl_alpha.
 DR InterPro: IPR000795; EFl_GTPbind.
 DR InterPro: IPR004160; EFTU_Cterm.
 DR InterPro: IPR004161; EFTU_D2.
 DR Pfam: PF00009; GTP_EFTU_D2.
 DR Pfam: PF00009; GTP_EFTU_D2; 1.
 DR Pfam: PF03143; GTP_EFTU_D3; 1.
 DR PRINTS: PR00315; ELONGATNFC1.
 DR TIGRFAMs: TIGR00483; EF-1_alpha; 1.
 DR PROSITE: PS00301; EFACITOR_GTP; 1.
 DR Elongation factor; Protein bioynthesis; GTP-binding;
 KW Multigene family.
 FT NP_BIND 14 21 GTP (BY SIMILARITY).
 FT NP_BIND 91 95 GTP (BY SIMILARITY).
 FT NP_BIND 153 156 GTP (BY SIMILARITY).
 SQ SEQUENCE 449 AA; 49174 MW; 21C76036B1ABE4DE CRC64;
 Query Match 38.3%; Score 46; DB 1; Length 449;
 Best Local Similarity 52.9%; Pred. No. 19;

Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 Qy 4 GWMYEGPLLEPPDALDI 20
 Db 212 GKMYKGPCLLEALDADC 228

RESULT 10
 FPRB_MYCLE STANDARD; PRT; 555 AA.
 AC 031064;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable ferredoxin/ferredoxin--NADP reductase (EC 1.18.1.2) (FNR).
 GN FPRB OR ML2134 OR MLCB57.39.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Biglmeier K., Parhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garner T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Dutoy S., Felwell T., Frazer A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jageley K., Lacroix C., Maclean J., Moulie S.,
 RA Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M.,
 RA Ruter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Batteil B.G.;
 RT "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 CC -1- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized
 ferredoxin + NADPH.
 CC -1- COFACTOR: FAD; PROBABLY BINDS ONE OR TWO 4FE-4S CLUSTERS.
 CC -1- SIMILARITY: IN THE N-TERMINAL, BELONGS TO THE BACTERIAL TYPE
 FERREDOXIN FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL, TO OTHER FERREDOXIN NADP
 REDUCTASES.

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 CC EMBL: Z99494; CAB16679.1; -.
 DR EMBL: AL583924; CAC31089.1; -.
 DR PIR: T45351; T45351.
 DR HSSP: P55907; IXER.
 DR Leptoma; ML2134;
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR000813; 7Fe_ferredoxin.
 DR InterPro: IPR000759; Adnrxn_reductase.
 DR InterPro: IPR001327; FAD_pyrid_redox.
 DR Pfam: PF00037; fer4_2.
 DR PRINTS: PR00354; 7FE8SFDOXIN.
 DR PRINTS: PR00419; ADKRDYASE.
 DR PRINTS: PR00368; FADPNR.
 DR PROSITE: PS00198; 4FE4S_FERREDOXIN; 1.
 DR Oxidoreductase; Flavoprotein; NADP; FAD; Electron transport;
 KW Iron-sulfur; 4Fe-4S; Complete proteome.
 FT DOMAIN 1 83 FERREDOXIN--NADP REDUCTASE.
 FT DOMAIN 115 555 FERREDOXIN-1 (BY SIMILARITY).
 FT METAL 9 9 IRON-SULFUR 1 (BY SIMILARITY).
 FT METAL 15 15 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 19 19 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 46 46 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 49 49 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 52 52 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
 FT METAL 56 56 IRON-SULFUR 1 (BY SIMILARITY).
 SQ SEQUENCE 555 AA; 59712 MW; 43C7292E6A2DFD9 CRC64;

Query Match

Best Local Similarity 32.1%; Score 45; DB 1; Length 555;
 Matches 9; Conservative 3; Mismatches 6; Indels 10; Gaps 1;

QY 3 NGCWYEGPLLEP-----RPDLD 20
 DB 481 NAGWLTDPVAEPALAKLVHARQPDIVD 508

RESULT 11

RS16_HELPD
 ID RS16_HELPD STANDARD; PRT; 76 AA.

AC 092K63;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S16.
 GN RPS16 OR JHP1078.

OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=85963;

SEQUENCE FROM N.A.

RA MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Carnes A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Werberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.V.;

RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).

CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.

CC -----

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DR EMBL; AE001535; AAD0658.1; -

DR PIR; C71852; C71852.

DR HSSP; P80379; IEMW.

DR HAMAP; MF_00385; -; 1.

DR InterPro: IPR000307; Ribosomal_S16.

DR Pfam: PF00886; Ribosomal_S16; 1.

DR ProDom: PD003791; Ribosomal_S16; 1.

DR TIGRFAMs; TIGR00002; S16; 1.

DR PROSITE; PS00732; RIBOSOMAL_S16; 1.

KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 76 AA; 8985 MW; FCF0FB21B58E230C8 CRC64;

Query Match

Best Local Similarity 37.1%; Score 44.5; DB 1; Length 76;
 Matches 9; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY 1 QONGGM-----YEGPLLEPRDLD 20
 DB 27 RRDGMWISIGYVNPSEPKDVID 51

RESULT 12

RS16_HELPD
 ID RS16_HELPD STANDARD; PRT; 76 AA.
 AC P56023;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S16.
 GN RPS16 OR HP1151

OS Helicobacter pylori (Campylobacter pylori).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.

OX NCBI_TaxID=210;

SEQUENCE FROM N.A.

RA STRAIN=26695 / ATCC 700392;
 RA MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirnse E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Melman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Kar P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;

RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori.";
 RL Nature 388:519-547(1997).

CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; AE000621; AAD08199.1; -

DR PIR; G64663; G64663.

DR HSSP; P80379; IEMW.

DR TIGR; HP1151; -

DR HAMAP; MF_00385; -; 1.

DR InterPro: IPR000307; Ribosomal_S16.

DR Pfam: PF00886; Ribosomal_S16; 1.

DR ProDom: PD003791; Ribosomal_S16; 1.

DR TIGRFAMs; TIGR00002; S16; 1.

DR PROSITE; PS00732; RIBOSOMAL_S16; 1.

KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 76 AA; 8971 MW; FCF0FB203D79ADFC8 CRC64;

Query Match

Best Local Similarity 37.1%; Score 44.5; DB 1; Length 76;
 Matches 9; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY 1 QONGGM-----YEGPLLEPRDLD 20
 DB 27 RRDGMWISIGYVNPSEPKDVID 51

RESULT 13

Y14D_BPT4
 ID Y14D_BPT4 STANDARD; PRT; 128 AA.
 AC P39507; Q9T0T2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 14.7 kDa protein in ftd-op32 intergenic region.
 GN Y14D OR PRD.2.
 OS Bacteriophage T4.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OX NCBI_TaxID=10665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Poglaзов A.B., Meeyanzhinov V.V., Kutter E.M.;


```

RN Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RT Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
RL "Bacteriophage T4 genome analysis."
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
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CC -----
DR EMBL; U20859; AAA62284.1; ALT INIT.
DR EMBL; AF158101; AAD42579.1; -.
DR InterPro; IPR004885; FRD2.
DR Pfam; PF03197; FRD2; 1.
KW Hypothetical protein.
SQ SEQUENCE 128 AA; 14741 MW; AE69390DBCFA6222 CRC64;

Query Match
Best Local Similarity 36.7%; Score 44; DB 1; Length 128;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QONGGWYE 8
DB 32 QONGGWFE 39

RESULT 14
Y14D_BPT6 STANDARD; PRT; 128 AA.
ID Y14D_BPT6
AC Q38169;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 14.8 kDa protein in frd-gp32 intergenic region.
OS FRD.2 OR FRD2.
GN Bacteriophage T6.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OX T4-like viruses.
RN NCBI_Taxid=10666;
RP SEQUENCE FROM N.A.
RA Fogelzov A.B., Porter D., Kutter E.M., Mesyanzhinov V.V.;
RT "DNA Sequences of the frd region in T4-related bacteriophages."
RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
CC -----
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CC -----
DR EMBL; L46846; AAA74669.1; -.
DR InterPro; IPR004885; FRD2.
DR Pfam; PF03197; FRD2; 1.
KW Hypothetical protein.
SQ SEQUENCE 128 AA; 14768 MW; 2CE311AF2D4372DC CRC64;

Query Match
Best Local Similarity 36.7%; Score 44; DB 1; Length 128;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QONGGWYE 8
DB 32 QONGGWFE 39

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RESULT 15
DDL_ENTHR
ID DDL_ENTHR STANDARD; PRT; 358 AA.
AC Q47827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE D-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase)
DE (D-Ala-D-Ala ligase).
GN DDL.
OS Enterococcus hirae.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_Taxid=1354;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 8043;
RX MEDLINE=96270057; PubMed=8662022;
RA Evers S., Casadewall B., Charles M., Dutka-Malen S., Galland M.,
RT Courvalin P.;
RT "Evolution of structure and substrate specificity in
RT D-alanine:D-alanine ligases and related enzymes."
RL J. Mol. Evol. 42:706-712(1996).
CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
CC alanyl-D-alanine.
CC -1- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
CC step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
CC -----
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CC -----
DR EMBL; U39788; AB01904.1; -.
DR HSP; P07862; I10W.
DR HAMAP; MF_00047; -.
DR InterPro; IPR005905; D_alal_D_alal.
DR Pfam; PF01820; Dala_dala_ligase; 1.
DR TIGRFAMs; TIGR01205; D_alal_D_alal; 1.
DR PROSITE; PS00843; DALA_DALA_LIGASE_1; 1.
DR PROSITE; PS00844; DALA_DALA_LIGASE_2; 1.
KW Ligase; Cell wall; Peptidoglycan synthesis.
SQ SEQUENCE 358 AA; 40128 MW; 225CF988A0A979F1 CRC64;

Query Match
Best Local Similarity 46.7%; Score 29;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 QONGWYEGPLLEBP 16
DB 42 KEGOWKGPILTEKP 56

```

Search completed: December 30, 2003, 10:55:51
 Job time : 2.12591 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 5.11779 Seconds

(without alignments)
1058.876 Million cell updates/sec

Title: US-09-674-752-29
Perfect score: 120
Sequence: 1 QOQNGWYEGPLPRPDALDI 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	44.2	408	5	Q96979	Q96979 paramorphys
2	52	43.3	98	4	Q96979	Q96979 paramorphys
3	51	42.5	175	16	Q8KBC1	Q8KBC1 chlorobium
4	50	41.7	205	5	Q00032	Q00032 brugia paha
5	50	41.7	343	1	Q9HH38	Q9HH38 methanobact
6	50	41.7	358	2	Q47755	Q47755 enterococcu
7	50	41.7	358	2	Q9F0M3	Q9F0M3 enterococcu
8	50	41.7	403	17	Q9YBR4	Q9YBR4 aeropyrum p
9	49	40.8	322	4	Q9H685	Q9H685 homo sapien
10	49	40.8	363	16	Q8EFW9	Q8EFW9 yersinia pe
11	49	40.8	384	16	Q8D080	Q8D080 yersinia pe
12	48.5	40.4	75	16	Q9ZME1	Q9ZME1 rhizobium m
13	48	40.0	190	16	Q8EKCS	Q8EKCS shewanella
14	48	40.0	346	9	Q98700	Q98700 rhizobium 1
15	48	40.0	354	9	Q80215	Q80215 methanobact
16	48	40.0	1235	11	Q9JLS3	Q9JLS3 rattus norv

17	48	40.0	1576	10	Q9FGX4	Q9FGX4 arabidopsis
18	47	39.2	362	16	Q8ZR27	Q8ZR27 salmonella
19	47	39.2	362	16	Q8Z8K6	Q8Z8K6 salmonella
20	47	39.2	362	16	Q8XBU7	Q8XBU7 escherichia
21	47	39.2	362	16	Q8FK14	Q8FK14 escherichia
22	47	39.2	409	5	Q9U9P4	Q9U9P4 paramecium
23	47	39.2	437	5	Q9U9C6	Q9U9C6 paramecium
24	47	39.2	4150	2	Q9KIV4	Q9KIV4 streptomyce
25	47	39.2	9477	2	Q9L4X3	Q9L4X3 streptomyce
26	46	38.3	190	5	Q17171	Q17171 brugia mala
27	46	38.3	310	16	Q8PK92	Q8PK92 xanthomonas
28	46	38.3	366	17	Q9HR12	Q9HR12 halobacteri
29	46	38.3	423	16	Q8UB66	Q8UB66 agrobacteri
30	46	38.3	524	3	Q00354	Q00354 coprinus ci
31	46	38.3	579	16	Q910U1	Q910U1 pseudomonas
32	46	38.3	627	2	Q9JHS6	Q9JHS6 bradyrhizob
33	46	38.3	647	12	Q9W9C4	Q9W9C4 human hefte
34	46	38.3	717	5	Q8MXN3	Q8MXN3 dictyostell
35	46	38.3	759	12	Q9PMX1	Q9PMX1 human hefte
36	46	38.3	825	5	Q21430	Q21430 caenorhabd
37	46	38.3	1062	4	Q9NSW2	Q9NSW2 homo sapien
38	46	38.3	1235	4	Q9UT54	Q9UT54 homo sapien
39	45.5	37.9	173	8	Q94SD1	Q94SD1 dactylopten
40	45.5	37.9	451	10	Q9ZSW2	Q9ZSW2 cyanophora
41	45.5	37.9	571	16	Q8KBC7	Q8KBC7 chlorobium
42	45.5	37.9	1349	16	Q8XG61	Q8XG61 escherichia
43	45.5	37.9	2380	16	Q8XYE8	Q8XYE8 ralatonia s
44	45.5	37.9	2425	17	Q28859	Q28859 archaeoglob
45	45.5	37.5	99	2	Q9AK08	Q9AK08 rhizobium m

ALIGNMENTS

RESULT 1
ID 096979 PRELIMINARY; PRT; 408 AA.
AC 096979;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE Translation elongation factor 1-alpha (Fragment).
TEFL.
OS Paramorphys carnifera.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Scuticociliatia;
OC Philasterida; Orchitophryidae; Paramorphys.
OX NCBI_TaxId=85900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152616; PubMed=10028290;
RA Moreira D., Le Guyader H., Philippe H.;
RT "Unusually high evolutionary rate of the elongation factor 1 alpha
genes from the Ciliophora and its impact on the phylogeny of
eukaryotes. ";
RL Mol. Biol. Evol. 16:234-245(1999).
DR EMBL; AF056103; AAD03258.1; -.
DR HSSP; P02990; 1FTU.
DR InterPro; IPR004539; BPI_alpha.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000795; EF_GTPbind.
DR Pfam; PF00009; GTP_EFTU_1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCF.
DR TIGRFAMs; TIGR00483; EF-1_alpha; 1.
DR PROSITE; PS00301; EFATOR_GTP; 1.
KW Elongation factor; GTP-binding; Protein biosynthesis.
FT NON_TER 1
FT NON_TER 408
SQ SEQUENCE 408 AA; 45067 MW; 384973BB7F3F5FA1 CRC64;
Query Match 44.2%; Score 53; DB 5; Length 408;

Best Local Similarity 55.6%; Pred. No. 8.5;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 NCGWYEGPLLEPPRDALD 20
Db 192 NAWPYKGPILCAALD 209

RESULT 2

Q96SFS PRELIMINARY; PRT; 98 AA.
AC Q96SFS;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE B555G22.1 (Hypothetical protein KIAA1008) (Fragment).
GN B555G22.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL391384; CAC39623.1; -.
KM Hypothetical protein.
FT NON_TER 98
SQ SEQUENCE 98 AA; 10403 MW; DSFF25DD73ACF578 CRC64;

Query Match 43.3%; Score 52; DB 4; Length 98;
Best Local Similarity 69.2%; Pred. No. 2.4;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGMWEGPLLEPPR 16
Db 40 GGAHEGPALPEPP 52

RESULT 3

Q8KBC1 PRELIMINARY; PRT; 175 AA.
AC Q8KBC1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein CT1868.
GN CT1868.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy K., Gwinn M.L., Nelson M.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouli H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL: AE012938; AAM73087.1; -.
DR TIGR: CT1868; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 175 AA; 19661 MW; 3C87FF6C5A7E930 CRC64;

Query Match 42.5%; Score 51; DB 16; Length 175;
Best Local Similarity 47.1%; Pred. No. 6.6;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPRDA 18
Db 138 ENGPWQDAVVERPDA 154

RESULT 4

Q00032 PRELIMINARY; PRT; 205 AA.
AC Q00032;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Major protein component of the microfilarial sheath.
GN MF22.
OS Brugia pahangi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91250404; PubMed=1710216;
RA Seikirk M., Yazdankhsh M., Freedman D., Baxter M., Cookson E.,
RA Jenkins R.E., Williams S.A.;
RT "A proline-rich structural protein of the surface sheath of larval
RT Brugia filarial nematode parasites."
RL J. Biol. Chem. 266:11002-11008(1991).
DR EMBL: X58063; CAA41094.1; -.
SQ SEQUENCE 205 AA; 22199 MW; CAD79DBFC7225041 CRC64;

Query Match 41.7%; Score 50; DB 5; Length 205;
Best Local Similarity 52.9%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPRDA 18
Db 162 QTPGWTPGPRLTPEKPTA 178

RESULT 5

Q9HH38 PRELIMINARY; PRT; 343 AA.
AC Q9HH38;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 38.6 kDa protein.
OS Methanobacterium wolfei.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=145261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429258; PubMed=11544247;
RA Luo Y., Pfeister P., Leisinger T., Wasserfallen A.;
RT "The Genome of Archaeal Prophage PsiM100 Encodes the Lytic Enzyme
RT Responsible for Autolysis of Methanothermobacter wolfeii."
RL J. Bacteriol. 183:5788-5792(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Luo Y.;
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF01375; AAG39973.1; -.
DR InterPro: IPR001993; Mitochondrion carrier.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
KM Hypothetical protein.
SQ SEQUENCE 343 AA; 38594 MW; 61D20A47A28905D3 CRC64;

Query Match 41.7%; Score 50; DB 1; Length 343;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

RESULT 10 748
US-09-880-748-1778
; Sequence 1778, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: p523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15

[illegible]

Qy	118	AMDVWGQGTVTVSS	132
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Db	117	DMDVWGRGTLTVSS	131

RESULT 12
US-09-880

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US-09-880-748-1425
Sequence 1425, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIORITY FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/212,210
PRIORITY FILING DATE: 2000-06-15
PRIORITY APPLICATION NUMBER: 60/240,816
PRIORITY FILING DATE: 2000-10-17
PRIORITY APPLICATION NUMBER: 60/276,248
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/277,379
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/293,499
PRIORITY FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1425
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1425

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Query Match	Score	DB	Length
72.2%	513	11	249

[illegible]

RESULT 13
US-09-880-748-1576
Sequence 1576, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
FILE REFERENCE: PFE23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1576

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; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1576

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Query Match	72.1%	Score 512.5;	DB 11;	Length 257;
Best Local Similarity	75.9%	Pred. No. 4.1e-41;		
Matches 101; Conservative	8;	Mismatches 21;	Indels 3;	Gaps 2

QY	1	QVOLLGSAETEXKKKGGASMKVSCMASGYPEFTSYDLSWVAQAPQOGLMMGWISISGNTDY	60
Db	1	QVOLLVGSAGAEYKKKGGASVKSCEASGYTFSTYSIGSWVAQAPQOGLMMGWISYGNTRY	60
QY	61	AQKQGRVMTTPTDSRRATAYMELRSLRSDPTAVVYCARDGGGAGAYEDVWSGEYP--EYAM	119
Db	61	PQKQGRVMTTPTDSTAYMDELRLSRSDPTAVVYCARD--GRLSYDILTGYARDYGM	118
QY	120	DVMGQGTVTIVSS	132
Db	119	DDMGRTMTIVSS	131

RESULT 14

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US-09-880-748-1562
Sequence 1562, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
FILE REFERENCE: pP523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,459
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1562
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1562

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Query Match	71.8%	Score 510.5;	DB 11;	Length 251;
Best Local Similarity	76.5%	Pred. No. 6.2e-41;		
Matches 101; Conservative	7;	Mismatches 17;	Indels 7;	Gaps 2

[illegible]

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RESULT 15
US-09-0880-748-1452
; Sequence 1452, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1452
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1452
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Query Match 71.8%; Score 510.5; DB 11; Length 259;

Best Local Similarity 73.9%; Pred. No. 6,4e-41;

Matches 99; Conservative 12; Mismatches 20; Indels 3; Gaps 2;

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Db 1 QMVLVQSGAEVKKPGASVKKVCKASGYFTNYGISWTRQAPGQGLEMMGWIISTYNGDNY 60

QY 61 AQKFGGVMTTDTDSRTAYMELSLRSDPTAVYYCARDDGGGAYEDVWSGEY--PEYVA 118
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Db 61 AQKLGQGVMTTDTSTSTAYMELSLRSDPTAVYYCARDRGASNY-DILGYIAPAGVA 119

QY 119 MDVWGQGTIVTSS 132
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 FDIWGRGTLVTSS 133
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Search completed: December 30, 2003, 11:45:22
Job time : 28.3087 secs

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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 13.4037 Seconds

(without alignments)
415.677 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711

Sequence: 1 QVOLLQSAIEVKKPGASMKV.....YPEYVMDVWGQITTVVSS 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	68.2	120	4	US-09-025-769B-36 Sequence 36, Appl
2	485	68.2	120	4	US-09-025-769B-59 Sequence 59, Appl
3	484.5	68.1	117	4	US-09-025-769B-22 Sequence 22, Appl
4	478.5	67.3	121	1	US-08-264-093-3 Sequence 3, Appl
5	476.5	67.0	129	2	US-08-561-521-45 Sequence 45, Appl
6	476.5	67.0	129	4	US-08-525-539A-77 Sequence 77, Appl
7	476.5	67.0	129	5	PCT-US95-01219-45 Sequence 45, Appl
8	476	66.9	128	1	US-08-202-047-22 Sequence 22, Appl
9	476	66.9	128	3	US-08-964-690-22 Sequence 22, Appl
10	471.5	66.3	125	3	US-09-199-149-3 Sequence 19, Appl
11	464	65.3	120	2	US-08-652-816A-19 Sequence 19, Appl
12	452.5	63.6	139	3	US-08-933-983-21 Sequence 21, Appl
13	450	63.3	117	3	US-08-545-809A-105 Sequence 105, Appl
14	448	63.0	139	1	US-08-253-877C-19 Sequence 19, Appl
15	448	63.0	139	2	US-08-452-164A-19 Sequence 19, Appl
16	448	63.0	139	3	US-08-603-024-16 Sequence 16, Appl
17	448	63.0	139	4	US-08-450-809-14 Sequence 14, Appl
18	447	62.9	123	3	US-09-049-672A-13 Sequence 13, Appl
19	444	62.4	120	4	US-09-025-769B-35 Sequence 35, Appl
20	444	62.4	120	4	US-09-025-769B-57 Sequence 57, Appl
21	443.5	62.4	119	2	US-08-561-521-10 Sequence 10, Appl
22	443.5	62.4	119	5	PCT-US95-01219-10 Sequence 10, Appl
23	440.5	62.0	146	1	US-08-276-852-155 Sequence 155, App
24	440.5	62.0	146	1	US-08-276-852-155 Sequence 155, App
25	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
26	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
27	440.5	62.0	146	5	PCT-US95-08743-155 Sequence 155, App

28	438	61.6	1	2	US-08-561-521-41 Sequence 41, Appl
29	438	61.6	1	5	PCT-US95-01219-41 Sequence 41, Appl
30	438	61.6	1	1	US-08-137-117D-102 Sequence 102, App
31	438	61.6	1	2	US-08-436-717-102 Sequence 102, App
32	436.5	61.4	1	1	US-08-300-386A-65 Sequence 65, Appl
33	436.5	61.4	1	3	US-08-931-645-65 Sequence 65, Appl
34	436.5	61.4	1	5	PCT-US95-11235-65 Sequence 65, Appl
35	435.5	61.3	1	2	US-08-561-521-12 Sequence 12, Appl
36	435.5	61.3	1	5	PCT-US95-01219-12 Sequence 12, Appl
37	434.5	61.1	1	1	US-08-477-877B-94 Sequence 94, Appl
38	434.5	61.1	1	2	US-08-477-877B-94 Sequence 94, Appl
39	434.5	61.1	1	3	US-08-477-877B-94 Sequence 94, Appl
40	433.5	61.0	1	3	US-08-836-561-63 Sequence 63, Appl
41	433.5	61.0	1	4	US-09-434-122-63 Sequence 63, Appl
42	433	60.9	1	1	US-08-137-117D-100 Sequence 100, App
43	433	60.9	1	2	US-08-436-717-100 Sequence 100, App
44	432	60.8	1	1	US-08-137-117D-112 Sequence 112, App
45	432	60.8	1	2	US-08-436-717-112 Sequence 112, App

ALIGNMENTS

```
RESULT 1
US-09-025-769B-36
Sequence 36, Application
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik,
APPLICANT: Pack, Pat
APPLICANT: 11ag, Vic
APPLICANT: Ge, Limin
APPLICANT: Moroney,
APPLICANT: Plueckhu
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESS: James F
STREET: 1251 Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FOR
MEDIUM TYPE: Flopp
COMPUTER: IBM PC C
OPERATING SYSTEM:
SOFTWARE: PatentIn
CURRENT APPLICATION D
APPLICATION NUMBER:
FILING DATE: 18-Fe
PRIOR APPLICATION DAT
APPLICATION NUMBER:
FILING DATE: 18-Au
ATTORNEY/AGENT INFORM
NAME: James F. Hal
REGISTRATION NUMBER
TELECOMMUNICATION INF
TELEPHONE: (212)596
TELEFAX: (212)596
INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
LENGTH: 120 amino
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: prote
US-09-025-769B-36
Query Match
Best Local Similarity
Matches 96; Conservat
2%; Score 485; DB 4; Length 120;
7%; Pred. No. 5.3e-39;
7; Mismatches 17; Indels 12; Gaps 1;
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QY 1 QVOLLGATATEYKKGASMKVSCMASGYPTFTSYDISWVROAPGQGLEMMGMIISYSGNTDY 60
Db 1 QVOLLVQSGAEVKKPGASVKSCKASGYFTFTSYMHMWRQAPGQGLEMMGMIINPNSGNTY 60
QY 61 AOKFGQGVMTTDTSRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWVGSEYPEYYAMD 120
Db 61 AOKFGQGVMTTDTSRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWVGSEYPEYYAMD 108
QY 121 VMGQGTIVTVSS 132
Db 109 YMGQGTIVTVSS 120

RESULT 2
US-09-025-769B-59
; Sequence 59, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhann, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-59

Query Match 68.2%; Score 485; DB 4; Length 120;
Best Local Similarity 72.7%; Pred. No. 5,3e-39;
Matches 96; Conservative 7; Mismatches 17; Indels 12; Gaps 1;

QY 1 QVOLLGATATEYKKGASMKVSCMASGYPTFTSYDISWVROAPGQGLEMMGMIISYSGNTDY 60
Db 1 QVOLLVQSGAEVKKPGASVKSCKASGYFTFTSYMHMWRQAPGQGLEMMGMIINPNSGNTY 60
QY 61 AOKFGQGVMTTDTSRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWVGSEYPEYYAMD 120
Db 61 AOKFGQGVMTTDTSRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWVGSEYPEYYAMD 108
QY 121 VMGQGTIVTVSS 132
Db 121 VMGQGTIVTVSS 132

Db 109 YMGQGTIVTVSS: 20

RESULT 3
US-09-025-769B-22
; Sequence 22, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhann, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-22

Query Match 81.1%; Score 484.5; DB 4; Length 117;
Best Local Similarity 72.7%; Pred. No. 5,7e-39;
Matches 96; Conservative 5; Mismatches 16; Indels 15; Gaps 1;

QY 1 QVOLLGATATEYKKGASMKVSCMASGYPTFTSYDISWVROAPGQGLEMMGMIISYSGNTDY 60
Db 1 QVOLLVQSGAEVKKPGASVKSCKASGYFTFTSYMHMWRQAPGQGLEMMGMIINPNSGNTY 60
QY 61 AOKFGQGVMTTDTSRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWVGSEYPEYYAMD 120
Db 61 AOKFGQGVMTTDTSRRTAYMELSLRSDDTAVYYCARDDGGGAYEDVWVGSEYPEYYAMD 105
QY 121 VMGQGTIVTVSS 132
Db 106 YMGQGTIVTVSS 117

RESULT 4
US-08-264-093-3
; Sequence 3, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:

```

APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-3

Query Match
Best Local Similarity 67.3%; Score 478.5; DB 1; Length 121;
Matches 95; Conservative 11; Mismatches 15; Indels 11; Gaps 3;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGGLWMGMISITVSGNTDY 60
DB 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGGLWMGMISITVSGNTDY 60
QY 61 AOKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYPEYYAM 120
DB 61 AOKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYPEYYAM 120
QY 121 VMGGCTVTVSS 132
DB 110 VMGGCTVTVSS 121

```

RESULT 5
US-08-561-521-45
Sequence 45, Application US/08561521

```

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA

```

```

ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC cc
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 42
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-JAN-94
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: R: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543,100
TELEFAX: 415-543,100
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-45

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Query Match
Best Local Similarity 0%; Score 476.5; DB 2; Length 129;
Matches 95; Conservative 4%; Pred. No. 3,7e-38;
11; Mismatches 22; Indels 5; Gaps 2;

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QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGGLWMGMISITVSGNTDY 59
DB 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGGLWMGMISITVSGNTDY 60
QY 60 YAKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYPEYYAM 119
DB 61 YAKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYPEYYAM 116
QY 120 DWVGCTVTVSS 32
DB 117 DWVGCTVTVSS 29

```

RESULT 6
US-08-525-539A-77
Sequence 77, Application /08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUO,
APPLICANT: CERTANI, J
APPLICANT: PETERSON,
TITLE OF INVENTION: COMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: ANTI-B46 ANTIBODY, METHODS OF USE THEREOF, AND
METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
STREET: 755 Page M
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC cc
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 5/08/525,539A
FILING DATE: 14-SEP-95

```

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
;
; TELETYPE: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-525-539A-77
;
; Query Match          67.0%; Score 476.5; DB 4; Length 129;
; Best Local Similarity 71.4%; Pred. No. 3.7e-38;
; Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;
;
QY 1 QVOLLQSAATEVKKKPGASMKVSCASGYPTSTDISWVRQAPGQGLEMMGWISIT-YSQNTD 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVOLLVSGAEVKKPGASVSKVSCASGYPTSTYSAISWVRQAPGQGLEMMGWIMPYGNQD 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YVAKFGGRVTMTDTRRTAYWELRSLRSDPTAVYYCARDGGGAYEDVWSGEPEPYAM 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YVAKFGGRVTITADISTRTAYWELSLRSDPTAVYYCARDAPYGGGCGCTRGD---YXF 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 DVMGQSTTVTVSS 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 117 DVMGQSTLVTVSS 129
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
;
; RESULT 7
; PCT-US95-01219-45
; Sequence 45, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saidanba, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 129 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
;
; PCT-US95-01219-45
;
; Query Match          67.0%; Score 476.5; DB 5; Length 129;
; Best Local Similarity 71.4%; Pred. No. 3.7e-38;
; Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;
;
QY 1 QVOLLQSAATEVKKKPGASMKVSCASGYPTSTDISWVRQAPGQGLEMMGWISIT-YSQNTD 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVOLLVSGAEVKKPGASVSKVSCASGYPTSTYSAISWVRQAPGQGLEMMGWIMPYGNQD 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YVAKFGGRVTMTDTRRTAYWELRSLRSDPTAVYYCARDGGGAYEDVWSGEPEPYAM 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YVAKFGGRVTITADISTRTAYWELSLRSDPTAVYYCARDAPYGGGCGCTRGD---YXF 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 DVMGQSTTVTVSS 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 117 DVMGQSTLVTVSS 129
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
;
; RESULT 8
; US-08-202-047-22
; Sequence 22, Application
; Patent No. 580815
; GENERAL INFORMATION:
; APPLICANT: CHESNOT,
; APPLICANT: POLLEY, N
; APPLICANT: PAULSON,
; APPLICANT: JONES, S
; APPLICANT: SALDANHA,
; APPLICANT: BENDIG, N
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend
; STREET: One Market
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC
; OPERATING SYSTEM:
; SOFTWARE: Patentin
; CURRENT APPLICATION I
; APPLICATION NUMBER:
; FILING DATE: 25-F
; CLASSIFICATION: 4
; ATTORNEY/AGENT INFOR
; NAME: Smith, Willia
; REGISTRATION NUMBER
; REFERENCE/DOCKET NU
; TELECOMMUNICATION IN
; TELEPHONE: 415-326
; TELEFAX: 415-326-
; INFORMATION FOR SEQ ID
; SEQUENCE CHARACTERIS
; LENGTH: 128 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION:
;
; US-08-202-047-22
; label= HUMAN_I
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```

Query Match      66.9%; Score 476; DB 1; Length 128;
Best Local Similarity 71.4%; Pred. No. 4.1e-38;
Matches 95; Conservative 11; Mismatches 21; Indels 6; Gaps 2;

Qy 1 QVOLLQSTAEVKKPPASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGWISITV-SGNTD 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLQSAEYKPPASVKKVSCKAGYFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 YAKFGQGRVTMTTDSRTAYAMELSLRSDPTAVYYCARDCGGAGYEDVMSGEYPEYYAM 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAKFGQGRVTITADTISTATAMELSLRSDPTAVYYCARAPGYSGGCGCTGDIY----F 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 120 DVMGQGTIVTVSS 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 DVMGQGTIVTVSS 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-08-964-690-22
; Sequence 22, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_1
US-08-964-690-22

Query Match      66.9%; Score 476; DB 3; Length 128;
Best Local Similarity 71.4%; Pred. No. 4.1e-38;
Matches 95; Conservative 11; Mismatches 21; Indels 6; Gaps 2;

```

```

Qy 1 QVOLLQSTAEVKKPPASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGWISITV-SGNTD 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLQSAEYKPPASVKKVSCKAGYFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 YAKFGQGRVTMTTDSRTAYAMELSLRSDPTAVYYCARDCGGAGYEDVMSGEYPEYYAM 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAKFGQGRVTITADTISTATAMELSLRSDPTAVYYCARAPGYSGGCGCTGDIY----F 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 120 DVMGQGTIVTVSS 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 DVMGQGTIVTVSS 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-199-149-3
; Sequence 3, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenek.
; APPLICANT: Taylor, Alex.
; APPLICANT: Trull, Jr., S.
; APPLICANT: Johnson, Ky.
; APPLICANT: Johnson, Ky.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; CURRENT FILING DATE: 1995-11-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 1.0
; SEQ ID NO 3
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Kabat VH subg
US-09-199-149-3

Query Match      63%; Score 471.5; DB 3; Length 125;
Best Local Similarity 71%; Pred. No. 1.1e-37;
Matches 96; Conservative 8; Mismatches 18; Indels 13; Gaps 3;

Qy 1 QVOLLQSTAEVKKPPASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGWISITVSGNTD 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLQSAEYKPPASVKKVSCKAGYFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 AAKFGQGRVTMTTDSRTAYAMELSLRSDPTAVYYCARDCGGAGYEDVMSGEYPEYY 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 AAKFGQGRVTITADTISTATAMELSLRSDPTAVYYCARAPGYSGGCGCTGDIY----GYM 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 118 AMDVWGQGTIVTVSS 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 YMGVWGQGTIVTVSS 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-08-652-816A-19
; Sequence 19, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Odbourn, J
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty
; TITLE OF INVENTION: Specific binding members, materials and methods.
; TITLE OF INVENTION: "
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall
; STREET: 6300 Sears
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

```


APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/Jp93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-105

Query Match 63.3%; Score 450; DB 3; Length 117;
Best Local Similarity 86.7%; Pred. No. 1,1e-35;
Matches 85; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLKMMGWISYSGNTDY 60
Db 20 QVOLLQSAATEVKKPGASVKSCKASGYFTSYDISWVRQAPQGLKMMGWISYSGNTDY 79

Qy 61 AOKFGQRTVMTTTSRTAYWELRLSRDDTAIVYCAR 98
Db 80 AOKFGQRTVMTTTSRTAYWELRLSRDDTAIVYCAR 117

RESULT 14
US-08-253-877C-19
Sequence 19, Application US/08253877C
Patent No. 5773001
GENERAL INFORMATION:
APPLICANT: Hamann, Phillip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Halleck, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrichio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3346
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-253-877C-19

Query Match 0%; Score 448; DB 1; Length 139;
Best Local Similarity 2%; Pred. No. 2e-35;
Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

Qy 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLKMMGWISYSGNTDY 60
Db 20 QVOLLQSAATEVKKPGASVKSCKASGYFTSYDISWVRQAPQGLKMMGWISYSGNTDY 79

Qy 61 AOKFGQRTVMTTTSRTAYWELRLSRDDTAIVYCAR 98
Db 80 AOKFGQRTVMTTTSRTAYWELRLSRDDTAIVYCAR 117

Qy 121 VMGGQTTVTVSS 12
Db 128 VMGGQTTVTVSS 19

RESULT 15
US-08-452-164A-19
Sequence 19, Application US/08452164A
Patent No. 5877296
GENERAL INFORMATION:
APPLICANT: Hamann, Phillip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Halleck, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrichio Antitumor
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 531
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-5858
TELEFAX: 201-683-4119
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-164A-19

Query Match 0%; Score 448; DB 2; Length 139;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 9.39399 Seconds

(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-27

Perfect score: 521
Sequence: 1 QVQLQSGATVEKPKGASMKV.....AYMELRLSRDPTAVYYCAR 98Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase :
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	87.5	98	2	S26919 Ig heavy chain V r
2	453	86.9	129	2	S36260 Ig heavy chain V r
3	451	86.6	122	2	S36271 Ig heavy chain V r
4	450	86.4	124	2	S19665 Ig heavy chain V r
5	432	82.9	131	2	S21924 Ig heavy chain V r
6	428	82.1	160	2	PL0105 anti-PR2 erythrocy
7	420	80.6	111	2	S21925 Ig heavy chain V r
8	407	78.1	98	2	S26918 Ig heavy chain V r
9	407	78.1	117	2	S18553 Ig heavy chain V r
10	407	78.1	136	2	S31600 Ig heavy chain V r
11	405	77.7	125	2	S68170 Ig heavy chain V r
12	401	77.0	98	2	S26938 Ig heavy chain V r
13	401	77.0	117	2	S31680 Ig heavy chain V r
14	401	77.0	117	2	S18551 Ig heavy chain V r
15	401	77.0	135	2	S49530 anti-sm antibody V
16	400	76.8	118	2	S36265 Ig heavy chain V r
17	397	76.2	104	2	S69899 Ig heavy chain V r
18	397	76.2	127	2	S34014 Ig heavy chain V r
19	393	75.4	98	2	S26912 Ig heavy chain V r
20	393	75.4	129	2	S46395 Ig heavy chain V r
21	391	75.0	117	2	S18552 Ig heavy chain V r
22	390	74.9	132	2	S31596 Ig heavy chain V r
23	389	74.7	110	2	PH1670 Ig heavy chain V r
24	389	74.7	123	2	D33548 Ig heavy chain V-1
25	388	74.5	98	2	S26920 Ig heavy chain V r
26	387	74.3	117	2	PT0371 Ig gamma chain pre
27	383	73.5	117	1	HVHUNG Ig heavy chain pre
28	383	73.5	148	2	S29257 Ig heavy chain V r
29	382	73.3	114	2	PH1667 Ig heavy chain V r

30	382	73.3	1	2	PH1666 Ig heavy chain V r
31	381	73.1	1	2	A32483 Ig heavy chain V r
32	380	72.9	1	2	S23623 Ig heavy chain V r
33	379	72.7	2	2	PH0871 Ig heavy chain V r
34	378	72.6	1	2	JN0295 Ig heavy chain V-D
35	377	72.4	1	2	S31657 Ig heavy chain V r
36	377	72.4	1	1	HVH05 Ig heavy chain pre
37	377	72.4	1	2	S31999 Ig heavy chain V r
38	377	72.4	1	2	B32274 Ig heavy chain pre
39	376	72.2	1	2	I44151 Ig heavy chain V r
40	372	71.4	2	2	S24680 Ig heavy chain V r
41	370	71.0	2	2	S26921 Ig heavy chain V r
42	369	70.8	1	2	PH1665 Ig heavy chain V r
43	369	70.8	1	2	PH1668 Ig heavy chain V r
44	367	70.4	2	2	S26915 Ig heavy chain V r
45	367	70.4	1	2	S31698 Ig heavy chain pre

ALIGNMENTS

RESULT 1

S26919 Ig heavy chain V region (D. 4) - human (fragment)
C:Species: Homo sapiens (m. _revision 10-Nov-1995 #text_change 23-Jul-1999
C:Date: 22-Nov-1993 #sequen
R:Accession: S26919
R:Tolsonson, I.M.; Walter, J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of man germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885 UID:9302117; PMID:1404388
A:Accession: S26919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-References: EMBL:Z12316; NID:G32855; PIND:CA79303.1; PID:G32856
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 456; DB 2; Length 98;
Best Local Similarity 87.8%; Pred. No. 1.76-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLQSGATVEKPKGASMKVSCMASGYPTSYDISWYRQAGGLEWYGSATNGNTHY 60
Db 1 QVQLVSGAEVKKPKGASVKSCASGTTFTSYGISWVQAGGLEWGMWISATNGNTY 60
Qy 61 AOKFQGRVTMTTDSRRRAYMELRLSRDPTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTRAYMELRLSRDPTAVYYCAR 98

RESULT 2

S36260 Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
R:Accession: S36260
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, A.; Title: Human anti-self antibodies with high specificity from phage display libraries
EMBO J. 12, 725-734, 1993
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36260
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-129 <GRI>
A:Cross-References: EMBL:Z18851; NID:G33124; PIND:CA79303.1; PID:G9339903
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 453; DB 2; Length 129;

Best Local Similarity 87.8%; Pred. No. 4.7e-39;
Matches 86; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
Db 1 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGWISAYNGNTY 60

Qy 61 AOKFGQGVMTTDTSRRTAYMELRLSRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 3
S36271
Ig heavy chain V region (clone alpha-THY-29) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36271
R:Giffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36271
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <GRI>
A:Cross-references: EMBL:Z18832; NID:G33115; PIDN:CAA79284.1; PID:G939895
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 451; DB 2; Length 122;
Best Local Similarity 87.6%; Pred. No. 7.1e-39;
Matches 85; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
Db 1 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGWISAYNGNTY 60

Qy 61 AOKFGQGVMTTDTSRRTAYMELRLSRSDDTAVYYCA 97
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCA 97

RESULT 4
S19665
Ig heavy chain V region (alpha-phoX15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Jun-2000
C:Accession: S19665; S24442
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Giffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage.
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19665
A:Molecule type: mRNA
A:Residues: 1-124 <MAR>
A:Cross-references: EMBL:X61647
R:Jones, P.T.
Submitted to the EMBL Data Library, October 1991
A:Reference number: S24442
A:Accession: S24442
A:Molecule type: mRNA
A:Residues: 1-40, 'GLSGMDGSAITMTVQSLDK', 61-118, 'T', 120-124 <JON>
A:Cross-references: EMBL:X61647; NID:G37667; PIDN:CAA43828.1; PID:G1335368
A:Note: the difference for residues 41-60 results from misplacement of 10 bases in the C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 450; DB 2; Length 124;
Best Local Similarity 86.7%; Pred. No. 9.1e-39;
Matches 85; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
Db 1 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGWISAYNGNTY 60

Qy 61 AOKFGQGVMTTDTSRRTAYMELRLSRSDDTAVYYCAR 98
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 5
S21924
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21924; S21923
R:Friedman, D.P.
Submitted to the EMBL Data Library, July 1991
A:Reference number: S21923
A:Accession: S21924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-131 <PRI>
A:Cross-references: EMBL:X60505; NID:G33565; PIDN:CAA43025.1; PID:G33566; EMBL:X60504;
C:Genetics:
A:Insertion: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 432; DB 2; Length 131;
Best Local Similarity 82.7%; Pred. No. 6.5e-37;
Matches 81; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
Db 20 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGWISAYNGNTY 79

Qy 61 AOKFGQGVMTTDTSRRTAYMELRLSRSDDTAVYYCAR 98
Db 80 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 117

RESULT 6
PL0105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C:Accession: PL0105
R:Silberstein, L.E.; Litwin, S.; Carmack, C.B.
U. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma B6
A:Reference number: PL0106; MUID:89235583; PMID:2541221
A:Accession: PL0105
A:Molecule type: mRNA
A:Residues: 1-160 <SL>
A:Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red b
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; hemagglutinin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:49-54/Region: complementarity-determining 1
F:69-84/Region: complementarity-determining 2
F:118-131/Domain: D region <DRG>
F:132-144/Domain: J4 segment <JSG>
F:145-160/Domain: C region <CRG>

Query Match 82.1%; Score 428; DB 2; Length 160;
Best Local Similarity 81.6%; Pred. No. 2.1e-36;
Matches 80; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60

Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYGISMVNQAPQGLEWMGMISAVNGNTY 79
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 98
Db 80 AOKLQGRVYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 117

RESULT 7

S21925
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21925
R:Friedman, D.F.
submitted to the EMBL Data Library, July 1991
A:Reference number: S21923
A:Accession: S21925
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <FRI>
A:Cross-references: EMBL:X60503; NID:g33626; PIDN:CAA43023.1; PID:g33627
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 80.6%; Score 420; DB 2; Length 111;
Best Local Similarity 87.0%; Pred. No. 9.1e-36;
Matches 80; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLEWMGMISAVNGNTY 60
Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYGISMVNQAPQGLEWMGMISAVNGNTY 79
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDTA 92
Db 80 AOKLQGRVYVTMTDTSRRTAYMELRSRSDTA 111

RESULT 8

S26918
Ig heavy chain V region (DP-15) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26918
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 407; DB 2; Length 98;
Best Local Similarity 78.6%; Pred. No. 1.7e-34;
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLEWMGMISAVNGNTY 60
Db 1 QVQLVQSGAEVKKPKASVAVSCASGYFTSYDISWVROATQGLEWMGMISAVNGNTY 60
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 98
Db 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 98

RESULT 9

S18553
Ig heavy chain V region precursor (VI-3b) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18553; S26916
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.;
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus:
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18553
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X62109
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26916
A:Molecule type: DNA
A:Residues: 20-117 <TOM>
A:Cross-references: EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID:g32872
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match

78.1%; Score 407; DB 2; Length 117;
Best Local Similarity 78.6%; Pred. No. 2e-34;
Matches 77; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLEWMGMISAVNGNTY 60
Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYAMHNVQAPQGLEWMGMISAVNGNTY 79
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 98
Db 80 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 117

RESULT 10

S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougeret, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from th
A:Reference number: S31585
A:Accession: S31600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUY>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 407; DB 2; Length 136;
Best Local Similarity 78.6%; Pred. No. 2.4e-34;
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLEWMGMISAVNGNTY 60
Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYDISWVROATQGLEWMGMISAVNGNTY 79
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 98
Db 80 AOKFGQRYVTMTDTSRRTAYMELRSRSDTAIVYVCAR 117

S49530
anti-Sm antibody VH chain (VH1/DK1 or DML/JH4b) - human

C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Maimoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies
A:Accession number: S48797
A:Reference: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL: Z46348; NID: G560839; PIDN: CAA66467.1; PID: G560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMW>

Query Match 77.0%; Score 401; DB 2; Length 135;
Best Local Similarity 77.6%; Pred. No. 9, 6e-34;
Matches 76; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQSATVEYKKPKASMKVSCMAGCYEFTSDISDWNRQAQGGLGEMVGWTSANGNTHY 60
 |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
DB 20 QVALQSAEAEVKKPPASVSKCSKASGYFTGTGMHWVAQAPQGLEMMGWIMPNSGGTNY 79
 |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY 61 AAKFGGRVTMTDTSRRRTAYMELSRLSPDDTAIVYYCAR 98
 |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
DB 80 AAKFGGRVTMTDRDISSTRAYMELSLRLSDDTAVYYCAR 117
 |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:

Search completed: December 30, 2003, 11:03:14
Job time : 9.39399 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 5.25426 Seconds
(without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-27

Perfect score: 521
Sequence: 1 QVOLLQATVEYKKGASMKV.....AYMEIRSLRSDDTAVYCAR 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	73.5	117	1	HV1B_HUMAN
2	377	72.4	117	1	HV1G_HUMAN
3	359	68.9	147	1	HV1C_HUMAN
4	340	65.3	117	1	HV52_MOUSE
5	331	63.5	117	1	HV1A_HUMAN
6	326	62.6	114	1	HV00_MOUSE
7	326	62.6	117	1	HV14_MOUSE
8	326	62.6	120	1	HV03_MOUSE
9	325	62.4	117	1	HV04_MOUSE
10	324	62.2	140	1	HV02_MOUSE
11	319	61.2	117	1	HV09_MOUSE
12	315	60.5	118	1	HV51_MOUSE
13	314	60.3	117	1	HV06_MOUSE
14	314	60.3	120	1	HV50_MOUSE
15	313	60.1	117	1	HV05_MOUSE
16	313	60.1	117	1	HV12_MOUSE
17	313	60.1	117	1	HV13_MOUSE
18	307	58.9	139	1	HV07_MOUSE
19	300	57.6	136	1	HV15_MOUSE
20	298	57.0	117	1	HV3C_HUMAN
21	297	57.0	117	1	HV10_MOUSE
22	297	57.0	117	1	HV49_MOUSE
23	295	56.6	137	1	HV11_MOUSE
24	294	56.4	138	1	HV48_MOUSE
25	292	56.0	121	1	HV3J_HUMAN
26	290	55.7	125	1	HV1F_HUMAN
27	289	55.5	117	1	HV55_MOUSE
28	284	54.5	119	1	HV3I_HUMAN
29	282	54.1	121	1	HV01_MOUSE
30	275.5	52.9	120	1	HV1H_HUMAN
31	274	52.6	119	1	HV3P_HUMAN
32	274	52.6	112	1	HV3G_HUMAN
33	272	52.2	136	1	HV16_MOUSE

34	270	51.8	122	1	HV3A_HUMAN	P01762	homo sapien
35	270	51.8	122	1	HV3H_HUMAN	P01769	homo sapien
36	269	51.6	114	1	HV3B_HUMAN	P01763	homo sapien
37	268	51.4	119	1	HV3M_HUMAN	P01774	homo sapien
38	266	51.1	117	1	HV54_MOUSE	P18525	mus musculus
39	265.5	51.0	97	1	HV56_MOUSE	P18527	mus musculus
40	265.5	51.0	116	1	HV05_CARAU	P19181	carabassus a
41	265	50.9	119	1	HV3L_HUMAN	P01773	homo sapien
42	264	50.7	126	1	HV3K_HUMAN	P01772	homo sapien
43	263.5	50.6	117	1	HV02_CARAU	P01785	canis fam11
44	263	50.5	117	1	HV03_CARAU	P19180	carabassus a
45	261.5	50.2	115	1	HV3F_HUMAN	P01767	homo sapien

ALIGNMENTS

RESULT 1

HV1B_HUMAN
ID HV1B_HUMAN STANDARD; PRT; 117 AA.

AC P01743;
DT 21-JUL-1986 (Rel. 01, Last Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region H33 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_Taxid=9606;

RN (1)

RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;

RA Reclavi G., Ram D., Glazer L., Zakut R., Givol D.;

RT "Evolutionary aspects of immunoglobulin heavy chain variable region

RT (VH) gene subgroups.";

RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC -----

DR EMBL; J00240; AAA52988.1; -.

DR PIR; A02024; HVH0HG.

DR HSSP; P01772; 2PB4.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_MHC.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_LIKE; 1.

DR Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H33.

FT DOMAIN 20 >117 IG-LIKE.

FT NON TER 117 117

SQ SEQUENCE 117 AA; 12946 MW; 203F92FC60CD1FE7 CRC64;

Query Match 73.5%; Score 383; DB 1; Length 117;

Best Local Similarity 75.5%; Pred. No. 1e-17;

Matches 74; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVOLLQATVEYKKGASMKVSCMASGYPTFSYDLSWTRQAGGLEGVGMISATNGNTHY 60
Db 20 QVOLLQATVEYKKGASMKVSCMASGYPTFSYDLSWTRQAGGLEGVGMISATNGNTHY 79

```

QY 61 AOKFGQGVMTTDTSTRTAYMELRSLSRSDDTAVYYCAR 98
DB 80 AOKFGQGVMTTDTSTRTAYMELRSLSRSDDTAVYYCAR 117

RESULT 2
HVLG HUMAN STANDARD; PRT; 117 AA.
AC P23063;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ono H., Fukushima S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBL J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
CC EMBL; X07448; -; NOT ANNOTATED_CDS.
CC PIR; S00476; HVHJ35.
CC HSSP; P01772; 2FBA4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117
FT TER 117
SQ SEQUENCE 117 AA; 13009 MM; BE61CE63F8CE97BD CRC64;

Query Match 72.4%; Score 377; DB 1; Length 117;
Best Local Similarity 74.5%; Pred. No. 5.1e-37;
Matches 73; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPFSTSYDISWVROAPGQGLEWVGWISAVNGNTHY 60
DB 20 QVOLLQSAATEVKKPGASMKVSCMASGYPFSTSYDISWVROAPGQGLEWVGWISAVNGNTHY 79

RESULT 3
HVLG HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (fragments).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT CHAIN 1 19
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON TER 147
FT TER 147
SQ SEQUENCE 147 AA; 16491 MM; 948F9F72A5366C20 CRC64;

Query Match 68.9%; Score 359; DB 1; Length 147;
Best Local Similarity 67.3%; Pred. No. 8.3e-35;
Matches 66; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPFSTSYDISWVROAPGQGLEWVGWISAVNGNTHY 60
DB 20 QVOLLQSAATEVKKPGASMKVSCMASGYPFSTSYDISWVROAPGQGLEWVGWISAVNGNTHY 79

RESULT 4
HVS2 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.

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RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
DR EMBL: M13787; AAA38499.1; -.
DR PIR: A02029; HVM5A1.
DR HSP: P01810; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 65.3%; Score 340; DB 1; Length 117;
Best Local Similarity 62.2%; Pred. No. 1e-32;
Matches 61; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

Qy 1 OVQLQSGATVEYKRGASMKVSCMASGYPTSYDISWVRQAPGQLEWVGWISANGNTYH 60
Db 20 QVQLVQSGAEVKKGQSLVKLSCKASGYTFTSYDINWVRQAPGQLEWVGWISANGNTYH 79
Qy 61 AQKFGKRVTTTDSRTATYMLSLRSDDTAVYYCA 98
Db 80 NEKFKGKATLTADKSSSTATYVQLSLTSNSAVYFCAR 117

RESULT 5
HVA HUMAN
ID _HVA_HUMAN STANDARD; PRT: 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Wexler M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
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RT Intrachain disulfide bonds.";
RL Biochemistry 9:3168-3196(1970).
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -----
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90563; G1H0EU.
DR HSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Pyrolydine carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLYDINE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADA8BD52818 CRC64;

Query Match 63.5%; Score 331; DB 1; Length 117;
Best Local Similarity 68.0%; Pred. No. 1.2e-31;
Matches 66; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

Qy 1 OVQLQSGATVEYKRGASMKVSCMASGYPTSYDISWVRQAPGQLEWVGWISANGNTYH 60
Db 1 QVQLVQSGAEVKKGQSLVKLSCKASGYTFTSYDINWVRQAPGQLEWVGWISANGNTYH 60
Qy 61 AQKFGKRVTTTDSRTATYMLSLRSDDTAVYYCA 97
Db 61 AQKFGKRVTTTDSRTATYMLSLRSDDTAVYYCA 97

RESULT 6
HVO0 MOUSE
ID _HVO0_MOUSE STANDARD; PRT: 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisencoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02022; G1MSA1.
DR HSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON_TER 114 114
```



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CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02030; HVM523.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 62.4%; Score 325; DB 1; Length 117;
Best Local Similarity 62.2%; Pred. No. 5.9e-31;
Matches 61; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

OY 1 OVOLLQSTAEVKKPGASMKVSCMASGYPTFSYDISWVROAPQGLWVGMISAVNGNTHY 60
DB 20 OVOLLQPGTELKPKASVSKASGYFTFSYGMWVQKRGQGLWVGMISAVNGNTHY 79
OY 61 AOKFGKVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98
DB 80 NEKFKSKTTLTVDKSSSTAYVQLSLTSBDSAVYYCAR 117

RESULT 10
HVO2_MOUSE STANDARD; PRT; 140 AA.
ID HVO2_MOUSE
AC P01746;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=83152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL: J00493; AAA8128.1; -.
DR PIR: A94264; HVM5G7.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR SMART, SM00406; IGV; 1.
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DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CB8E31DA5CE8 CRC64;

Query Match 62.2%; Score 324; DB 1; Length 140;
Best Local Similarity 59.2%; Pred. No. 9.5e-31;
Matches 58; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

OY 1 OVOLLQSTAEVKKPGASMKVSCMASGYPTFSYDISWVROAPQGLWVGMISAVNGNTHY 60
DB 20 EVOLLQSGAEVLVRAKSSVSKASGYFTFSYGMWVQKRGQGLWVGMISAVNGNTHY 79
OY 61 AOKFGKVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98
DB 80 NEKFKSKTTLTVDKSSSTAYVQLSLTSBDSAVYYCAR 117

RESULT 11
HVO9_MOUSE STANDARD; PRT; 117 AA.
ID HVO9_MOUSE
AC P01753; P11271;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-JUN-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paekind M., Reith W., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
DR PIR: D90809; HVM561.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A086CB17F5A CRC64;

Query Match 61.2%; Score 319; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 2.9e-30;
Matches 59; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

OY 1 OVOLLQSTAEVKKPGASMKVSCMASGYPTFSYDISWVROAPQGLWVGMISAVNGNTHY 60
DB 20 OVOLLQSGAEVLVRAKSSVSKASGYFTFSYGMWVQKRGQGLWVGMISAVNGNTHY 79
OY 61 AOKFGKVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98
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DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009851; AA09851.1; -
 DR InterPro; IPR000005; HTHArac.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KM Hypothetical protein.
 SQ SEQUENCE 614 AA; 67921 MW; 55EFS36E77AA9BBB CRC64;

Query Match 71.2%; Score 371; DB 4; Length 614;
 Best Local Similarity 70.4%; Pred. No. 1.7e-32;
 Matches 69; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 QVOLLGATATEVKKPGASMKVSCASGYPTSDISWVRAPQGLGEMVGMISAVNGNTNY 60
 Db 20 QVOLLVSGAEVKKGTSSVSCASGYTFTYRLHVRQAPQALEMGMWITPFGNTNY 79
 OY 61 AOKFQGRVTMTTDSRTTAYMELRLSRSDTAIVYCAR 98
 Db 80 AOKFQGRVTITRDRSMNTAYMELSLRSRSDTAIVYCAR 117

RESULT 6
 Q96QSO PRELIMINARY; PRT; 159 AA.
 ID Q96QSO;
 AC Q96QSO;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DE Putative matrix cell adhesion molecule-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tilson M.D.;
 RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
 RL mRNA (Matrix Cell Adhesion molecule-3, Mat-CAM 3).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY039025; AA02649.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537EB81FAF02 CRC64;

Query Match 69.7%; Score 363; DB 4; Length 159;
 Best Local Similarity 69.4%; Pred. No. 2.6e-32;
 Matches 68; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

OY 1 QVOLLGATATEVKKPGASMKVSCASGYPTSDISWVRAPQGLGEMVGMISAVNGNTNY 60
 Db 20 QVOLLVSGAEVKKGTSSVSCASGYTFTYRLHVRQAPQALEMGMWITPFGNTNY 79

OY 61 AOKFQGRVTMTTDSRTTAYMELRLSRSDTAIVYCAR 98
 Db 80 AOKFQGRVTITRDRSMNTAYMELSLRSRSDTAIVYCAR 117

RESULT 7
 Q9GYZ2 PRELIMINARY; PRT; 119 AA.
 ID Q9GYZ2;
 AC Q9GYZ2;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
 DE (Fragment).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RL Schistosoma japonicum";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282622; AA01452.1; -
 DR HSPB; P01772; 2F84.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFACAB CRC64;

Query Match 68.7%; Score 358; DB 5; Length 119;
 Best Local Similarity 68.4%; Pred. No. 6.7e-32;
 Matches 67; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

OY 1 QVOLLGATATEVKKPGASMKVSCASGYPTSDISWVRAPQGLGEMVGMISAVNGNTNY 60
 Db 1 QVOLLVSGAEVKKGTSSVSCASGYTFTYRLHVRQAPQALEMGMWITPFGNTNY 79
 OY 61 AOKFQGRVTMTTDSRTTAYMELRLSRSDTAIVYCAR 98
 Db 61 AOKFQGRVTITRDRSMNTAYMELSLRSRSDTAIVYCAR 117

RESULT 8
 Q8WY24 PRELIMINARY; PRT; 497 AA.
 ID Q8WY24;
 AC Q8WY24;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
 DE SMC66 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
 RT "Identification and characterization of SMC66, a Ig-like gene which is
 RT down-regulated in colorectal cancer";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282666; AA036987.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.

DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 4.
DR PROSITE: PS00290; IG_MHC: 1.
SQ SEQUENCE 497 AA; 5365 MM; F24D08DFA5A63E5 CRC64;

Query Match
Best Local Similarity 68.3%; Score 357; DB 4; Length 497;
Matches 65; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEKKPKGASKMKVSCASGYPTSYDISWVROAPQGGLVWGMISAYNGNTYH 60
DB 20 QEQLEQSGAEVTKPKGASVSKVSCASGYPTFIAYDINVRQAPQGGLVWGMNPNQNTNTEF 79
QY 61 AOKFGQRYVMTTDSRTAYMELRSRSDPTAVYYCA 98
DB 80 AOKFGQRLTFSRDTSINTAYMVLSTLSEDSAYIFCAR 117

RESULT 9
Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035025; AAD56261.1; -.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR007110; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12605 MM; C8F913DE13EA898 CRC64;

Query Match
Best Local Similarity 65.3%; Score 340; DB 4; Length 116;
Matches 67; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 5 LQSADEVKPKGASKMKVSCASGYPTSYDISWVROAPQGGLVWGMISAYNGNTYH 64
DB 1 VQSGAEVKKPKGASVSKVSCASGYPTSSYSAISWVROAPQGGLVWGMRIIPILGIANYAKKF 60
QY 65 QGRVTMTTDSRTAYMELRSRSDPTAVYYCA 97
DB 61 QGRVTITADKSTAYMELSLRSEDTAVYYCA 93

RESULT 10
Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MRJ.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL: AF240166; AAK43731.1; -.
DR InterPro: IPR007110; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 1.
SQ SEQUENCE 147 AA; 16274 MM; 800594A12B97191F CRC64;

Query Match
Best Local Similarity 64.7%; Score 337; DB 11; Length 147;
Matches 63; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEKKPKGASKMKVSCASGYPTSYDISWVROAPQGGLVWGMISAYNGNTYH 60
DB 3 QVQLHQSGEVVKKPKGASVSKVSCASGYPTSYDISWVROAPQGGLVWGMIPPGEGSTREY 62
QY 61 AOKFGQRYVMTTDSRTAYMELRSRSDPTAVYYCA 98
DB 63 NEKFKRATLSVDKSSSTAYMELTRLTSEDSAVYFCAR 100

RESULT 11
Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC013490; AAH13490.1; -.
DR InterPro: IPR007110; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 4.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 4.
DR PROSITE: PS00290; IG_MHC: 2.
KM Hypothetical protein
SQ SEQUENCE 481 AA; 52105 MM; 97DF68D159463F65 CRC64;

Query Match
Best Local Similarity 64.3%; Score 335; DB 11; Length 481;
Matches 62; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

Qy	1	QVOLLQSAATEVKKPKASMKVSCMASGYPFTSYDISWVAQAPQGLWVGMISAVXGNTHY	60
Db	20	QVOLLQSGPELVPKASVAKISCKASGYTFTSYIHWKQRPQGLWVIGWIPGDKTKY	79
Qy	61	AQKFGARVTMTTDTTSRRTAYMELRLSRSDDTAVYYCAR	98
Db	80	NEKFGKTTTLTADKSSSTAYMFLSSLTSDSAVYFCTR	117
RESULT 12			
Qy	Q9Y298	PRELIMINARY; PRT; 150 AA.	
ID	Q9Y298		
AC	Q9Y298:		
DT	01-NOV-1999	(TREMBLrel. 12, Created)	
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	IGG VH protein precursor (Fragment).		
GN	IGG VH.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OK	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98322155; PubMed=9657749;		
RA	Jacquelin M.G., Vander Elst L.P.L.;		
RT	"Mechanism and kinetics of factor VIII inactivation: study with an		
RT	IGG monoclonal antibody derived from a hemophilia A patient with		
RT	inhibitor.";		
RL	Blood 92:496-506(1998).		
DR	EMBL: AJ224083; CAA11829.1; -.		
DR	HSSP: P01772; 2F84.		
DR	InterPro: IPR007110; IG-like.		
DR	InterPro: IPR003006; IG_MHC.		
DR	InterPro: IPR003596; IG_V.		
DR	Pfam: PF00047; IG_1.		
DR	SMART: SMO0406; IGV; 1.		
DR	PROSITE: PS50835; IG_LIKE; 1.		
KW	Signal.		
FT	SIGNAL. 1 19	POTENTIAL.	
FT	NON_TER 150 150		
SO	SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;		
Query Match	64.1%;	Score 334; DB 4; Length 150;	
Best Local Similarity	67.0%;	Pred. No. 4e-29;	
Matches	65; Conservative 8; Mismatches 24; Indels 0; Gaps 0		
Qy	1	QVOLLQSAATEVKKPKASMKVSCMASGYPFTSYDISWVAQAPQGLWVGMISAVXGNTHY	60
Db	20	QVOLLQSGPELVPKASVAKISCKASGYTFTSYIHWKQRPQGLWVIGWIPGDKTKY	79
Qy	61	AQKFGARVTMTTDTTSRRTAYMELRLSRSDDTAVYYCA	97
Db	80	AREFGSVTMTADTSDIAYMELSLRSDDTAVYYCA	116
RESULT 13			
ID	Q8K024	PRELIMINARY; PRT; 480 AA.	
AC	Q8K024:		
DT	01-OCT-2002	(TREMBLrel. 22, Created)	
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	Similar to expressed sequence A1893585.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OK	NCBI_TaxId=10090;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Breast tumor;		
RA	Straussberg R.;		

RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: BC029188; AAH29188.1; -		
DR	InterPro: IPR003599; IG_1-like.		
DR	InterPro: IPR007110; IG_1-like.		
DR	InterPro: IPR003597; IG_C1.		
DR	InterPro: IPR003006; IG_MHC.		
DR	InterPro: IPR003596; IG_V.		
DR	Pfam: PF00047; Ig_4		
DR	SMART: SM00409; Ig_3.		
DR	SMART: SM00407; Igc1; 3.		
DR	SMART: SM00406; IGV; 1.		
DR	PROSITE: PS50835; IG_LIKE; 4.		
DR	PROSITE: PS00290; IG_MHC; 2.		
SD	SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;		
Query Match			
Best Local Similarity		63.5%; Score 331; DB 11; Length 480;	
Matches 59; Conservative 18; Mismatches 21; Indels 0; Gaps 0;			
Qy	1 QVOLLQSTAEVKKKGASMKVSCMASGYPTFSYDLSMWROAGCGGLEWVGWISATNGNTHY 60		
Db	20 QVOLLQSQSTELVKKGASVKLSCKASGYPTFSYDLSMWKQRPQGPWIGWISPGDSSEY 79		
Qy	61 AAKFGARVTMTDTSRRATAYMELSLRSDPTAVYYCAR 98		
Db	80 NEKFKGKATLTADKSSNTATYMHLSLTSENSAVYFCAR 117		
RESULT 14			
ID	Q8VJ1	PRELIMINARY;	PRT; 123 AA.
AC	Q8VJ1.		
DT	01-MAR-2002 (TREMBLrel. 20; Created)		
DT	01-MAR-2002 (TREMBLrel. 20; Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23; Last annotation update)		
DE	Anti-DNA heavy chain (Fragment).		
GN	U558.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C3H/HeJ-lpr/lpr;		
RA	MEDLINE=96409289; PubMed=8814271;		
RA	Wlodeh M.K., Alexander A.L., Pippen A.M., Piszczak D.S., Gilkeson G.S.;		
RT	"Differences in V kappa gene utilization and VH CDR3 sequence among		
RT	anti-DNA from C3H-lpr mice and lupus mice with nephritis.";		
RL	Eur. J. Immunol. 26:2225-2233(1996).		
DR	EMBL: U59154; AAB02916.1; -		
DR	InterPro: IPR007110; IG_1-like.		
DR	InterPro: IPR003006; IG_MHC.		
DR	InterPro: IPR003596; IG_V.		
DR	Pfam: PF00047; Ig_1.		
DR	SMART: SM00406; IGV; 1.		
DR	PROSITE: PS50835; IG_LIKE; 1.		
FT	NON TER		
FT	NON TER		
SD	SEQUENCE 123 AA; 13806 MW; CC0037A806E9911B CRC64;		
Query Match			
Best Local Similarity		63.3%; Score 330; DB 11; Length 123;	
Matches 59; Conservative 19; Mismatches 20; Indels 0; Gaps 0;			
Qy	1 QVOLLQSTAEVKKKGASMKVSCMASGYPTFSYDLSMWROAGCGGLEWVGWISATNGNTHY 60		
Db	1 EIQLLQSQSTELVKKGASVKLSCKASGYPTGYNNWVWQSHKSLWVGIDINPYGGTRY 60		
Qy	61 AAKFGARVTMTDTSRRATAYMELSLRSDPTAVYYCAR 98		
Db	61 SAKFKGKATLTADKSSNTATYMHLSLTSENSAVYFCAR 98		

RA Venter C.J.;
 RT "Potential virulence determinants in terminal regions of variola
 smallpox virus genome."
 RL Nature 366:748-751 (1993).
 DR EMBL; L22579; AAA60931.1; -
 SQ SEQUENCE 1897 AA; 213641 MW; 0B33A13F6753B08F CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1897;
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 6 AYEDVWSGSEYPER 18
 DB 1560 SYED1WKSDDPDX 1572

RESULT 13

O934G8 PRELIMINARY; PRT; 420 AA.
 AC O934G8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase.
 GN GNGC.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_Taxid=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC10543;
 RA Ashida H., Anderson K., Li S., Li Y.;
 RT "Cloning and expression of the gene encoding GlcNAc-alpha-1,4-Gal-
 releasing endo-beta-galactosidase from Clostridium perfringens."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB059351; BAB69460.1; -
 FT CHAIN 18 420 POTENTIAL.
 SQ SEQUENCE 420 AA; 49377 MW; F288D16FA0E5FB6D CRC64;

Query Match 38.8%; Score 52; DB 2; Length 420;
 Best Local Similarity 45.5%; Pred. No. 60;
 Matches 10; Conservative 4; Mismatches 4; Indels 4; Gaps 1;

OY 1 DGGGAYEDVWSGSEYPERYAMD 22
 DB 255 DAGSGAHNDVW----PKWAIID 272

RESULT 14

O94MR7 PRELIMINARY; PRT; 536 AA.
 AC O94MR7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE P52.
 OS Bacteriophage Mx8.
 OC Viruses.
 OX NCBI_Taxid=49964;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA "Genome organization of temperate Myxococcus phage Mx8."
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF396866; AAK94387.1; -
 SQ SEQUENCE 536 AA; 56864 MW; 08BCA8810380E0BD CRC64;

Query Match 38.8%; Score 52; DB 9; Length 536;
 Best Local Similarity 50.0%; Pred. No. 78;
 Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 GGGGAYE-----DVWSGEY 15

DB 474 GSGGTWDSGTWDVWWSGEY 493

RESULT 15

O9FGH6 PRELIMINARY; PRT; 857 AA.
 AC O9FGH6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Na/H+ antiporter-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosida II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB025632; BAB10261.1; -
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 SQ SEQUENCE 857 AA; 95833 MW; 5EA87F54AC2EBE73 CRC64;

Query Match 38.8%; Score 52; DB 10; Length 857;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DGGGAYEDVW 11
 DB 253 DGGGAYISVIW 263

Search completed: December 30, 2003, 11:01:07
 Job time : 7.6052 secs

RT "Terminal region sequence variations in variola virus DNA."
 RL Virology 221:291-300(1996).
 DR EMBL: U18341; AAA69465.1; -
 SQ SEQUENCE 1896 AA; 213552 MW; 70444A0DAE289E37 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1896;
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AYEDVWSGEYPEY 18
 Db 1559 SYEDIWKSMDPDY 1571

RESULT 10

089096 PRELIMINARY; PRT; 1896 AA.
 AC 089096;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE DiR protein (ORF1R).
 OS DiR.
 OS Variola virus, and
 OS Variola minor virus.
 OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10255, 53258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Variola virus; STRAIN=GARCIA-1966;
 RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Totmenin A.V., Shchelkunov S.N., Esposto J.J.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Variola minor virus; STRAIN=GARCIA-1966;
 RA Shchelkunov S.N., Totmenin A.V., Gutarov V.V., Safronov P.F.,
 RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Esposto J.J., Sonovtsev S.;
 RL "Analysis of the complete coding sequence of DNA of alastrim variola
 minor virus strain Garcia-1966."
 RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Variola virus; STRAIN=garcia-1966;
 RA Shchelkunov S.N., Blinov V.M., Totmenin A.V., Resenchuk S.M.,
 RA Sandakhchiev L.S.;
 RT "XhoI-I, P DNA fragments of variola minor virus strain Garcia-1966."
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U18339; AAA69405.1; -
 DR EMBL: Y16780; CAA54796.1; -
 DR EMBL: X70841; CAA50189.1; -
 SQ SEQUENCE 1896 AA; 213565 MW; 564F2B5276BF7D40 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1896;
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AYEDVWSGEYPEY 18
 Db 1559 SYEDIWKSMDPDY 1571

RESULT 11

089192 PRELIMINARY; PRT; 1896 AA.
 AC 089192;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE B26R protein.
 GN B26R.

OS Variola virus.
 OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967;
 RA Blinov V.M.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967;
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 protective mechanisms."
 RL FEBS Lett. 319:80-83(1993).

Qy 6 AYEDVWSGEYPEY 18
 Db 1559 SYEDIWKSMDPDY 1571

RESULT 12

085406 PRELIMINARY; PRT; 1897 AA.
 AC 085406;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE B22R.
 GN B22R.
 OS Variola major virus.
 OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=12870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bangladesh-1975;
 RA Masung R.F., Esposto J.J., Liu L., Qi J., Uteerback T.R.,
 RA Knight J.C., Aubin L., Yuzen T.E., Parsons J.M., Loparev V.N.,
 RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,

Qy 6 AYEDVWSGEYPEY 18
 Db 1559 SYEDIWKSMDPDY 1571

Query Match 39.6%; Score 53; DB 12; Length 1896;
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

RA McCombie W.R.:
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC078944; AAK92619.1; -
DR Gramene: Q94HL8; -
SQ SEQUENCE 221 AA; 23356 MW; 7C80178EDBA46E6 CRC64;

Query Match 39.6%; Score 53; DB 10; Length 221;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 DGGGAYEDVWSGEY 16
DB 6 DRGGALTEWMSGFCP 21

RESULT 6
089230 PRELIMINARY; PRT; 1264 AA.

AC 089230:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE (XhoI-F.O.H.P.Q genome fragment) genes.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RA Kolykhalov A.V., Blinov V.M., Gytarov V.V., Pozdnyakov S.G.,
RA Chizhikov V.E., Frolov I.V., Totmenin A.V., Shchelkunov S.N.,
RA Sandakchiev L.S.;
RT "Nucleotide sequence analysis of the region of Variola virus XhoI F O
RT H P Q genome fragment."
RT Submitted (Apr-1992) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RA Shchelkunov S.N., Marenikova S.S., Totmenin A.V., Blinov V.M.,
RA Chizhikov V.E., Gytarov V.V., Saitonov P.F., Pozdnyakov S.G.,
RA Shchukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakchiev L.S.;
RT "Constructions of clones of the genomic fragments of poxvirus and
RT study of structural and functional organization of host range viral
RT genes."
RL Dokl. Akad. Nauk SSSR 321:404-406(1991).
DR EMBL: X67117; CAA47538.1; -
SQ SEQUENCE 1264 AA; 142967 MW; DBYF0989CB794FD CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1264;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEY 18
DB 927 SYEDIMKSDMPDY 939

RESULT 7
08927 PRELIMINARY; PRT; 1869 AA.
AC 08927:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE CMP202R.
GN
OS Camelopox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=203174;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CMS;
RX PubMed=11907336;
RA Gubser C., Smith G.L.;
RT "The sequence of camelopox virus shows it is most closely related to
RT variola virus, the cause of smallpox."
RL J. Gen. Virol. 83:855-872(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CMS;
RA Gubser C., Smith G.L.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY009089; AAG37713.1; -
SQ SEQUENCE 1869 AA; 210470 MW; 06054FCCDD94722C6 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1869;
Best Local Similarity 46.2%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 6 AYEDVWSGEYPEY 18
DB 1532 SYEDIMKSDMPDY 1544

RESULT 8
08V2H2 PRELIMINARY; PRT; 1869 AA.

AC 08V2H2:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE B22R-like protein.
OS Camelopox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=203174;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-96;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA Kerebekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT "The genome of camelopox virus."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF48185; AAL73914.1; -
SQ SEQUENCE 1869 AA; 210498 MW; 64ABEF98F88237A9 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1869;
Best Local Similarity 46.2%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEY 18
DB 1532 SYEDIMKSDMPDY 1544

RESULT 9
089117 PRELIMINARY; PRT; 1896 AA.
AC 089117:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE B22R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxId=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Somalia-1977;
RX MEDLINE=96395428; PubMed=8661439;
RA Maesung R.F., Loparev V.N., Knight J.C., Totmenin A.V.,
RA Chizhikov V.E., Parsons J.M., Saitonov P.F., Gytarov V.V.,
RA Shchelkunov S.N., Espósito J.J.;

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SQ SEQUENCE 168 AA; 18515 MW; 4265E31505E0657 CR; 4;
Query Match 44.4%; Score 59.5; DB 11; Length 168;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21
DB 23 DGGGAHTWAPEDAMWGTHPKYLEM 46

RESULT 2
Q8R3W5 PRELIMINARY; PRT; 168 AA.
AC Q8R3W5;
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE Similar to RIKEN CDNA 5730449L18 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strusberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ data bases.
DR EMBL; BC024342; AAB24342.1; -
SQ SEQUENCE 168 AA; 18530 MW; 99DBE6E14C2FCFA0 CR; 4;

Query Match 44.4%; Score 59.5; DB 11; Length 168;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21
DB 23 DGGGAHTWAPEDAMWGTHPKYLEM 46

RESULT 3
Q8RW01 PRELIMINARY; PRT; 171 AA.
AC Q8RW01;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiida; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strusberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ data bases.
DR EMBL; BC022030; AAB22030.1; -
KW Hypothetical protein.
SQ SEQUENCE 171 AA; 18641 MW; E728BF39A89D1FB CF; 4;

Query Match 44.4%; Score 59.5; DB 4; Length 171;
Best Local Similarity 50.0%; Pred. No. 2.2;
Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21
DB 26 DGGGAPSWAPEDAMWGTHPKYLEM 49

RESULT 4
Q9BZ05 PRELIMINARY; PRT; 197 AA.
AC Q9BZ05;

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DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Clorf19 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21218927; PubMed=11318611;
RA Sood R., Bonner T.I., Malakowska I., Stephan D.A., Robbins C.M.,
RA Conners T.D., Korgenshieser S.D., Su K., Faruque M.U., Pinkett H.,
RA Graham C., Baxevanis A.D., Klingner K.W., Landes G.W., Trent J.M.,
RA Carpen J.D.;
RT "Cloning and characterization of 13 novel transcripts and the human
RT RGS8 gene from the 1q25 region encompassing the hereditary prostate
RT cancer (hpc1) locus."
RL Genomics 73:211-222(2001).
DR EMBL; AF288394; AAG60614.1; -
DR Genew; HGNC:16791; Clorf19.
FT NON TER
SQ SEQUENCE 197 AA; 21077 MW; 58B73731FA5E127 CRC64;

Query Match 44.4%; Score 59.5; DB 4; Length 197;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21
DB 52 DGGGAPSWAPEDAMWGTHPKYLEM 75

RESULT 5
Q94HL8 PRELIMINARY; PRT; 221 AA.
AC Q94HL8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaraloideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA Spiegel L., de la Bastide M., Nacimiento L., Kirchoff K., King L.,
RA Preston R., Vili M.D., Baker J., Bell M., Zutavern T., Santos L.,
RA Miller B., Kuit K., Rodriguez S., Cunnus D.M., Balija V., Shah R.,
RA Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;
RT "Genomic Sequence for Oryza sativa, Nipponbare strain, clone
RT OSUBa0089D15, from Chromosome 10, complete sequence."
RN Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA McCombie W.R.;
RN Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA McCombie W.R.;
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA Palmer L.E., Spiegel L., de la Bastide M., Nacimiento L., Kirchoff K.,
RA King L., Preston R., Vili M.D., Baker J., Bell M., Zutavern T.,
RA Santos L., Miller B., Kuit K., Rodriguez S., Cunnus D.M., Balija V.,
RA Shah R., Bahret A., Bal H., O'Shaughnessy A., Dedhia N.,

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search tim 5.6052 Seconds
(without alignments)
1058.876 Mill on cell updates/sec

Title: US-09-674-752-30
Perfect score: 134
Sequence: 1 DGGGAGYEDVWSGEYPERYAMDV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 30525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPRTEMBL.23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by choice to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59.5	44.4	168	11	O9CY15 mus musculus
2	59.5	44.4	168	11	O8R3W5 mus musculus
3	59.5	44.4	171	4	O8W01 homo sapien
4	59.5	44.4	197	4	O9b2q5 homo sapien
5	53	39.6	221	10	O94HL8 oryza sativ
6	53	39.6	1264	12	O89230 variola vir
7	53	39.6	1869	12	O8QPE27 variola vir
8	53	39.6	1869	12	O8V2H2 camelopox vi
9	53	39.6	1869	12	O89117 variola vir
10	53	39.6	1869	12	O89096 variola vir
11	53	39.6	1869	12	O89192 variola vir
12	53	39.6	1897	12	O85406 variola maj
13	52	38.8	420	2	O934G8 clostridium
14	52	38.8	420	2	O94MR7 bacteriophage
15	52	38.8	857	10	O9FGH6 arabidopsis
16	52	38.8	1482	16	O8ER16 oceanobacill

17	51	38.1	187	10	O8H564	O8H564 oryza sativ
18	51	38.1	554	10	O94129	O94129 oryza sativ
19	51	38.1	800	2	O52998	O52998 escherichia
20	50.5	37.7	433	13	O91859	O91859 xenopus lae
21	50	37.3	292	5	O62458	O62458 caenorhabdi
22	50	37.3	360	16	O9RDA4	O9RDA4 streptomyces
23	50	37.3	531	10	O94B16	O94B16 vitis vinif
24	50	37.3	1933	12	O72759	O72759 cowpox viru
25	49	36.6	509	16	O9A962	O9A962 caulobacter
26	49	36.6	527	10	O9FMH4	O9FMH4 arabidopsis
27	49	36.6	1340	3	O9P3C8	O9P3C8 neurospora
28	49	36.6	1879	12	O8V407	O8V407 monkeypox v
29	48.5	36.2	166	16	O97M64	O97M64 clostridium
30	48.5	36.2	262	16	O9FC56	O9FC56 streptomyces
31	48	35.8	139	17	O96XMS	O96XMS sulfolobus
32	48	35.8	461	13	O90WQ7	O90WQ7 oncorhynchus
33	48	35.8	464	13	O90WQ6	O90WQ6 oncorhynchus
34	48	35.8	840	10	O9AV49	O9AV49 oryza sativ
35	47.5	35.4	178	5	O8IH71	O8IH71 drosoophila
36	47.5	35.4	260	10	O8H6Q2	O8H6Q2 phycophthor
37	47.5	35.4	308	5	O8INH1	O8INH1 drosoophila
38	47.5	35.4	321	5	O8MSY1	O8MSY1 drosoophila
39	47.5	35.4	344	5	O9VET6	O9VET6 drosoophila
40	47.5	35.4	558	3	O43071	O43071 schizosacch
41	47	35.1	156	4	O961F7	O961F7 homo sapien
42	47	35.1	159	4	O96E20	O96E20 homo sapien
43	47	35.1	188	4	O9B4P1	O9B4P1 diadarma ba
44	47	35.1	216	15	O9YX19	O9YX19 human immun
45	47	35.1	316	2	O9K1X4	O9K1X4 bradyrhizob

ALIGNMENTS

RESULT 1

ID O9CY15 PRELIMINARY; PRT; 168 AA.

AC O9CY15; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE 57304491LBR1k protein.

GN 57304491LBR1k.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Fiedelmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Mashio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Guernincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Mombarts P.,

RA Nordene P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzukit H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,

RA Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK017650; BMB30855.1; -;

DR MGD; MGI:1913887; 57304491LBR1k.

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CC -----
DR EMBL; AL627275; CAD02714.1; -.
DR EMBL; AE016835; AA068065.1; -.
DR HAMAP; MF_00378; -; 1.
DR InterPro; IPR003753; Exonuc_VII_L.
DR InterPro; IPR004365; tRNA_anti.
DR Pfam; PF02601; Exonuc_VII_L; 1.
DR TIGRFAMs; TIGR00237; xseA; 1.
DR HydroLase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 449 AA; 50720 MW; 511957DEC878F5D2 CRC64;

Query Match 33.6%; Score 45; DB 1; Length 449;
Best Local Similarity 70.0%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGAYEDVWS 12
Db 206 GCGSLDPLWS 215
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Search completed: December 30, 2003, 10:55:52
Job time : 2.2314 secs

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CC or send an email to license@sib.ch).
CC -----
DR EMBL; AF198100; AAF44578.1; -.
DR EMBL; D00295; BAA00209.1; ALT_FRAME.
DR EMBL; D00295; BAA00207.1; ALT_FRAME.
DR HSSP; P25963; INRI.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 7.
DR SMART; SM00248; ank; 6.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS50297; ANK_RBP_REGION; 1.
KW Hypothetical protein; Repeat; ANK repeat.
FT REPEAT 6 35 ANK 1.
FT REPEAT 39 68 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 103 132 ANK 4.
FT REPEAT 137 169 ANK 5.
FT REPEAT 174 202 ANK 6.
FT REPEAT 206 238 ANK 7.
FT REPEAT 242 271 ANK 8.
SQ SEQUENCE 428 AA; 49194 MW; C71BEAF74687EE8F CRC64;

Query Match 33.6%; Score 45; DB 1; Length 428;
Best Local Similarity 56.2%; Pred. No. 74;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 8 EDVMSGEYPEYAMDV 23
Db 133 EDGANGKPIHYAMKV 148

RESULT 14
EX7L_RICCN STANDARD; PRT; 444 AA.
AC 092GUF6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
GN (Exonuclease VII large subunit).
OS XSEA OR RCI026.
OC Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audifren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RT Science 293:2093-2098(2001).
CC -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large
CC acid-insoluble oligonucleotides, which are then degraded further
CC into small acid-soluble oligonucleotides (By similarity).
CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -1- SUBUNIT: Heterooligomer composed of large and small subunits (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE XSEA FAMILY.
CC -----
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CC -----
CC EMBL; AE008654; AAL03564.1; ALT_INIT.

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DR HAMAP; MF_00378; -. 1.
DR InterPro; IPR003753; Exonuc_VII_L.
DR InterPro; IPR004365; rRNA_ant1.
DR Pfam; PF02601; Exonuc_VII_L; 1.
DR Pfam; PF01336; tRNA_ant1; 1.
DR TIGRPFAM; TIGR00237; xsea; 1.
KW Hydroxylase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 444 AA; 49886 MW; CAB0B6B843f4768 CRC64;

Query Match 33.6%; Score 45; DB 1; Length 444;
Best Local Similarity 70.0%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GCGAYEDVMS 12
Db 211 GCGSIDLMS 220

RESULT 15
EX7L_SALTI STANDARD; PRT; 449 AA.
AC 0824Q1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE (Exonuclease VII large subunit).
GN XSEA OR STY2753 OR T0345.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Baeham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jegerle K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RT Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=2253167; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodymani V., Schwartz D.C., Blatner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RT J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large
CC acid-insoluble oligonucleotides, which are then degraded further
CC into small acid-soluble oligonucleotides (By similarity).
CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -1- SUBUNIT: Heterooligomer composed of large and small subunits (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE XSEA FAMILY.
CC -----
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CC SEVERAL TRANSCRIPTION FACTORS.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity) .
CC -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=Long;
CC      IsoId=O61985-1; Sequence=Displayed;
CC      Name=Short;
CC      IsoId=O61985-2; Sequence=VSP_000580, VSP_000581;
CC      Note=No experimental confirmation available;
CC      -1- TISSUE SPECIFICITY: Widely expressed.
CC      -1- PM: COULD BE DEPENDENT ON CKII PHOSPHORYLATION FOR BINDING.
CC      -1- SIMILARITY: Belongs to the bzfp family. CNC subfamily.
-----
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-----
DR EMBL; X78709; CAA55362.1; -.
DR EMBL; AF015881; AAC40108.1; -.
DR PIR; I48694; I48694.
DR HSSP; P34707; ISKN.
DR MGD; MGI:99421; Nfe2l1.
DR InterPro; IPRO04827; TF_bZIP.
DR SMART; SMO0338; BRLZ; 1.
DR PROSITE; PS50217; BZIP; 1.
DR PROSITE; PS00036; BZIP_BASIC; 1.
DR KW DNA-binding; Nuclear protein; Phosphorylation; Alternative splicing.
FT DOMAIN 125 259
FT FT ASP/GLU-RICH (ACIDIC).
FT FT POLY-SER.
FT FT ASP/GLU-RICH (ACIDIC).
FT FT BASIC MOTIF (BY SIMILARITY).
FT FT LEUCINE-ZIPPER (BY SIMILARITY).
FT FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT FT MISSING (in isoform short).
FT FT /Ftld=VSP_000580.
FT FT Missing (in isoform short).
FT FT /Ftld=VSP_000581.
FT FT VARSPLIC 447 583
FT FT CONFLICT 318 318 S->T (IN REF. 2).
FT FT CONFLICT 387 387 P->L (IN REF. 2).
SQ SEQUENCE 741 AA; 81545 MW; C01E89DD26E7CDFE CRC64;
Query Match 34.3%; Score 46; DB 1; Length 741;
Best Local Similarity 50.0%; Pred. NO. 96;
Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 4 GGAGEDVWSGEPYPYAMDV 23
Db 210 GRERDTWSGEGALARDL 229
| | | | | :
| | | | | :
RESULT 12
CIBA_PAEPP STANDARD; PRT; 675 AA.
ID CIBA_PAEPP
AC P57091;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Parasporal crystal protein cry18Ba (Parasporal delta-endotoxin
DE CryXIIB(a)) (Crystalline parasporal protoxin) (76 kDa crystal
DE protein).
DN CRYI8BA OR CRYXVIIIB(A).
OS Paenibacillus popilliae (Bacillus popilliae).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
RN NCBI_Taxid=78057;
RP SEQUENCE FROM N.A. [1]
RA STRAIN=B93;
RA Patel R., Yousten A.A., Ripperre K.;
RA "Detection of two new cry genes in Paenibacillus popilliae.";
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RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCABAB
CC LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORIULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT (BY SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; AF169250; AAF69667.1; -
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
KW Toxin; Sporulation.
FT DOMAIN 101 104 POLY-LEU.
FT DOMAIN 199 204 POLY-LEU.
SQ SEQUENCE 675 AA; 75848 MW; 823B588B4AB81D75 CRC64;
QY Query Match 34.0%; Score 45.5; DB 1; Length 675;
Db Best Local Similarity 36.4%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
QY 2 GGGGAYEDVWSGGEYPERYAMDV 23
Db 455 GLGTGYASAWT-SYDPDYITNI 475
-----
RESULT 13
V234_FOWPV STANDARD; PRT; 428 AA.
ID _V234_FOWPV
AC P14368; P14367; Q9501;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative ankryrin-repeat protein FFW234 (BamHI-ORF12/ORF13).
GN FFW234.
OS Fowlpox virus (PPV).
OC Viruses; dsDNA viruses, no RNA stage; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
OX [1]
SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Alfonsio C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of Fowlpox virus."
RL J. Virol. 74:3815-3831(2000).
[2]
SEQUENCE OF 65-428 FROM N.A.
RP STRAIN=FP-9 / Isolate HP-438;
RX MEDLINE=88223622; PubMed=2835548;
RA Tomley F., Blinn M., Campbell J., Bourneill M.E.G.;
RT "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
RT of fowlpox virus."
RL J. Gen. Virol. 69:1025-1040(1988).
CC -1- SIMILARITY: Contains 8 ANK repeats.
CC -1- CAUTION: Ref.29 sequence differs from that shown due to frameshifts
CC in position 204, 219 and 237.
CC -----
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RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58";
RT Science 294:2317-2323(2001).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Gurolo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Hounmel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Seear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58";
RT Science 294:2323-2328(2001).
-----
CC -1- FUNCTION: Catalyzes the ferrous insertion into protoporphyrin IX.
CC -1- CATALYTIC ACTIVITY: Protoporphyrin + Fe(2+) = protoheme + 2 H(+).
CC -1- PATHWAY: Protoheme biosynthesis; last step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the ferrochelatase family.
-----
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CC EMBL; AE009308; AAL44581.1;
CC EMBL; AE008306; AAK89636.1; ALT_INIT.
CC PIR; AG3020; AG3020.
DR HAMAP; MF_00323; -; 1.
DR InterPro; IPR001015; Ferrochelatase.
DR Pfam; PF00762; Ferrochelatase; 1.
DR Prodom; PD002792; Ferrochelatase; 1.
DR TIGRFAMs; TIGR00109; hemH; 1.
DR PROSITE; PS00534; FERROCHELATASE; 1.
KW Porphyrin biosynthesis; Heme biosynthesis; Lyase; Iron;
KW Complete proteome.
FT METAL 214 IRON (BY SIMILARITY).
FT METAL 295 IRON (BY SIMILARITY).
SQ SEQUENCE 344 AA; 39472 MW; 33890E7A3BA0F32 CRC64;
Query Match 34.3%; Score 46; DB 1; Length 344;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 4 GGAYEDVWSGEYPEY 19
DB 76 GKAYEIMWHERNEST 91
RESULT 10
YK09_CABEL STANDARD; PRT; 643 AA.
AC PJ4304;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C06E1.9 in chromosome III.
GN C06E1.9
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

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RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnson L., Jones M., Kershaw J., Kiresten B., O'Callaghan M.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sime W., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sprat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RT Nature 368:32-38(1994).
RL Nature 368:32-38(1994).
RN [2]
RN REVISIONS.
RA Waterston R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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-----
CC EMBL; L16559; AAA27929.2;
CC WormPep; C06E1.9; CE24790.
DR WormPep; C06E1.9; CE24790.
KW Hypothetical protein.
SQ SEQUENCE 643 AA; 72354 MW; CF83BECFC880A10A CRC64;
Query Match 34.3%; Score 46; DB 1; Length 643;
Best Local Similarity 46.7%; Pred. No. 83;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DGGGAYEDVWSGEY 15
DB 537 DGGNGVDYDEYDER 551
RESULT 11
NFL1_MOUSE STANDARD; PRT; 741 AA.
AC Q61985; O70234;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nuclear factor erythroid 2 related factor 1 (NFE2 related factor 1)
DE (NFE2-related factor 1) (Nuclear factor, erythroid derived 2, like 1).
GN NFE2L1 OR NFE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=95278942; PubMed=7759107;
RA Prieaschi E.E., Novotny V., Geonga R., Jaksche D., Elbe-Bueger A.,
RA Thum W., Auer M., Stingl G., Baumruker T.;
RT "A novel splice variant of the transcription factor Nfe1 interacts
RT with the typhalpa promoter and stimulates transcription.";
RL Nucleic Acids Res. 26:2291-2297(1998).
CC -1- FUNCTION: THE SHORT ISOFORM INTERACTS WITH THE EXTENDED KAPPA 3
CC SITE OF THE TNF ALPHA PROMOTER AFTER FC GAMMA RI1 STIMULATION AND
CC PARTICIPATES IN THE INDUCTION OF THIS CYTOKINE. THE LONG ISOFORM
CC IS EITHER INACTIVE OR REPRESSSES THE TRANSCRIPTIONAL ACTIVATION.
CC -1- SUBUNIT: HETERODIMER (PROBABLE). IT MAY FORM A HETERODIMER WITH

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ID AMYG CANAL STANDARD; PRT; 946 AA.
AC 074254;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucosylase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
DE (1,4-alpha-D-glucan glucohydrolase).
GN GAM1 OR GCA1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC5314;
RX MEDLINE=99451422; PubMed=10520161;
RA Sturtevant J., Dixon F., Madsworth E., Laige J.-P., Zhao X.-J.,
RA Calderone R.;
RT "Identification and cloning of GCA1, a gene that encodes a cell
RT surface glucosylase from Candida albicans.";
RL Med. Mycol. 37:357-366(1999).
CC -1 CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
CC glucose residues successively from non-reducing ends of the chains
CC with release of beta-D-glucose.
CC -1 SUBCELLULAR LOCATION: CELL WALL ASSOCIATED.
CC -1 SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL: AF082188; AAC1968.1; -
DR InterPro: IPR00322; Glyco_hydro_31.
DR Pfam: PF01055; Glyco_hydro_31; 1.
DR PROSITE: PS00129; GLYCOSYL_HYDROL_F31_1; 1.
DR PROSITE: PS00707; GLYCOSYL_HYDROL_F31_2; 1.
KM Hydrolyase; Glycosidase; Polysaccharide degradation; Glycoprotein;
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 946 GLUCOSYLASE 1.
FT ACT SITE 462 462 BY SIMILARITY.
FT DOMAIN 519 532 SER/THR-RICH.
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 505 505 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 801 801 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 895 895 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 912 912 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 946 AA; 105804 MW; BD6B640C4EEF1F70 CRC64;

Query Match 34.7%; Score 46.5; DB 1; Length 946;
Best Local Similarity 45.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 3 GGGAYEDVWSGE-YPEYAM 21
Db 617 GSGKYMGMGSDNADYNNM 636

RESULT 8

VG38_BPARI
ID VG38_BPARI STANDARD; PRT; 259 AA.
AC Q9G0B4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Receptor recognizing protein (Protein Gp38).
GN 38.
OS Bacteriophage ARI.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=66711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485545; PubMed=11029414;
RA Yu S.L., Ko K.L., Chen C.S., Chang Y.C., Syu W.J.;
RT "Characterization of the distal tail fiber locus and determination of
RT the receptor for phage ARI, which specifically infects Escherichia
RT coli O157:H7.";
RL J. Bacteriol. 182:5962-5968(2000).
CC -1 FUNCTION: VG38 IS AT THE TIP OF THE LONG TAIL FIBERS AND SERVES
CC AS THE PHAGE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.
CC -1 MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEIN OMPA AS A
CC RECEPTOR.
CC -----
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CC -----
DR EMBL: AF208841; AAC29755.1; -
DR Pfam: PF05268; GP38; 1.
KM Fiber protein; Phage recognition.
SQ SEQUENCE 259 AA; 26277 MW; 042225B00128A5B8 CRC64;

Query Match 34.3%; Score 46; DB 1; Length 259;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GGGAYEDV--WSGEY 15
Db 154 GGGGYSGQANWAGKY 169

RESULT 9
HEMZ_AGR75 STANDARD; PRT; 344 AA.
ID HEMZ_AGR75
AC Q8U9F7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ferrochelatase (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme
DE synthetase).
GN HEHMZ OR ATU3771 OR AGR_L 2129.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kirajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D., Str.,
RA Chapman P., Clendinning J., Deachere G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Best Local Similarity 29.4%; Pred. No. 87;
Matches 10; Conservative 5; Mismatches 4; Indels 15; Gaps 2;

OY 2 GCGGAYEDVWSGE-----YPEYAMD 22
Db 212 GCGGAYEDVWSGE-----YPEYAMD 243

RESULT 5
FAED_ECOLI STANDARD; PRT; 812 AA.
ID FAED_ECOLI P06970;
AC P06970;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane usher protein faed precursor.
GN FAED.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=86176742; PubMed=2870470;
RA Mooi F.R., Claassen I., Bakker D., Kuipers H., de Graaf F.K.;
RT "Regulation and structure of an Escherichia coli gene coding for an
RT outer membrane protein involved in export of K88ab fimbriae
RT subunita.";
RL Nucleic Acids Res. 14:2443-2457(1986).
[2]
REVISIONS.
RA Oudega B.;
RN Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RX MEDLINE=96020654; PubMed=8577257;
RA Valent O.A., Zaai J., de Graaf F.K., Oudega B.;
RT "Subcellular localization and topology of the K88 usher faed in
RT Escherichia coli.";
RL Mol. Microbiol. 16:1243-1257(1995).
[4]
SEQUENCE OF 794-812 FROM N.A.
RX MEDLINE=91312125; PubMed=1713284;
RA Bakker D., Vader C.E.M., Roosaendaal B., Mooi F.R., Oudega B.,
RA de Graaf F.K.;
RT "Structure and function of periplasmic chaperone-like proteins
RT involved in the biosynthesis of K88 and K99 fimbriae in
RT enterotoxigenic Escherichia coli.";
RL Mol. Microbiol. 5:875-886(1991).
[1]
FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF K88AB FIMBRIAL
SUBUNITS ACROSS THE OUTER MEMBRANE.
[2]
SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
(By similarity).
[3]
SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
[4]
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CC EMBL; X03675; CAA27310.1; -;
CC EMBL; X56002; CAA39476.1; -;
CC EMBL; X56003; CAA39477.1; -;
CC PIR; S24931; MMECOF.
CC InterPro; IPR000015; Fimb_usher.
CC Pfam; PF00577; Usher, 1.
CC PROSITE; PS01151; FIMBRIAL_USHER, 1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.
FT SIGNAL 1 35

FT CHAIN 36 812 OUTER MEMBRANE USHER PROTEIN FAED.
FT DISULFID 793 811 POTENTIAL.
SQ SEQUENCE 812 AA; 85496 MW; C6DAACA4AD8BDAPC CRC64;

Query Match 35.1%; Score 47; DB 1; Length 812;
Best Local Similarity 42.3%; Pred. No. 78;
Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 2;

OY 2 GCGGAYEDVW---SGEY-PEYAMDV 23
Db 46 GCGGAYEDVW---SGEY-PEYAMDV 71

RESULT 6
YGB4_METTH STANDARD; PRT; 431 AA.
ID YGB4_METTH
AC O27119;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MTH1684.
GN MTH1684.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Viare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Carno A., Bush D., Sater H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
[1]
SIMILARITY: STRONG, TO M.JUNNASCHEI MJ1681.

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CC EMBL; AE000926; AAB86156.1; -;
CC PIR; B69092; B69092.
CC HSSP; P00198; 2FDN.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC InterPro; IPR002708; DUF39.
CC Pfam; PF01837; DUF39, 1.
CC Pfam; PF00037; fer4, 2.
CC ProDom; PD011569; DUF39, 1.
CC PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 431 AA; 46950 MW; 802FA3957194B85 CRC64;

Query Match 34.7%; Score 46.5; DB 1; Length 431;
Best Local Similarity 56.2%; Pred. No. 47;

Matches 9; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

OY 7 YEDVWSGE-----YPE 17
Db 328 YEDVWSGDVRPVHPE 343

RESULT 7
AMYG_CANAL

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CC -----
DR EMBL; S61875; AAB26988.1; -.
DR EMBL; S62100; AAB26989.1; -.
DR EMBL; S61875; AAB26989.1; JOINED.
DR EMBL; S62537; CAA44503.1; -.
DR EMBL; X62638; CAA44504.1; -.
DR PIR; A47369; A47369.
DR PIR; B41732; B41732.
DR PIR; B47369; B47369.
DR HSSP; P09651; 1HA1.
DR FlyBase; FBgn003498; sqd.
DR GO; GO:005717; C:chromatin; IDA.
DR GO; GO:0016607; C:nuclear speck; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS00102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW RNA-binding; Nuclear protein; Ribonucleoprotein; Alternative splicing;
FT DOMAIN 56 138 RNA-BINDING (RRM) 1.
FT DOMAIN 136 213 RNA-BINDING (RRM) 2.
FT DOMAIN 221 337 GLY-RICH.
FT VARSPLIC 286 345
FT FT
FT FT
FT VARSPLIC 286 322
FT FT
FT CONFLICT 169 169
FT FT SEQUENCE 345 AA; 36207 MM; 47.5% ID; 17 Gaps; 1;
SQ SEQUENCE 345 AA; 36207 MM; 47.5% ID; 17 Gaps; 1;
Query Match 35.4%; Score 47.5; DB 1; Length 345;
Best Local Similarity 27.8%; Pred. No. 27;
Matches 10; Conservative 3; Mismatches 6; Indels 17; Gaps 1;
OY 2 GGGGAYEDVMSGE-----YPEYYA 20
DB 239 GGGGYNQMDQGSYGSGYGSGYGAGGYGYA 274
RESULT 4
ITAS_XENLA
ID _ITAS_XENLA STANDARD; PRT; 1050 AA.
AC 006274;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin alpha-5 precursor (Fibronectin receptor alpha subunit)
DE (Integrin alpha-5) (VLA-5).
DS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
CX NCBI_Taxid=8355;
CX (1)
RX SEQUENCE FROM N.A.
RX MEDLINE=95344994; PubMed=7619730;
RA Joos T.O., Whitaker C.A., Meng F., Deslome D.W., Gnan V.,
RA Hansen P.;
RT "Integrin alpha 5 during early development of Xenopus laevis.";
RL Mech. Dev. 50:187-199(1995).
RX SEQUENCE OF 318-393 FROM N.A.
RX MEDLINE=94008528; PubMed=8404528;
RA Whitaker C.A., Deslome D.W.;
RT "Integrin alpha subunit mRNAs are differentially expressed in early
RT Xenopus embryos.";
CC -1- FUNCTION: INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN.

```

CC		IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
CC	-I-	SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
CC		SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
CC		DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
CC	-I-	SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I-	SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC	-I-	SIMILARITY: Contains 7 FG-GAP repeats.
CC		-----
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CC		-----
DR	EMBL; U12683;	AAA9668.1; -.
DR	EMBL; L10191;	AAA16249.1; -.
DR	PIR; I51527;	I51527.
DR	HSSP; P06756;	IUV2.
DR	InterPro; IPRO00413;	Integrin_alpha.
DR	Pfam; PF01839;	FG-GAP; 4.
DR	Pfam; PF00357;	Integrin_A; 1.
DR	PRINTS; PR01185;	INTEGRINA.
DR	SMART; SMO0191;	Int_alpha; 5.
DR	PROSITE; PS00242;	INTEGRIN_ALPHA; 1.
KW	Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;	
KW	Signal; Repeat.	
FT	SIGNAL	1..32
FT	CHAIN	33..1050
FT	CHAIN	33..932
FT	CHAIN	933..1050
FT	DOMAIN	33..996
FT	TRANSMEM	997..1022
FT	DOMAIN	1023..1050
FT	REPEAT	48..110
FT	REPEAT	120..188
FT	REPEAT	189..246
FT	REPEAT	259..312
FT	REPEAT	313..373
FT	REPEAT	379..438
FT	REPEAT	442..494
FT	CA_BIND	324..332
FT	CA_BIND	390..398
FT	CA_BIND	454..462
FT	SITE	1025..1029
FT	DISULFID	90..99
FT	DISULFID	145..166
FT	DISULFID	182..195
FT	DISULFID	502..513
FT	DISULFID	519..575
FT	DISULFID	636..642
FT	DISULFID	708..721
FT	DISULFID	862..910
FT	DISULFID	917..922
FT	CARBOHYD	75..75
FT	CARBOHYD	95..95
FT	CARBOHYD	98..98
FT	CARBOHYD	172..172
FT	CARBOHYD	287..287
FT	CARBOHYD	297..297
FT	CARBOHYD	306..306
FT	CARBOHYD	507..507
FT	CARBOHYD	515..515
FT	CARBOHYD	521..521
FT	CARBOHYD	600..600
FT	CARBOHYD	649..649
FT	CARBOHYD	714..714
FT	CARBOHYD	763..763
FT	CARBOHYD	861..861
SEQ	SEQUENCE	1050 AA; 115961 MW; 10ED96153B8D918 CRC64;

35.4%; Score 47.5; DB 1; Length 1050;

Matches 11; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

QY 3 GCGAYEDVMSGEY-----PEYAM 21
 Db 42 GCGSVRDVLGHYPPLGKPKHPEYFLM 67

RESULT 2
 SYCL_MYCTU STANDARD; PRT; 469 AA.

AC P96862;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cysteine--tRNA synthetase 1 (EC 6.1.1.16) (Cysteine--tRNA ligase 1)
 DE (CYRSB 1).
 GN CYSS1 OR CYSS OR RV3580C OR MT3686 OR MTCY06G11.27C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_Taxid=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gao S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Deavin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagals K., Krogh J., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickley B.,
 RA Kojanay J.F., Nelson W.C., Umayam L.A., Ernolova M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
 CC diphosphate + L-cysteineyl-tRNA(Cys).
 CC -1- SUBUNIT: Monomer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC Strong, to methionyl-tRNA synthetase.
 CC
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 CC -----
 DR EMBL, Z92774; CAB07154.1; -;
 DR EMBL, AE007169; AAK48044.1; -;
 DR PIR, B70607; B70607.
 DR TIGR, MT3686; -;
 DR TubercuList; RV3580c; -;
 DR HAMAP, MF_00041; -; 1.
 DR InterPro, IPR002308; Cys_tRNA-synt_1a.
 DR InterPro, IPR001412; tRNA-synt_1.
 DR Pfam, PF01406; tRNA-synt_1e; 1.
 DR PRINTS, PR00983; TRNASYNTHCS.
 DR TIGRFAMs, TIGR00435; cys5; 1.

DR PROSITE, PS00178; AA tRNA_LIGASE_I, FALSE NEG.
 KM Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KM Complete proteome.
 FT SITE 35 45 "HIGH" REGION.
 FT SITE 267 271 "KMSKS" REGION.
 FT BINDING 270 270 ATP (BY SIMILARITY).
 FT CONFLICT 457 457 D -> E (IN REF. 2).
 SQ SEQUENCE 469 AA; 51854 MW; 515F9D19482ADC0E CRC64;

Query Match 35.8%; Score 48; DB 1; Length 469;
 Best Local Similarity 64.7%; Pred. No. 32;
 Matches 11; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 2 GCGAYEDVMSGEYPEY 18
 Db 142 GCGDVYFDVLS--YPEY 156

RESULT 3
 SOD_DROME STANDARD; PRT; 345 AA.

AC Q08473;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE RNA-binding protein squid (Heterogeneous nuclear ribonucleoprotein 40)
 DE (HNRNP 40).
 GN SOD OR HRP40.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=93279471; PubMed=7684991;
 RA Kelley R.L.;
 RT "Initial organization of the Drosophila dorsoventral axis depends on
 RT an RNA-binding protein encoded by the squid gene."
 RL Genes Dev. 7:948-960(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=92112968; PubMed=1730754;
 RA Matunis E.L., Matunis M.J., Dreyfuss G.;
 RT "Characterization of the major hnRNP proteins from Drosophila
 RT melanogaster."
 RL J. Cell Biol. 116:257-269(1992).
 CC -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE
 CC NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING
 CC MORPHOGEN (DM) ORIGINATING IN THE GERMAL VESICLE. AT LEAST ONE
 CC OF THE ISOFORMS IS ESSENTIAL IN SOMATIC TISSUES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. IT IS POSSIBLE THAT
 CC SOME ISOFORMS ARE FOUND ONLY IN ONE OF THESE LOCATIONS.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=3;
 CC Comment-Additional isoforms seem to exist;
 CC Name=sqds; Synonyms=HRP40.2;
 CC IsoId=Q08473-1; Sequence=Displayed;
 CC Name=sqda; Synonyms=HRP40.1;
 CC IsoId=Q08473-2; Sequence=VSP_005876;
 CC Name=sqdb;
 CC IsoId=Q08473-3; Sequence=VSP_005877;
 CC -1- DISEASE: FEMALES WITH MUTATIONS IN SOD ARE STERILE AND LAY EGGS
 CC THAT DISPLAY ONLY DORSAL STRUCTURES.
 CC -1- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
 CC
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 1.23314 Seconds
(without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-30

Perfect score: 134
Sequence: 1 DGGGAYEDVMSGEYPEYAMDV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49.5	36.9	220	Y1CG_HAEIN	P45122 haemophilus
2	48	35.8	469	SYCL_MYCTU	P96862 mycobacteri
3	47.5	35.4	345	SOD_DROME	Q08473 drosophila
4	47.5	35.1	1050	ITAS_XENLA	Q06274 xenopus lae
5	47	35.1	812	PABD_ECOLI	P06370 escherichia
6	46.5	34.7	431	YG84_METTH	Q27719 methanobact
7	46.5	34.7	946	AMYG_CANAL	Q74254 candida alb
8	46	34.3	259	VG38_BRAP1	Q99484 bacterioph
9	46	34.3	344	HEMZ_MARTS	Q809T7 bacterioph
10	46	34.3	643	YKQ9_CAEL	P34304 caenorhabdi
11	46	34.0	741	NFL1_MOUSE	P61985 mus musculu
12	45.5	34.0	675	CIBA_PAEPP	P57091 paenibacill
13	45	33.6	428	V234_ROMPV	P14368 fowlpox vir
14	45	33.6	444	EX7L_RICCN	Q92966 rickettsia
15	45	33.6	449	EX7L_SALTI	Q824q1 salmoneila
16	45	33.6	449	EX7L_SALTY	Q82588 salmoneila
17	45	33.6	453	EX7L_RICPR	Q82588 salmoneila
18	45	33.6	456	EX7L_ECOS7	Q82588 salmoneila
19	45	33.6	456	EX7L_ECOS1	Q82588 salmoneila
20	45	33.6	458	EX7L_ECOS6	Q82588 salmoneila
21	45	33.6	459	EX7L_YERPE	Q82588 salmoneila
22	45	33.6	463	ANX7_MOUSE	Q82588 salmoneila
23	45	33.6	532	EX7L_AGRIS	Q82588 salmoneila
24	45	33.6	542	EX7L_AGRIS	Q82588 salmoneila
25	45	33.6	1131	APCE_ANASP	Q82588 salmoneila
26	44.5	33.2	115	YAT7_RHOBL	P05450 rhodospheudo
27	44	32.8	79	RLJ1_ANASP	Q82588 salmoneila
28	44	32.8	159	CUP9_DROME	Q82588 salmoneila
29	44	32.8	207	ECG2_SCHUA	P27781 drosophila
30	44	32.8	210	Y593_CAMUE	Q91969 schistosoma
31	44	32.8	212	EGG1_SCHUA	Q91969 schistosoma
32	44	32.8	284	HSR4_ARATH	Q96120 arabidopsis
33	44	32.8	325	Y893_MYCTU	Q10552 mycobacteri

34	44	32.8	352	1	PRK1_SCHPO	O13958 schizosacch
35	44	32.8	466	1	ANX7_HUMAN	P20073 homo sapien
36	44	32.8	704	1	GLGB_YEAST	P32775 saccharomyc
37	44	32.8	729	1	PABD_ECOS7	Q82588 salmoneila
38	44	32.8	729	1	PABD_ECOS1	Q82588 salmoneila
39	44	32.8	729	1	PABD_SALTI	Q82588 salmoneila
40	44	32.8	729	1	PABD_SALTY	Q82588 salmoneila
41	44	32.8	774	1	SCA_DROME	P21520 drosophila
42	44	32.8	1173	1	DPOL_RCWMV	Q85428 rat cytoleg
43	43.5	32.5	102	1	SGP3_CHRYI	O52055 chromatiu
44	43.5	32.5	378	1	Y952_ARCFU	O293170 archaeoglob
45	43.5	32.5	451	1	EX7L_NEIMA	O93178 neisseria m

ALIGNMENTS

RESULT 1	
Y1CG_HAEIN	STANDARD; PRT; 220 AA.
ID Y1CG_HAEIN	P45122;
AC	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Hypothetical protein H11240.
GN	H11240.
OC	Haemophilus influenzae.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC	Pasteurellaceae; Haemophilus.
OX	NCBI_TaxId=727;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=RD / KW20 / ATCC 51907;
RX	MEDLINE=95350630; PubMed=7542800;
RA	Pfeischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA	McKenny K., Sutton G., Fitzhugh W., Fields C.A., Kelley J.M.,
RA	Scott J.D., Shiley R., Liu L.-I., Glodex A., Kelley J.M.,
RA	Weldman J.F., Phillips C.A., Spirigs T., Hedblom E., Cotton M.D.,
RA	Ueterbach T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA	Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA	Venter J.C.;
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae
RT	strain RD.";
RL	Science 269:496-512(1995).
CC	- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC	- SIMILARITY: BELONGS TO THE UPF0126 FAMILY. STRONG. TO E.COLI Y1CG.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
DR	EMBL: U32804; AAC22893.1; -
DR	PIR: B64169; E64169.
DR	TIGR: H11240; -
DR	InterPro: IPR005115; UPF0126.
DR	Pfam: PF03458; UPF0126; 2.
KW	Hypothetical protein; Transmembrane; Complete proteome.
FT	TRANSMEM 26 46
FT	TRANSMEM 65 85
FT	TRANSMEM 92 112
FT	TRANSMEM 116 136
FT	TRANSMEM 152 172
FT	TRANSMEM 175 195
SO	SEQUENCE 220 AA; 24228 MW; 58506FAFLCS570BF CRC64;
Query Match	36.9%; Score 49.5; DB 1; Length 220;
Best Local Similarity	42.3%; Pred. No. 9.1;

Best Local Similarity 69.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAYEDVWSGE 14
Db 124 GGGGAYEDVWFRE 136

RESULT 8
E64169
conserved hypothetical protein H11240 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999

C/Accession: E64169
R:Platichmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirnesh, E.F.; Kervilave, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: E64169
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-220 <TIGR>
A:Cross-references: GB:U32804; GB:L42023; NID:g1574170; PIDN:AC22893.1; PID:g1574172; C:Superfamily: hypothetical protein b1832

Query Match 36.9%; Score 49.5; DB 2; Length 220;
Best Local Similarity 42.3%; Pred. No. 16;
Matches 11; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

Qy 3 GGGAYEDVWSGEY-----PEYYAM 21
Db 42 GGGSVRVLLGHVPLGKVKRPEYFLM 67

RESULT 9
H87389

conserved hypothetical protein CC1132 (imported) - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C/Accession: H87389
R:Merlan, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frazer, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87389
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-509 <STO>
A:Cross-references: GB:AE005673; NID:g13422446; PIDN:AAK23116.1; GSPDB:GN00148

C:Genetic: A:Gene: CC1132

Query Match 36.6%; Score 49; DB 2; Length 509;
Best Local Similarity 52.6%; Pred. No. 47;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 DGGGAYEDVWSGEYPEY 19
Db 321 DGG----EDFWPGRYSKTY 335

RESULT 10
H96940

hypothetical protein CAC0334 (imported) - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: H96940
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; Lee,

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C

A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H96940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78315.1; PID:g15023180; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetic: A:Gene: CAC0334

Query Match 36.2%; Score 48.5; DB 2; Length 166;
Best Local Similarity 41.7%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

Qy 5 GAYEDVWSGEYPE-----YAMDV 23
Db 141 GGFPCGMDPEYPRGIVAYPKSV 164

RESULT 11
B70607

probable cysB protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C/Accession: B70607
R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltri, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Ralandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Sgarer, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:9825987; PMID:9634230

A:Accession: B70607
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-469 <COL>

A:Cross-references: GB:292774; GB:AL123456; NID:g3261729; PIDN:CA807154.1; PID:g1877311
A:Experimental source: strain H37Rv
C:Genetic: A:Gene: cysB

C:Superfamily: cysteine-tRNA ligase

Query Match 35.8%; Score 48; DB 2; Length 469;
Best Local Similarity 64.7%; Pred. No. 59;
Matches 11; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GGGAYEDVWSGEYPEY 18
Db 142 GGGDYVFDVLS--YPEY 156

RESULT 12
B47369

RNA-binding protein (alternatively spliced) SqdB - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999

C/Accession: B47369
R:Kelley, R.L. Genes Dev. 7, 948-960, 1993
A:Title: Initial organization of the Drosophila dorsoventral axis depends on an RNA-bind
A:Reference number: A47369; MUID:93279471; PMID:7684991
A:Accession: B47369

A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-308 <XEL>

A:Cross-references: GB:S62100; NID:g185453; PIDN:AA26989.1; PID:g185455
A:Note: sequence extracted from NCBI backbone (NCBIN:132997, NCBIN:132999, NCBI:133001)
C:Genetic: A:Gene: FlyBase:sgd
A:Cross-references: FlyBase:FBgn0003498

C/Superfamily: immunoglobulin V region; immunoglobulin homology C; **Keywords:** heterotetramer; immunoglobulin

A; Cross-references: EMBL:Z188034; NID:g33116; PIDN:CAA19286..1; PUD:g935896
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

A; Cross-references: EMBL:Z188034; NID:g33116; PIDN:CAA19286..1; PUD:g935896
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNONOT01
CLONE: 3551457
US-09-049-672A-13

Query Match 65.5%; Score 431; DB 3; Length 236;
Best Local Similarity 66.4%; Pred. No. 1.1e-39;
Matches 81; Conservative 13; Mismatches 22; Indels 6; Gaps 1;

QY 1 OVQLQSGADYKPKGASVKSCTASGYIFTSYDINMVRQATGGLEWGMNPNNSGNAGF 60
DB 20 OVQLVQSGAEVKKPKGASVKSCTASGYIFTSYDINMVRQATGGLEWGMNPNNSGNAGF 79
QY 61 AOKFKGRLLTRDSTSTAYMELRLSEEDTAVYVCARCDTLLIFGPAPYYDSMGCGT 120
DB 80 SQNFQGRITTRDSTSTAYMELRLSEEDTAVYVCARCDTLLIFGPAPYYDSMGCGT 133
QY 121 LV 122
DB 134 LV 135

RESULT 11
US-08-264-093-3
Sequence 3, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-3

Query Match 65.3%; Score 429.5; DB 1; Length 121;
Best Local Similarity 66.4%; Pred. No. 7.2e-40;
Matches 81; Conservative 17; Mismatches 19; Indels 5; Gaps 1;

QY 1 OVQLQSGADYKPKGASVKSCTASGYIFTSYDINMVRQATGGLEWGMNPNNSGNAGF 60
DB 1 OVQLVQSGAEVKKPKGASVKSCTASGYIFTSYDINMVRQATGGLEWGMNPNNSGNAGF 60
QY 61 AOKFKGRLLTRDSTSTAYMELRLSEEDTAVYVCARCDTLLIFGPAPYYDSMGCGT 120
DB 61 AOKFKGRVSWTTRDSTSTAYMELRLSEEDTAVYVCARCDTLLIFGPAPYYDSMGCGT 115
QY 121 LV 122
DB 116 LV 117

RESULT 12
US-08-561-521-45
Sequence 45, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-45

Query Match 65.1%; Score 428.5; DB 2; Length 129;
Best Local Similarity 64.0%; Pred. No. 1e-39;
Matches 87; Conservative 10; Mismatches 14; Indels 25; Gaps 3;

QY 1 OVQLQSGADYKPKGASVKSCTASGYIFTSYDINMVRQATGGLEWGMNPNNSGNAGF 59
DB 1 OVQLVQSGAEVKKPKGASVKSCTASGYIFTSYDINMVRQATGGLEWGMNPNNSGNAGF 60

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_1
US-08-202-047-22

Query Match 66.1%; Score 435; DB 1; Length 128;
Best Local Similarity 64.4%; Pred. No. 1.9e-40;
Matches 87; Conservative 11; Mismatches 13; Indels 24; Gaps 3;

QY 1 OVOLQSAADYKKPGASVKSCTASGYFTSYDINMVRQATGGLEMMGMNP-NSGNAG 59
DB 1 OVOLVQSAEAVKPGASVKSCTASGYFTSYAISWVRQAPGGLEMMGMNPYNGNDTN 60
QY 60 FAKFKGRLLTLTRDSTSTAYMELRLSEEDTAVYYCARCOTLLIMFGAP----- 111
DB 61 YAKFGGRVITITADTSTAYMELSLRSEDIAVYYCAR-----APGYSGGGCC 109
QY 112 ----YDSMGQGTLY 122
DB 110 YRGDYFDYWGQGTLY 124

RESULT 9
US-08-964-690-22
Sequence 22, Application US/08964690
Patent No. 6033667
GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: POLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,690
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: /label= HUMAN_1
US-08-964-690-22

Query Match 66.1%; Score 435; DB 3; Length 128;
Best Local Similarity 64.4%; Pred. No. 1.9e-40;
Matches 87; Conservative 11; Mismatches 13; Indels 24; Gaps 3;

QY 1 OVOLQSAADYKKPGASVKSCTASGYFTSYDINMVRQATGGLEMMGMNP-NSGNAG 59
DB 1 OVOLVQSAEAVKPGASVKSCTASGYFTSYAISWVRQAPGGLEMMGMNPYNGNDTN 60
QY 60 FAKFKGRLLTLTRDSTSTAYMELRLSEEDTAVYYCARCOTLLIMFGAP----- 111
DB 61 YAKFGGRVITITADTSTAYMELSLRSEDIAVYYCAR-----APGYSGGGCC 109
QY 112 ----YDSMGQGTLY 122
DB 110 YRGDYFDYWGQGTLY 124

RESULT 10
US-09-049-672A-13
Sequence 13, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Maria R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-472-281A-94

Query Match 66.5%; Score 437.5; DB 2; Length 123;
Best Local Similarity 69.7%; Pred. No. 9.7e-41;
Matches 85; Conservative 13; Mismatches 21; Indels 3; Gaps 1;
QY 1 OVOLLOSADYKKKQASVSCASGYFTSYDINMTRQATGCGLEMMGMNPNNSGNAGF 60
DB 1 OVOLVQSAEYKKQASVSCASGYFTGYVMHWRAQGOGLMMGRINPNSGCTNY 60
QY 61 AOKFKGRLLTRDSTSTAYMELRLSESDTAVYYCARCDTLLIMFGAPAYDSMGCGT 120
DB 61 AOKFGQRYTMRDTSISTAYMELRLSDDTAVYYCARGRTYIV--VAEGFDYWGQGT 117
QY 121 LV 122
DB 118 LV 119

RESULT 7
US-08-477-989B-94
Sequence 94, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Hervy
APPLICANT: Latine, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kiebert-Emmons, Thomas
APPLICANT: Polesma, Christina E.
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Giffillan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable
US-08-477-989B-94

Query Match 66.5%; Score 437.5; DB 2; Length 123;
Best Local Similarity 69.7%; Pred. No. 9.7e-41;
Matches 85; Conservative 13; Mismatches 21; Indels 3; Gaps 1;
QY 1 OVOLLOSADYKKKQASVSCASGYFTSYDINMTRQATGCGLEMMGMNPNNSGNAGF 60
DB 1 OVOLVQSAEYKKQASVSCASGYFTGYVMHWRAQGOGLMMGRINPNSGCTNY 60
QY 61 AOKFKGRLLTRDSTSTAYMELRLSESDTAVYYCARCDTLLIMFGAPAYDSMGCGT 120
DB 61 AOKFGQRYTMRDTSISTAYMELRLSDDTAVYYCARGRTYIV--VAEGFDYWGQGT 117
QY 121 LV 122
DB 118 LV 119

RESULT 8
US-08-202-047-22
Sequence 22, Application US/08202047
Patent No. 5800815
GENERAL INFORMATION:
APPLICANT: CHESNUT, Robert W.
APPLICANT: FOLLEY, Margaret J.
APPLICANT: PAULSON, James C.
APPLICANT: JONES, S. Tarran
APPLICANT: SALDANHA, Jose W.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994

```

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-22

Query Match 67.1%; Score 441.5; DB 4; Length 117;
Best Local Similarity 69.7%; Pred. No. 3.3e-41;
Matches 85; Conservative 11; Mismatches 17; Indels 9; Gaps 1;

QY 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVRQATGQGLNMGWNPNSGNAGF 60
DB 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVRQATGQGLNMGWNPNSGNAGTNY 60
QY 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120
DB 61 AOKFGKRVMTTRDTSTSTAYMELSLRSDDTAVYYCAR-----DGDGFPYWGQGT 111

QY 121 LV 122
DB 112 LV 113

RESULT 5
US-08-477-877B-94
Sequence 94, Application US/08477877B
Patent No. 5730979
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latime, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cecchi, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS

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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,877B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-477-877B-94

Query Match 66.5%; Score 437.5; DB 1; Length 123;
Best Local Similarity 69.7%; Pred. No. 9.7e-41;
Matches 85; Conservative 13; Mismatches 21; Indels 3; Gaps 1;

QY 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVRQATGQGLNMGWNPNSGNAGF 60
DB 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVRQATGQGLNMGWNPNSGCTNY 60
QY 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120
DB 61 AOKFGKRVMTTRDTSTSTAYMELSLRSDDTAVYYCARGTETIV--VAEGFPYWGQGT 117

QY 121 LV 122
DB 118 LV 119

RESULT 6
US-08-472-281A-94
Sequence 94, Application US/08472281A
Patent No. 5817311
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latime, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cecchi, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 12.3883 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 658
Sequence: 1 OVALLOSADVKKPKGASVKV.....LLIWGPAPYDSMGQGLTV 122Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCtus.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	451	68.5	120	4	US-09-025-769B-36 Sequence 36, Appl
2	451	68.5	120	4	US-09-025-769B-59 Sequence 39, Appl
3	449	68.2	117	3	US-08-545-809A-96 Sequence 96, Appl
4	441.5	67.1	117	4	US-09-025-769B-22 Sequence 22, Appl
5	437.5	66.5	123	1	US-08-477-877B-94 Sequence 94, Appl
6	437.5	66.5	123	2	US-08-477-281A-94 Sequence 94, Appl
7	437.5	66.5	123	2	US-08-477-989B-94 Sequence 94, Appl
8	435	66.1	128	1	US-08-202-047-22 Sequence 22, Appl
9	435	66.1	128	3	US-08-964-690-22 Sequence 22, Appl
10	431	65.5	236	3	US-09-049-672A-13 Sequence 13, Appl
11	429.5	65.3	121	1	US-08-264-093-3 Sequence 3, Appl
12	428.5	65.1	129	2	US-08-561-521-45 Sequence 45, Appl
13	428.5	65.1	129	4	US-08-525-539A-77 Sequence 77, Appl
14	428.5	65.1	129	5	PCT-US95-01219-45 Sequence 45, Appl
15	424	64.4	139	1	US-08-253-877C-19 Sequence 19, Appl
16	424	64.4	139	2	US-08-452-164A-19 Sequence 19, Appl
17	424	64.4	139	3	US-08-603-024-18 Sequence 18, Appl
18	424	64.4	139	4	US-08-450-809-14 Sequence 14, Appl
19	423	64.3	118	1	US-08-491-845-14 Sequence 14, Appl
20	423	64.3	137	3	US-08-513-968-38 Sequence 38, Appl
21	422.5	64.2	135	3	US-09-199-149-3 Sequence 3, Appl
22	421.5	64.1	119	2	US-08-561-521-10 Sequence 10, Appl
23	421.5	64.1	119	5	PCT-US95-01219-10 Sequence 10, Appl
24	418.5	63.6	119	4	US-09-438-954-41 Sequence 41, Appl
25	415	63.0	245	4	US-10-039-785-46 Sequence 46, Appl
26	414.5	63.0	139	3	US-08-933-983-21 Sequence 21, Appl
27	414	62.9	117	3	US-08-545-809A-90 Sequence 90, Appl

28	411.5	62.5	121	1	US-08-202-047-23 Sequence 23, Appl
29	411.5	62.5	121	3	US-08-964-690-23 Sequence 23, Appl
30	406.5	61.8	119	1	US-08-478-039-65 Sequence 65, Appl
31	406.5	61.8	119	1	US-08-476-349A-65 Sequence 65, Appl
32	405.5	61.6	119	2	US-08-561-521-12 Sequence 12, Appl
33	405.5	61.6	119	5	PCT-US95-01219-12 Sequence 12, Appl
34	405.5	61.6	123	1	US-08-482-882-86 Sequence 86, Appl
35	405.5	61.6	123	2	US-08-483-389-86 Sequence 86, Appl
36	405.5	61.6	123	2	US-08-487-113D-86 Sequence 86, Appl
37	405.5	61.6	123	2	US-08-473-503-86 Sequence 86, Appl
38	405.5	61.6	123	2	US-08-483-932-86 Sequence 86, Appl
39	405.5	61.6	123	3	US-08-720-420A-86 Sequence 86, Appl
40	405.5	61.6	123	3	US-08-714-017-86 Sequence 86, Appl
41	405.5	61.6	123	3	US-08-475-680-86 Sequence 86, Appl
42	403.5	61.3	140	3	US-08-836-561-63 Sequence 63, Appl
43	403.5	61.3	140	3	US-08-569-147-82 Sequence 82, Appl
44	403.5	61.3	140	4	US-09-434-122-63 Sequence 63, Appl
45	402.5	61.2	119	1	US-08-491-845-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-36
Sequence 36, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-36
Query Match 68.5%; Score 451; DB 4; Length 120;
Beet Local Similarity 71.5%; Pred. No. 3,1e-42;
Matches 88; Conservative 9; Mismatches 18; Indels 8; Gaps 2;


```
Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-204
```

```
Query Match 71.9%; Score 473; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 5e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;
```

```
QY 1 QVQLQSSADPVKPKGASVSVKSTASGYIFTSYDINVRQATGQGLEMGMMNPNSGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVSVKSCASGYSTSYDINVRQATGQGLEMGMMNPNGNTGY 60
QY 61 AOKFKRLTLTRDTSSTAYMELRLSEEDTAVYVCARCDTLLIFGAPAYY---DSWG 117
DB 61 AOKFGQRTVMTRNTSISTAYMELSLRSEDTAVYVCAR---DIVVVYATDYIYGMDWVG 117
QY 118 QGTLV 122
DB 118 QGTTV 122
```

```
RESULT 13
US-10-041-860-241
; Sequence 241, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-241
```

```
Query Match 71.9%; Score 473; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 5e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;
```

```
QY 1 QVQLQSSADPVKPKGASVSVKSTASGYIFTSYDINVRQATGQGLEMGMMNPNSGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVSVKSCASGYSTSYDINVRQATGQGLEMGMMNPNGNTGY 60
```

```
QY 61 AOKFKRLTLTRDTSSTAYMELRLSEEDTAVYVCARCDTLLIFGAPAYY---DSWG 117
DB 61 AOKFGQRTVMTRNTSISTAYMELSLRSEDTAVYVCAR---DIVVVYATDYIYGMDWVG 117
QY 118 QGTLV 122
DB 118 QGTTV 122
RESULT 14
US-10-041-860-349
; Sequence 349, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-349
```

```
Query Match 71.9%; Score 473; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 5e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;
```

```
QY 1 QVQLQSSADPVKPKGASVSVKSTASGYIFTSYDINVRQATGQGLEMGMMNPNSGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVSVKSCASGYSTSYDINVRQATGQGLEMGMMNPNGNTGY 60
QY 61 AOKFKRLTLTRDTSSTAYMELRLSEEDTAVYVCARCDTLLIFGAPAYY---DSWG 117
DB 61 AOKFGQRTVMTRNTSISTAYMELSLRSEDTAVYVCAR---DIVVVYATDYIYGMDWVG 117
QY 118 QGTLV 122
DB 118 QGTTV 122
```

```
RESULT 15
US-10-041-860-38
; Sequence 38, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
```



```

QY      1 QVQLLOSLADPVKKRPGASVNVSCYASGYITSTSDIMNRAQTGGLEWMGNPNSSGNAGF 60
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 QVQLVQSGAEVKKRPGASVNVSCASGYITSTSDIMNVQAQTGGLEWMGNPNSSGNATGY 60
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      61 AOKFKRLTLTRDPTSTSTAYMELRLRESEDTAVVYCARCDTLLIWFSPAPY---DSWG 117
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 AOKFKQGVMTNRTNSTISTAYMELSLRSEDTAVVYCAEGIAVA---GTYYIYGMQVWG 117
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      118 QGTLV 122
      ||| |
Db      118 QGTLV 122

```

```

RESULT 9
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvahan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gagit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabab, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX. 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

```

Query Match	72.0%	Score 474;	DB 12;	Length 126;
Best Local Similarity	74.4%	Pred. No. 3.9e-41;		
Matches	93;	Conservative	8;	Mismatches 18; Indels 6; Gaps 2
Qy	1	QVOLLQSLADYVKKPGASVAVKSCSTAGYIFTSYDINNVRQATGGLEMMGMNPNNSGNAGF	60	
Db	1	QVQLVDSGAEVKKPGASVAVKSCASYYTTSYDINNVRQATGGLEMMGMNPNNSGNTGY	60	
Qy	61	AKPKRGLTLTRDTSSTSTAYMELRLRESEDDTAVYYCARCDTLLILWFGPAPY--DSWG	117	
Db	61	AKPKQGRVMTMTNTISTAYMELSLRSDDTAVYYCARGLIAVA--GTYYYYYGMDWG	117	
Qy	118	QGLTV	122	
Db	118	QGLTV	122	

```

RESULT 10
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R. F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Beasbuh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PGSD AND USES
; THEREOF
; FILE REFERENCE: ABGENIX 051A

```

```

:
: CURRENT APPLICATION NUMBER: US-10/041,860
:
: CURRENT FILING DATE: 2002-01-07
:
: NUMBER OF SEQ ID NOS: 377
:
: SOFTWARE: FASTSEQ for Windows Version 4.0.
:
: SEQ ID NO 288
:
: LENGTH: 126
:
: TYPE: PRT
:
: ORGANISM: homo sapiens
:
: US-10-041-860-288

```

Query Match	72.0%	Score 474;	DB 12;	Length 126;
Best Local Similarity	74.4%	Pred. NO. 3.9e-41;		
Matches 93; Conservative	8;	Mismatches 18;	Indels 6;	Gaps 2;

```
QY      1 QVQLLOSLADAVKKPGASVYNVSCTASGTYFTSYDINMWRQAATGGLEWMGMNPNPSGNAGF 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      1 QVQLVSGAEVKKPGASVYSVCSKASGYFTSYDINMWRQAQGLEWMGMNPNPSGNITGY 60
QY      61 AQKEKRLLTLTRDTSTSTAAMELRLESEDPAYVCARCDTLLIMFGPAPYY---DSWG 117
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 AQQEGRVTMTNTNSTISTAYNELSSLRSEDDTAIVYCAREGIAYA---GTYYYYYGMDVMG 117
QY      118 QGTLV 122
        ||| |
Db      118 QGITV 122
```

```

RESULT 11
US-10-041-860-40
; Sequence 40, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R. F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABEENIX. 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-40

```

Query	Match Similarity	71.9%	Score 473;	DB 12;	Length 126;
Best Local	Similarity	72.8%	Pred. No. 56-41;		
Matches	91; Conservative	11; Mismatches	17; Indels	6; Gaps	2
Oy	1	QVOLLQSADYVKPGSAVKVSCTASGYIFTSYDINWVRQATGQLGEEMGMNPNNSGNAGF	60		
Db	1	QVQLVDSGAEVKKPKAPSVKVSCKASGYSTSYDINWVRQATGQLGEEMGMNPNNGNTGY	60		
Oy	61	AOKFKGRLLTLTRDISTSTANMELRLSESDTAVYYCARCDITLLILFGAPFY---DSWG	117		
Db	61	AOKFGGRVTMTNTISTAYMELSLRSEDITAVYYCAR---DIVVVVATDYDYGGDWVG	117		
Oy	118	OGLTV	122		
Db	118	OGLTV	122		

RESULT 12
US-10-041-860-204
; Sequence 204, Application US/10041860

APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041.860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-37

Query Match 72.2%; Score 475; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 3.1e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVOLLGSAADVKKFGASVKVSCYIFTSYDINWYRQATGQGLEWGMNPNNGNAGF 60
DB 1 QVOLLGSAEYKKGASVKVSCYIFTTYDINWYRQATGQGLEWGMNPNNGNAGTGY 60
QY 61 AOKFKGRLTLTRDTSTSTAYWELRLSEDTAYVYCARCOTLLIWFGPAPY---DSWG 117
DB 61 AOKFGQVMTMTSLSTAYWELSLRSEDTAYVYCAR---DIVVVAATNYNGMDVWG 117
QY 118 QGTLV 122
DB 118 QGTLV 122

RESULT 6
US-10-041-860-202
Sequence 202, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041.860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 202
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-202

Query Match 72.2%; Score 475; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 3.1e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVOLLGSAADVKKFGASVKVSCYIFTSYDINWYRQATGQGLEWGMNPNNGNAGF 60
DB 1 QVOLLGSAEYKKGASVKVSCYIFTTYDINWYRQATGQGLEWGMNPNNGNAGTGY 60
QY 61 AOKFKGRLTLTRDTSTSTAYWELRLSEDTAYVYCARCOTLLIWFGPAPY---DSWG 117
DB 61 AOKFGQVMTMTSLSTAYWELSLRSEDTAYVYCAR---DIVVVAATNYNGMDVWG 117
QY 118 QGTLV 122
DB 118 QGTLV 122

RESULT 7
US-10-041-860-239
Sequence 239, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041.860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 239
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-239

Query Match 72.2%; Score 475; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 3.1e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVOLLGSAADVKKFGASVKVSCYIFTSYDINWYRQATGQGLEWGMNPNNGNAGF 60
DB 1 QVOLLGSAEYKKGASVKVSCYIFTTYDINWYRQATGQGLEWGMNPNNGNAGTGY 60
QY 61 AOKFKGRLTLTRDTSTSTAYWELRLSEDTAYVYCARCOTLLIWFGPAPY---DSWG 117
DB 61 AOKFGQVMTMTSLSTAYWELSLRSEDTAYVYCAR---DIVVVAATNYNGMDVWG 117
QY 118 QGTLV 122
DB 118 QGTLV 122

RESULT 8
US-10-041-860-19
Sequence 19, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041.860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-19

Query Match 72.0%; Score 474; DB 12; Length 126;
Best Local Similarity 74.4%; Pred. No. 3.3e-41;
Matches 93; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

OY 118 OCTLV 122
DB 118 OCTTV 122

RESULT 2

US-10-041-860-199
; Sequence 199, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-199

Query Match 72.6%; Score 478; DB 12; Length 126;
Best Local Similarity 74.4%; Pred. No. 1.5e-41;
Matches 93; Conservative 10; Mismatches 16; Indels 6; Gaps 2;

OY 1 0VOLQISADYKKPGASVKSCTASGYIFTSYDINWROATGQGLEMMGMNPNNGNAGF 60
DB 1 0VOLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQGLEMMGMNPNNGNAGTGY 60
OY 61 AOKFKGRLTLTRDSTSTAYMELRLSESDTAIVYVCARDTLLIMFGPAPY---DSWG 117
DB 61 AOKFGQRYMTNRNISTAYMELSLRSESDTAIVYCAR--DWMITFGVIVHYGMDVWG 117
OY 118 OCTLV 122
DB 118 OCTTV 122

RESULT 3

US-10-041-860-236
; Sequence 236, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-236

Query Match 72.6%; Score 478; DB 12; Length 126;
Best Local Similarity 74.4%; Pred. No. 1.5e-41;
Matches 93; Conservative 10; Mismatches 16; Indels 6; Gaps 2;

OY 1 0VOLQISADYKKPGASVKSCTASGYIFTSYDINWROATGQGLEMMGMNPNNGNAGF 60
DB 1 0VOLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQGLEMMGMNPNNGNAGTGY 60
OY 61 AOKFKGRLTLTRDSTSTAYMELRLSESDTAIVYVCARDTLLIMFGPAPY---DSWG 117
DB 61 AOKFGQRYMTNRNISTAYMELSLRSESDTAIVYCAR--DWMITFGVIVHYGMDVWG 117
OY 118 OCTLV 122
DB 118 OCTTV 122

RESULT 4

US-10-041-860-294
; Sequence 294, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-294

Query Match 72.6%; Score 478; DB 12; Length 126;
Best Local Similarity 74.4%; Pred. No. 1.5e-41;
Matches 93; Conservative 10; Mismatches 16; Indels 6; Gaps 2;

OY 1 0VOLQISADYKKPGASVKSCTASGYIFTSYDINWROATGQGLEMMGMNPNNGNAGF 60
DB 1 0VOLVQSGAEVKKPGASVKSCKASGYFTSYDINWROATGQGLEMMGMNPNNGNAGTGY 60
OY 61 AOKFKGRLTLTRDSTSTAYMELRLSESDTAIVYVCARDTLLIMFGPAPY---DSWG 117
DB 61 AOKFGQRYMTNRNISTAYMELSLRSESDTAIVYCAR--DWMITFGVIVHYGMDVWG 117
OY 118 OCTLV 122
DB 118 OCTTV 122

RESULT 5

US-10-041-860-37
; Sequence 37, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 26.1641 Seconds
(Without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 658
Sequence: 1 QVQLVDSADYKPKGASVKV.....LLIWFPGAPYYSWGQGLT 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	478	72.6	126	US-10-041-860-21 Sequence 21, Appl
2	478	72.6	126	US-10-041-860-199 Sequence 199, Appl
3	478	72.6	126	US-10-041-860-236 Sequence 236, Appl
4	478	72.6	126	US-10-041-860-294 Sequence 294, Appl
5	475	72.2	126	US-10-041-860-37 Sequence 37, Appl
6	475	72.2	126	US-10-041-860-202 Sequence 202, Appl
7	475	72.2	126	US-10-041-860-239 Sequence 239, Appl
8	474	72.0	126	US-10-041-860-19 Sequence 19, Appl
9	474	72.0	126	US-10-041-860-201 Sequence 201, Appl
10	474	72.0	126	US-10-041-860-288 Sequence 288, Appl
11	473	71.9	126	US-10-041-860-40 Sequence 40, Appl
12	473	71.9	126	US-10-041-860-204 Sequence 204, Appl
13	473	71.9	126	US-10-041-860-241 Sequence 241, Appl
14	473	71.9	126	US-10-041-860-349 Sequence 349, Appl
15	472.5	71.8	125	US-10-041-860-38 Sequence 38, Appl

16	472.5	71.8	125	US-10-041-860-293	Sequence 293, Appl
17	472.5	71.8	125	US-10-041-860-240	Sequence 240, Appl
18	472.5	71.8	125	US-10-041-860-343	Sequence 343, Appl
19	469	71.3	120	US-10-269-805-47	Sequence 47, Appl
20	468	71.1	146	US-09-925-299-1050	Sequence 1050, Ap
21	468	71.1	146	US-09-925-299-1050	Sequence 1050, Ap
22	466	70.8	122	US-10-269-805-61	Sequence 61, Appl
23	465	70.7	127	US-09-880-748-927	Sequence 927, Appl
24	465	70.7	247	US-09-880-748-948	Sequence 948, Appl
25	464.5	70.6	127	US-10-041-860-44	Sequence 44, Appl
26	464.5	70.6	127	US-10-041-860-205	Sequence 205, Appl
27	464.5	70.6	127	US-10-041-860-242	Sequence 242, Appl
28	464.5	70.6	127	US-10-041-860-360	Sequence 360, Appl
29	462.5	70.3	125	US-10-041-860-48	Sequence 48, Appl
30	462.5	70.3	125	US-10-041-860-200	Sequence 200, Appl
31	462.5	70.3	125	US-10-041-860-237	Sequence 237, Appl
32	462.5	70.3	125	US-10-041-860-372	Sequence 372, Appl
33	460	69.9	125	US-10-041-860-238	Sequence 238, Appl
34	453.5	68.9	248	US-09-880-748-1721	Sequence 1721, Ap
35	449	68.2	98	US-10-041-860-289	Sequence 289, Appl
36	449	68.2	98	US-10-041-860-290	Sequence 290, Appl
37	449	68.2	98	US-10-041-860-295	Sequence 295, Appl
38	449	68.2	98	US-10-041-860-296	Sequence 296, Appl
39	449	68.2	98	US-10-041-860-342	Sequence 342, Appl
40	449	68.2	98	US-10-041-860-344	Sequence 344, Appl
41	449	68.2	98	US-10-041-860-348	Sequence 348, Appl
42	449	68.2	98	US-10-041-860-361	Sequence 361, Appl
43	449	68.2	99	US-10-041-860-1	Sequence 1, Appl1
44	449	68.2	251	US-09-880-748-1389	Sequence 1389, Ap
45	447.5	68.0	251	US-09-880-748-930	Sequence 930, Appl

ALIGNMENTS

RESULT 1

US-10-041-860-21

Sequence 21, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvatan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Peng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazic, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezaheh, Banyan

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ. ID NOS: 377

SOFTWARE: FastSeq for Windows Version 4.0

SEQ. ID NO 21

LENGTH: 126

TYPE: PRT

ORGANISM: homo sapiens

US-10-041-860-21

Query Match 72.6%; Score 478; DB 12; Length 126;

Best Local Similarity 74.4%; Pred. No. 1.5e-41;

Matches 93; Conservative 10; Mismatches 16; Indels 6; Gaps 2;

QY 1 QVQLVDSADYKPKGASVKSCSTASGIFITSYINWRAQTGGLEMGWNNNSGAGF 60

DB 1 QVQLVDSADYKPKGASVKSCSTASGIFITSYINWRAQTGGLEMGWNNNSGAGF 60

QY 61 AQKFKRLTTRTSTSTAYMELRLSEEDTAYYYCARCCTLLIWFPGAPYV---DSWG 117

DB 61 AQKFKRLTTRTSTSTAYMELRLSEEDTAYYYCARCCTLLIWFPGAPYV---DSWG 117

CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M131, by PCR
CC amplification using primers AAQ78917-38. The genes are subdivided into 5
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA
CC fragments were isolated from high molecular weight DNA from human
CC placenta. The DNA was partially digested with TagI restriction enzyme.
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions
CC were collected. The fragments were ligated with ClaI-digested cosmid
CC vector pJB81. The ligation products were in vitro packed and infected
CC into E.coli 490A. The fragments were then subcloned by colony
CC hybridization. The Vh genes and the DNA fragments encoding them are
CC useful in producing human immunoglobulin in mammalian hosts.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 117 AA;

Query Match 68.2%; Score 449; DB 16; Length 117;
Best Local Similarity 84.7%; Pred. No. 1,1e-35;
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLLOSADVKKPGASVKVSCTASGYSFTSYDINWVROATGQGLEPMGMNPNNGNAGF 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVDSGAEVKKPGASVKVSCTASGYSFTSYDINWVROATGQGLEPMGMNPNNGNTGY 79
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFKGRLTLTRDSTSTAYMELRLESEDTAYYCAR 98
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 AOKFQGRVTMTNTSISTAYMELSLRSEDTAYYCAR 117
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: December 30, 2003, 10:54:34
Job time : 40.3295 sec

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet adhesion or aggregation, for
 CC increasing mortality of tumour or leukaemia cells, for increasing the
 CC susceptibility of diseased cells to damage by anti-disease, anti-cancer
 CC or anti-leukaemia agents, or for decreasing the number of tumour or
 CC leukaemia cells in a patient, or in the manufacture of a medicament for
 CC the above mentioned purposes. The epitopes are useful for diagnosing and
 CC treating diseases such as cancer, leukaemia, autoimmune diseases,
 CC inflammatory diseases, cardiovascular diseases such as myocardial
 CC infarction, retinopathic diseases and other diseases mediated by abnormal
 CC platelet function and diseases caused by sulphated tyrosine-dependent
 CC protein-protein interactions. This sequence represents a human antibody
 CC fragment of the invention.

XX Sequence 98 AA;

Query Match 68.2%; Score 449; DB 23; Length 98;

Best Local Similarity 84.7%; Pred. No. 8.9e-36;

Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVOLLQSAADYKPKGASVKSCTASGYIFTSYDINWVRQATGQGLEMMGMNPNNGNAF 60
 DB 1 QVOLLQSGAEVKKPKGASVKSCKASGYFTFTSYDINWVRQATGQGLEMMGMNPNNGNTGY 60

OY 61 AOKFKRLTLTRDTSTSTAYMELRLBSEDPTAVYYCAR 98
 DB 61 AOKFOGRVMTNRTNISSTAYMELSLRSEDPTAVYYCAR 98

RESULT 14

ID ABG78170 standard; Protein; 98 AA.

AC ABG78170;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #45.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

PN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US49440.

PR 29-DEC-2000; 2000US-0751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

PI Plaksin D, Peretz T;

DR MPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favour of other
 PT cells -

XX Claim 13; Page 168-169; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention.

XX Sequence 98 AA;

Query Match 68.2%; Score 449; DB 23; Length 98;

Best Local Similarity 84.7%; Pred. No. 8.9e-36;

Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVOLLQSAADYKPKGASVKSCTASGYIFTSYDINWVRQATGQGLEMMGMNPNNGNAF 60
 DB 1 QVOLLQSGAEVKKPKGASVKSCKASGYFTFTSYDINWVRQATGQGLEMMGMNPNNGNTGY 60

OY 61 AOKFKRLTLTRDTSTSTAYMELRLBSEDPTAVYYCAR 98
 DB 61 AOKFOGRVMTNRTNISSTAYMELSLRSEDPTAVYYCAR 98

RESULT 15

ID AAR66302 standard; Protein; 117 AA.

AC AAR66302;

DT 25-MAR-2003 (updated)

DT 02-AUG-1995 (first entry)

DE Human immunoglobulin variable heavy chain #8.

XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;

KM cosmid; placenta; vector; pJBB1; E.coli; mammalian.

OS Homo sapiens.

PN WO9426895-A1.

PD 24-NOV-1994.

PF 10-MAY-1993; 93WO-JP00603.

PR 10-MAY-1993; 93WO-JP00603.

PA (NIBS) JAPAN TOBACCO INC.

PI Honjo T, Matsuda F;

DR MPI; 1995-006791/01.

DR N-PSDB; AAQ78946.

PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts

PS Claim 17; Page 41-42; 130pp; Japanese.

XX Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
 CC chain sequences encoded by novel isolated genes. The genes
 CC (AAQ78939-79002) were isolated and cloned from a series of cosmid

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XX PN MO9708320-A1.
XX PT
XX PD 06-MAR-1997.
XX PF
XX PF 19-AUG-1996; 96MO-EP03647.
XX PR 18-AUG-1995; 95EP-0113021.
XX PA (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
XX PI Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckhuhn A;
XX PT WPI; 1997-179277/16.
XX DR N-PSDB; AAT87949.
XX PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX PS
XX PS Example 1; Fig 5B; 436bp; English.
XX CC The present sequence is the human antibody heavy chain
CC variable region synthetic sequence VH18, used in the preparation of
CC a human derived antibody gene library.
XX SQ Sequence 120 AA;

Query Match 68.5%; Score 451; DB 18; Length 120;
Best Local Similarity 71.5%; Pred. No. 7.2e-36;
Matches 88; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

QY 1 QVQLVDSADVKKPGASVKVCTASGYIFTSYDINWVROATGCGLEWMGMNPNNSGNAGF 60
DB 1 QVQLVDSGAEVKKRPGASVKVCSKASGYTFTSYHWVRQAPGQGLEWMGINPNSSGNTY 60
QY 61 AQRFKGRLLTTRDTSTSTAYMELRLSEPTAVYYCARCTTLIIFGPAPY-YDSWGQG 119
DB 61 AQRFKGRVMTTRDTSTSTAYMELSLRSEPTAVYYCAR-----WGQDGFYAMDYWGQG 113
QY 120 TLV 122
DB 114 TLV 116

RESULT 12
AAV50958
ID AAV50958 standard; Protein; 98 AA.
XX AC AAV50958;
XX XX
XX XX 23-MAR-2000 (first entry)
XX XX
XX XX Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
XX XX
XX XX Human; heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; scFv; A3-C1.
XX OS
XX OS Homo sapiens.
XX PN MO958680-A2.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99MO-NL00285.
XX PR 08-MAY-1998; 98EP-0201543.
XX PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX DR WPI; 2000-053102/04.

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XX PT New polynucleotide, polypeptide and antibody useful for diagnosing the
XX PT presence of neutralizing antibodies against factor VIII and for
XX PT treatment of hemophilia A patients with these antibodies -
XX PS
XX PS Example 8; Fig 9A; 61bp; English.
XX CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC factor VIII antibody A3-C1 specific scFv protein DP-15 which is used
CC in the method of the invention.
XX SQ Sequence 98 AA;

Query Match 68.2%; Score 449; DB 21; Length 98;
Best Local Similarity 84.7%; Pred. No. 8.9e-36;
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVDSADVKKPGASVKVCTASGYIFTSYDINWVROATGCGLEWMGMNPNNSGNAGF 60
DB 1 QVQLVDSGAEVKKRPGASVKVCSKASGYTFTSYDINWVROATGCGLEWMGMNPNNSGNTGY 60
QY 61 AQRFKGRLLTTRDTSTSTAYMELRLSEPTAVYYCAR 98
DB 61 AQRFKGRVMTTRDTSTSTAYMELSLRSEPTAVYYCAR 98

RESULT 13
ABG91861
ID ABG91861 standard; Protein; 98 AA.
XX AC ABG91861;
XX XX
XX XX 04-DEC-2002 (first entry)
XX XX
XX XX Human antibody fragment #45.
XX DE
XX XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM metastasis; hypervariable region; autoimmune disease; thrombosis;
KM rectorosis; leukaemia; inflammatory disease; cardiovascular disease;
KM myocardial infarction; retinopathic disease; abnormal platelet function;
KM sulphated tyrosine-dependent protein-protein interaction.
XX OS
XX OS Homo sapiens.
XX PN WO200253700-A2.
XX PD 11-JUL-2002.
XX PF 31-DEC-2001; 2001WO-US49442.
XX PR 29-DEC-2000; 2000US-258948P.
XX PR 29-DEC-2000; 2000US-0751181.
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX PI Stanhon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX DR WPI; 2002-674776/72.
XX PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer -
XX PS Disclosure; Page 246; 310pp; English.

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XX The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of
 CC TIMP-1. The antibody comprises a variable heavy chain (VH)CD3 region and
 CC a variable light chain (VL)CD3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostatic hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 230 AA;

Query Match 68.7%; Score 452; DB 24; Length 230;
 Best Local Similarity 70.6%; Pred. No. 1.2e-35;
 Matches 89; Conservative 11; Mismatches 18; Indels 8; Gaps 2;

OY 1 OVQLQSNADYKKGASVKSCTASGYIFTSYDINMVRQATGQGLEMMGMNPNNGNAGF 60
 DB 1 OVQLQSGAEVKKPGASVKSCKASGYFTSYHMVWQAPQGLEMMGMNPNNGNAGF 60
 OY 61 AOKFKGRLLTRDSTSTAYMELRLSEBDTAVVYCARCDTTLIMFGPAP---YYISW 116
 DB 61 AOKFKGRVYTMTRDISISTAYMELSLRSEBDTAVVYCAR---LVGIVGKKPDELILYFDW 116
 OY 117 GGGTLV 122
 DB 117 GGGTLV 122

RESULT 10

ABBS7555
 ID ABB57555 standard; Peptide; 116 AA.

XX ABB57555;

DT 18-MAR-2002 (first entry)

DE HLA-DR-specific protein MS-GPC3 VH sequence.

XX Immunomodulatory human MHC class II antigen-binding protein; HLA;
 KM human leukocyte antigen; immune system; immunosuppression; antibody;
 KM major histocompatibility complex; antirheumatic; antiarthritic;
 KM neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;
 KM immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;
 KM thyrometetic; hepatotropic; immune response suppressor; narcolepsy;
 KM rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;
 KM Grave's disease; insulin-dependent diabetes; Hashimoto's disease;
 KM systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;
 KM transplant rejection; graft versus host disease; pemphigus vulgaris;
 KM glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;
 KM irritable bowel disease; Sjogren's syndrome.

OS Homo sapiens.

OS Synthetic.

XX WO200187338-A1.

XX 22-NOV-2001.

PD 14-MAY-2001; 2001WO-US15626.

XX 12-MAY-2000; 2000EP-0110063.

PR 06-OCT-2000; 2000US-238762P.

XX (GPCB-) GPC BIOTECH AG.

PA (MORP-) MORPHOSYS AG.

PI Nagy Z, Teasar M, Thomassen-Wolf E;

XX WPI: 2002-075289/10.

XX Composition for suppressing immune response, treating diseases of
 PT immune system, has polypeptide comprising antibody-based
 PT antigen-binding domain of human composition, which binds antigen
 PT expressed on a cell surface -
 XX Example; Fig 15; 139pp; English.

XX The present invention describes a composition (I), comprising a
 CC polypeptide comprising an antibody-based antigen-binding domain of human
 CC composition with binding specificity for an antigen expressed on the
 CC surface of a cell, where treating cells expressing the antigen with the
 CC polypeptides leads to suppression of an immune response, and the IC50 for
 CC the suppression of immune response is 1 microm or less. (I) has
 CC antineumatic, antiarthritic, immunosuppressive, dermatological,
 CC antidiabetic, antipsoriatic, neuroprotective, antiinflammatory,
 CC antithyroid, nephrotropic, thyromimetic and hepatocytic activities, and
 CC can be used as a suppressor of immune response. (I) is useful for
 CC suppressing activation or proliferation of a cell of the immune system,
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the
 CC immune system with another cell, immunosuppressing a patient and for
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR
 CC on the surface of the cell, where neither cytotoxic entities nor
 CC immunological mechanisms are needed to cause or lead to the killing.
 CC (I) (optionally linked to cytotoxic or immunogenic agent) is useful for
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in
 CC the exemplification of the present invention.

XX Sequence 116 AA;

Query Match 68.5%; Score 451; DB 23; Length 116;
 Best Local Similarity 70.5%; Pred. No. 6.9e-36;
 Matches 86; Conservative 10; Mismatches 16; Indels 10; Gaps 1;

OY 1 OVQLQSNADYKKGASVKSCTASGYIFTSYDINMVRQATGQGLEMMGMNPNNGNAGF 60
 DB 1 OVQLQSGAEVKKPGASVKSCKASGYFTSYHMVWQAPQGLEMMGMNPNNGNAGF 60
 OY 61 AOKFKGRLLTRDSTSTAYMELRLSEBDTAVVYCARCDTTLIMFGPAPYYDSMGQGT 120
 DB 61 AOKFKGRVYTMTRDISISTAYMELSLRSEBDTAVVYCARLSTRM-----DPMGQGT 110
 OY 121 LV 122
 DB 111 LV 112

RESULT 11

AAW27551
 ID AAW27551 standard; Protein; 120 AA.

XX AAW27551;

DT 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH18 consensus.

XX Human; antibody; preparation; library; VH18; variable region;

XX heavy chain; consensus.

OS Homo sapiens.

DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 1533-1534; 3148bp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytotoxic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
 CC and so may be used to detect and quantitate the presence of BLYS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLYS. They may also be
 CC administered to treat diseases associated with aberrant BLYS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 SQ Sequence 247 AA:
 Query Match 70.7%; Score 465; DB 23; Length 247;
 Best Local Similarity 72.2%; Pred. No. 7.1e-37;
 Matches 91; Conservative 9; Mismatches 16; Indels 10; Gaps 2;
 QY 1 QVQLQSGADYKPKGASVSKCTASGYIFTSYDINMVRQATGQGLEWMGMNPNNGNAGF 60
 Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYITFTYGISVROAPQGLEWMGMNPNNGNAGY 60
 QY 61 AOKFKGRILTLTRDTSTSTAYMELRLRLESEDTAVYYCARCD---TTLTIWGPAPYYDSW 116
 Db 61 AOKFGQGRVITMTNTSISTAYMELSLRSEDTAVYYCARQGYDILTYWFPD-----W 114
 QY 117 GGGTLV 122
 Db 115 GGGTLV 120
 Db
 RESULT 6
 AAB62747
 ID AAB62747 standard; Protein; 120 AA.
 XX
 AC AAB62747;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 46.
 XX
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis.
 XX
 OS Homo sapiens.
 OS
 PN WO200100678-A1.
 PN
 PD 04-JAN-2001.
 PD
 PF 23-JUN-2000; 2000MO-US17327.
 PF
 PR 30-JUN-1999; 99US-0141701.
 PR
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 PI Wackins BA, Reitz MS;
 PI
 PT WPI; 2001-112438/12.
 PT
 DR N-PSDB; AAF29048.
 DR

XX
 PT Novel human monoclonal antibody immunoreactive with human
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal -
 XX
 PS Claim 1; Page 51-52; 81pp; English.
 XX
 CC The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection.
 XX
 SQ Sequence 120 AA;
 Query Match 70.1%; Score 461.5; DB 22; Length 120;
 Best Local Similarity 73.2%; Pred. No. 7e-37;
 Matches 90; Conservative 10; Mismatches 14; Indels 9; Gaps 2;
 QY 1 QVQLQSGADYKPKGASVSKCTASGYIFTSYDINMVRQATGQGLEWMGMNPNNGNAGF 60
 Db 2 EVQLQSGAEVKKPGASVRSCKASGYITFTSYDINMVRQATGQGLEWMGMNPNNGNAGY 61
 QY 61 AOKFKGRILTLTRDTSTSTAYMELRLRLESEDTAVYYCARCOTTLTIWGPAPYYDS -WGQ 119
 Db 62 AOKFGQGRVITMTNTSISTAYMELSLRSEDTAVYYCAR-----QSSRGVWVSWGQ 113
 QY 120 TLV 122
 Db 114 TLV 116
 Db
 RESULT 7
 AAB45710
 ID AAB45710 standard; Protein; 248 AA.
 XX
 AC AAB45710;
 XX
 DT 19-AUG-2002 (first entry)
 DT
 DE Human BlyS binding scFv SEQ ID 1721.
 DE
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytotoxic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 OS
 PN WO200202641-A1.
 PN
 PD 10-JAN-2002.
 PD
 PF 15-JUN-2001; 2001WO-US19110.
 PF
 PR 16-JUN-2000; 2000US-212210P.
 PR
 PR 17-OCT-2000; 2000US-240816P.
 PR
 PR 16-MAR-2001; 2001US-276248P.
 PR
 PR 21-MAR-2001; 2001US-277379P.
 PR
 PR 25-MAY-2001; 2001US-293499P.
 PR
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI
 PT WPI; 2002-114799/15.
 PT
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX

CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.

CC Sequence 146 AA;

Query Match 71.1%; Score 468; DB 21; Length 146;
 Best Local Similarity 74.6%; Pred. No. 2e-37;
 Matches 91; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 1 QVQLQSADPVKPKGASVYKSCSTASGYIFTSYDINMVRQATGGGLEMGMMNNSGNAGF 60
 DB 25 QVQLVSGAEVKKPKGASVYKSCASGYFTFSYDINMVRQATGGGLEWGMNPNNSANTGY 84
 QY 61 AOKFKRLTLTRDPTSTSTAYMELRLSEEDTAVYYCARCDTLLIFGPAPYYDSWGQGT 120
 DB 85 AOKFGQRTVMTTRTSTISTAYMELSLRSEDTAVYYCARXRMRLL--GMMDTFDYGQGT 142

QY 121 LV 122
 DB 143 LV 144

RESULT 4
 ABP44916
 ID ABP44916 standard; Protein; 247 AA.

AC ABP44916;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 927.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PI WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 1508-1509; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 247 AA;

Query Match 70.7%; Score 465; DB 23; Length 247;
 Best Local Similarity 72.2%; Pred. No. 7.1e-37;
 Matches 91; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 1 QVQLQSADPVKPKGASVYKSCSTASGYIFTSYDINMVRQATGGGLEMGMMNNSGNAGF 60
 DB 1 QVQLVSGAEVKKPKGASVYKSCASGYFTFSYDINMVRQATGGGLEWGMNPNNSANTGY 60
 QY 61 AOKFKRLTLTRDPTSTSTAYMELRLSEEDTAVYYCARCD---TLLIFGPAPYYDSW 116
 DB 61 AOKFGQRTVMTTRTSTISTAYMELSLRSEDTAVYYCARQGYDILTYGMFDP-----W 114

QY 117 GQGTIV 122
 DB 115 GKGTIV 120

RESULT 5
 ABP44937
 ID ABP44937 standard; Protein; 247 AA.

AC ABP44937;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 948.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PT treatment of hemophilia A patients with these antibodies -
 XX
 PS Example 8; Fig 9B; 61pp; English.
 XX
 CC This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specifically which has
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides in the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents a fragment
 CC of the human factor VIII antibody heavy chain variable region protein B38
 CC which is used in the method of the invention.
 XX
 SQ Sequence 122 AA:
 Query Match 100.0%; Score 658; DB 21; Length 122;
 Best Local Similarity 100.0%; Pred. No. 8.6e-56;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OVQLQSAADVKKPGASVKSCTASGYFTSYDINMVRQATGCGLEWGMNPNNGNAGF 60
 DB 1 OVQLQSAADVKKPGASVKSCTASGYFTSYDINMVRQATGCGLEWGMNPNNGNAGF 60
 QY 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQT 120
 DB 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQT 120
 QY 121 LV 122
 DB 121 LV 122
 RESULT 2
 AAY50959
 ID AAY50959 standard; Protein; 122 AA.
 XX
 AC AAY50959;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human FVIII antibody A3-C1 scFv heavy chain protein B38.
 XX
 KW Human; heavy chain; antibody; factor VIII; hemostatic;
 KW hemophilia A; scFv; A3-C1.
 XX
 OS Homo sapiens.
 XX
 PN WO9558680-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-NL00285.
 XX
 PR 08-MAY-1998; 98EP-0201543.
 XX
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
 XX
 PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
 XX
 DR WPI; 2000-053102/04.
 XX
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for
 PT treatment of hemophilia A patients with these antibodies -
 XX
 PS Example 8; Fig 9A; 61pp; English.
 XX
 CC This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specificity which has
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents the human
 CC factor VIII antibody A3-C1 specific scFv protein B38 which is used
 CC in the method of the invention.
 XX
 SQ Sequence 122 AA:
 Query Match 95.9%; Score 631; DB 21; Length 122;
 Best Local Similarity 96.7%; Pred. No. 3.4e-53;
 Matches 118; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 OVQLQSAADVKKPGASVKSCTASGYFTSYDINMVRQATGCGLEWGMNPNNGNAGF 60
 DB 1 OVQLQSAADVKKPGASVKSCTASGYFTSYDINMVRQATGCGLEWGMNPNNGNAGF 60
 QY 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQT 120
 DB 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQT 120
 QY 121 LV 122
 DB 121 LV 122
 RESULT 3
 AAB53510
 ID AAB53510 standard; Protein; 146 AA.
 XX
 AC AAB53510;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human colon cancer antigen protein sequence SEQ ID NO:1050.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200055351-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05883.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587534/55.
 DR N-PSDB; AAC98267.
 XX
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX
 PS Claim 11; Page 1631; 2104pp; English.
 XX
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53334 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 39.2461 Seconds
(without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 1 QVQLQSGADVKKPKGASVKV.....LLIWFGPAPYDMSWGQTLV 122

Sequence: 658

Scoring table: BLAST62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	122	21	AA150966 Human FVIII antibo
2	631	95.9	122	21	AA150959 Human FVIII antibo
3	468	71.1	146	21	AA153510 Human FVIII antibo
4	465	70.7	247	23	ABP44916 Human BLYS binding
5	465	70.7	247	23	ABP44937 Human BLYS binding
6	461.5	70.1	120	22	AA152747 Human HIV-1 monocl
7	453.5	68.9	248	23	ABP45710 Human BLYS binding
8	452.5	68.8	245	22	AA157619 Human Leukocyte an
9	452	68.7	230	24	ABR01514 Human anti-TIMP-1

10	451	68.5	116	23	AB157555 HLA-DR-specific pr
11	451	68.5	120	18	AA127551 Human Ab heavy cha
12	449	68.2	98	21	AA150958 Human FVIII antibo
13	449	68.2	98	23	ABG1961 Human antibody fra
14	449	68.2	98	23	ABG78170 Human Fv molecule
15	449	68.2	117	16	AA166302 Human immunoglobul
16	449	68.2	251	23	ABP45378 Human BLYS binding
17	447.5	68.0	251	23	ABP44919 Human BLYS binding
18	447	67.9	100	24	ABJ18673 Antibody library r
19	447	67.9	130	24	ABJ18719 Antibody library r
20	446	67.8	247	23	ABP45718 Human BLYS binding
21	445.5	67.7	199	20	AA134302 IGM antibody CEM 1
22	445.5	67.7	251	23	ABP45575 Human BLYS binding
23	444	67.5	251	23	ABP46020 Human BLYS binding
24	443.5	67.4	251	23	ABP45859 Human BLYS binding
25	443	67.3	249	23	ABP45624 Human BLYS binding
26	442.5	67.2	146	18	AA122641 Human anti-tumour
27	442.5	67.2	248	23	ABP45461 Human BLYS binding
28	442	67.2	228	23	ABR01526 Human anti-TIMP-1
29	442	67.2	241	23	ABP45937 Human BLYS binding
30	441.5	67.1	248	23	ABP44882 Human BLYS binding
31	441.5	67.1	248	23	ABP45860 Human BLYS binding
32	441.5	67.1	251	23	ABP45858 Human BLYS binding
33	441.5	67.1	470	23	AA174286 Anti-human AL10 m
34	440.5	66.9	251	23	ABP45727 Human BLYS binding
35	440.5	66.9	476	20	AA188464 Monoclonal antibod
36	439.5	66.8	251	23	ABP45551 Human anti-TIMP-1
37	438.5	66.6	221	24	ABR01537 Human anti-TIMP-1
38	438.5	66.6	251	23	ABP45861 Human BLYS binding
39	438	66.6	238	23	ABP45886 Human BLYS binding
40	438	66.6	249	23	ABP44908 Human BLYS binding
41	438	66.6	250	23	ABP45549 Human BLYS binding
42	437.5	66.5	133	19	AA179228 Heavy chain variab
43	437.5	66.5	248	23	ABP45866 Human BLYS binding
44	437.5	66.5	250	23	ABP45711 Human BLYS binding
45	437.5	66.5	251	23	ABP45867 Human BLYS binding

ALIGNMENTS

RESULT 1	AA150966	AA150966 standard; Protein; 122 AA.
XX	AA150966	
AC	AA150966	
XX	23-MAR-2000 (first entry)	
XX		
DE	Human FVIII antibody heavy chain variable region B38 protein fragment.	
XX		
KW	Human; heavy chain; antibody; factor VIII; hemostatic; variable region;	
KW	hemophilia A.	
XX		
OS	Homo sapiens.	
XX		
PN	W0958680-A2.	
XX		
PD	18-NOV-1999.	
XX		
XX		
PP	07-MAY-1999; 99WO-NL00285.	
XX		
PR	08-MAY-1998; 98BP-0201543.	
XX		
PA	(SAND-) STICHTING SANDUIN BLOEDVOORZIEENING.	
XX		
PI	Voorberg JJ, Van Den Brink EN, Turenhout EM;	
XX		
DR	WPI: 2000-053102/04.	
XX		
DR	N-PSDB; AA243863.	
XX		
XX	New polynucleotide, polypeptide and antibody useful for diagnosing the	
PT	presence of neutralizing antibodies against factor VIII and for	


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QY      121 LV 122
DB      135 MV 136

RESULT 11
095978      PRELIMINARY; PRT; 157 AA.
AC 095978;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE VHL protein precursor (Fragment).
GN VHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularly Hodgkin's disease is associated with
RT somatic mutations within the untranscribed regions of rearranged and
RT class switch recombined Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005570; CAA06599.1; -.
DR HSPB; P01772; 2PB4.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT NON_TER 157 157 POTENTIAL.
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA8488B5 CRC64;

Query Match      55.9%; Score 367.5; DB 4; Length 157;
Best Local Similarity 59.0%; Pred. No. 8,7e-32;
Matches 72; Conservative 15; Mismatches 30; Indels 5; Gaps 1;

QY      1 OVOLLOSADVKKPGASVKVCTASGYIFTSYDINVRQATGQGLEWMGMNPNNSGNAGF 60
DB      20 QVOLVSGAELVKRPGASVKVHCKTSGVFTSYIHVWRQPRGQGLEWMGGIGPEVGSITMC 79
QY      61 AOKFKRLTLTRDTSTSTAYMELRLSEEDTAVYYCARCCTLLIMFGPAPYYDSMGCGT 120
DB      80 AENKQGLTITRNSTTTVMELSLRLFDPAVAVFCGRGR-----WRSGNYNHMGCGT 134
QY      121 LV 122
DB      135 PV 136

RESULT 12
08VCX4      PRELIMINARY; PRT; 489 AA.
AC 08VCX4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 53.2 kDa protein.
GN IGH-V0558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC      TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAH18322.1; -.
DR MGD; MGI:96486; Igh-V0558.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00280; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;

Query Match      54.9%; Score 361.5; DB 11; Length 489;
Best Local Similarity 55.9%; Pred. No. 1.5e-30;
Matches 71; Conservative 19; Mismatches 26; Indels 11; Gaps 3;

QY      1 OVOLLOSADVKKPGASVKVCTASGYIFTSYDINVRQATGQGLEWMGMNPNNSGNAGF 60
DB      20 KVQLQSGAELVFKPGASVKLSCKASGYTFSDYFIHWIKRSGCGLEWIGWFNPGSGSIKF 79
QY      61 AOKFKRLTLTRDTSTSTAYMELRLSEEDTAVYYCARCCTLLIMFGPAPYYDS 115
DB      80 NEFKKQKATLTADKSTTYVMDLSRLTSEDSAVYFCARHEDRGNYDGLAMF----VY-- 133
QY      116 WGQSTLV 122
DB      134 WGQSTLV 140

RESULT 13
0920E8      PRELIMINARY; PRT; 120 AA.
AC 0920E8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotypic heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horatius O., Cotton R.G.H.;
RT "Definition of the idiotype of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307936; AAL09420.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;

Query Match      54.8%; Score 360.5; DB 11; Length 120;
Best Local Similarity 55.3%; Pred. No. 3.6e-31;
Matches 68; Conservative 25; Mismatches 23; Indels 7; Gaps 2;

QY      1 OVOLLOSADVKKPGASVKVCTASGYIFTSYDINVRQATGQGLEWMGMNPNNSGNAGF 60
DB      1 EVOLQSGPELKRPGASVKISCKASGYTFGYNMWNVQSGSLWIGNIDIPYCGTSY 60
QY      61 AOKFKRLTLTRDTSTSTAYMELRLSEEDTAVYYCARCCTLLIMFGPAPYYDSMGCG 119
DB      61 NOKFKKATLTVDKSSSTAYMQLKSLTSEDSAVYCA-----VIYGNPAMFAYWGCG 114
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QY 61 AOKFKRLTLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 120
 Db 63 NEKFKRATLSVSKSSSTAYMELRLTSEDSAVYFCARGDY-----RRYFDLWGCGT 115
 QY 121 LV 122
 Db 116 TV 117

RESULT 8

QY 61 AOKFKRLTLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 120
 Db 63 NEKFKRATLSVSKSSSTAYMELRLTSEDSAVYFCARGDY-----RRYFDLWGCGT 115
 QY 121 LV 122
 Db 116 TV 117

RESULT 8
 ID Q9UL89 PRELIMINARY; PRT; 116 AA.
 AC Q9UL89;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035025; AAD56261.1; -.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG_V; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13A898 CRC64;

Query Match 57.9%; Score 381; DB 4; Length 116;
 Best Local Similarity 64.4%; Pred. No. 2, 1e-33;
 Matches 76; Conservative 14; Mismatches 22; Indels 6; Gaps 1;

QY 5 LOSADYVKKPGASVYKSTAGYIFTSYDINWVROATGQGLEWGMNPNNSGNAGPAOKF 64
 Db 1 VQSGAEVKKPGSSVKSCAKSGTFSSYALISWVROAPGQGLEWVGRIIPILGIANYAKKF 60
 QY 65 KGRLLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 122
 Db 61 QGRVTLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 112

RESULT 9
 ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
 AC Q9GYZ2;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region (Fragment).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 NC NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Song X.T., Feng Z.Q., Guan X.H.;
 RA "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of

RT Schistosoma japonicum";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282622; AAG01452.1; -.
 DR HSSP; P01772; 2FBJ.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG_V; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FA6AB CRC64;

Query Match 56.9%; Score 374.5; DB 5; Length 119;
 Best Local Similarity 57.0%; Pred. No. 1, 1e-32;
 Matches 73; Conservative 15; Mismatches 21; Indels 19; Gaps 2;

QY 1 QVOLLGADYVKKPGASVYKSTAGYIFTSYDINWVROATGQGLEWGMNPNNSGNAGF 60
 Db 1 QVLLVSGAEVKKPGASVYKSTAGYIFTSYDINWVROAPGQGLEWVGRIIPILGIANYAKKF 60
 QY 61 AOKFKRLTLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 115
 Db 61 NOFKKRVLTTRDSTSTAYMELRLSRLSADSAYTCAR-----YDDHYCUD 107
 QY 116 -WGCGT 122
 Db 108 YWGCGT 115

RESULT 10
 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
 AC Q96GA6;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009851; AA09851.1; -.
 DR InterPro; IPR000005; HTHARC.
 DR InterPro; IPR007110; Ig_1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG_V; 1.
 DR PROSITE; PSS0041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PSS0835; IG_LIKE; 5.
 DR PROSITE; PSS00290; IG_MHC; 3.
 DR Hypothetical protein.
 SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 56.8%; Score 373.5; DB 4; Length 614;
 Best Local Similarity 59.8%; Pred. No. 1e-31;
 Matches 73; Conservative 18; Mismatches 26; Indels 5; Gaps 2;

QY 1 QVOLLGADYVKKPGASVYKSTAGYIFTSYDINWVROATGQGLEWGMNPNNSGNAGF 60
 Db 20 QMOLVSGAEVKKPGSSVKSCAKSGTFSSYALISWVROAPGQGLEWVGRIIPILGIANYAKKF 79
 QY 61 AOKFKRLTLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 120
 Db 80 AOKFKRLTLTRDSTSTAYMELRLSEEDTAVYCARCOTLLIWFGPAPYDSWGCGT 114


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OY 61 AOKFKGRLTLTRDSTSTAYMELRLSEDTAVYVCARCDTLLIMFGPAPYDSMGQGT 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFKGRLTLTRDSTSTAYMELRLSEDTAVYVCARCDTLLIMFGPAPYDSMGQGT 138
OY 121 LV 122
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 LV 140

RESULT 5
O960S0 PRELIMINARY; PRT: 159 AA.
AC O960S0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibillar protein with Ig-like domain 3
RL Submitted (JUN-2001) to the EMBL/Genbank/DBD databases.
DR EMBL; AY039025; AAK82649.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 62.2%; Score 409; DB 4; Length 159;
Best Local Similarity 64.3%; Pred. No. 3e-36;
Matches 83; Conservative 16; Mismatches 20; Indels 10; Gaps 3;

OY 1 OVQLQSAADVKKPGASVYKVSCTASGYIFTSYDINMVRQATGGLGEMGMNPNNGNAGF 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 OVQLQSAADVKKPGASVYKVSCTASGYIFTSYDINMVRQATGGLGEMGMNPNNGNAGF 79
OY 61 AOKFKGRLTLTRDSTSTAYMELRLSEDTAVYVCARCDTLLIMFGPAPYDSMGQGT 113
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFKGRLTLTRDSTSTAYMELRLSEDTAVYVCARCDTLLIMFGPAPYDSMGQGT 136
OY 114 DSMGQGTLY 122
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 DSMGQGTLY 145

RESULT 6
O9BRV0 PRELIMINARY; PRT: 500 AA.
AC O9BRV0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=prostate;
RA Straubeberg R.;
RL Submitted (APR-2001) to the EMBL/Genbank/DBD databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV LIKE; 4.
DR PROSITE; PS00290; IGV_MHC; 1.
DR Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 59.9%; Score 394; DB 4; Length 500;
Best Local Similarity 59.7%; Pred. No. 4.8e-34;
Matches 77; Conservative 13; Mismatches 27; Indels 12; Gaps 2;

OY 1 OVQLQSAADVKKPGASVYKVSCTASGYIFTSYDINMVRQATGGLGEMGMNPNNGNAGF 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 OVQLQSAADVKKPGASVYKVSCTASGYIFTSYDINMVRQATGGLGEMGMNPNNGNAGF 79
OY 61 AOKFKGRLTLTRDSTSTAYMELRLSEDTAVYVCARCDTLLIMFGPAPYDSMGQGT 113
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFKGRLTLTRDSTSTAYMELRLSEDTAVYVCARCDTLLIMFGPAPYDSMGQGT 134
OY 114 DSMGQGTLY 122
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 DSMGQGTLY 143

RESULT 7
O92SS3 PRELIMINARY; PRT: 147 AA.
AC O92SS3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice."
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain."
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 58.0%; Score 381.5; DB 11; Length 147;
Best Local Similarity 61.5%; Pred. No. 2.5e-33;
Matches 75; Conservative 14; Mismatches 26; Indels 7; Gaps 1;

OY 1 OVQLQSAADVKKPGASVYKVSCTASGYIFTSYDINMVRQATGGLGEMGMNPNNGNAGF 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 OVQLQSAADVKKPGASVYKVSCTASGYIFTSYDINMVRQATGGLGEMGMNPNNGNAGF 62
```

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Db      1 EVOLVESGAEVKKPGASVKSCKASGYTFTGYMHVWROAPGQGLEMMGNINPNSWTNYY 60
QY      61 AOKFKRLTLTRDTSTSTAYMELRLESEDTAVYYCARCOTLLIFGAPAYDSMGCGT 120
      61 AOKFKQAVTMTKDTSTSTAYMELSRLESDTAVYYCARGS-----GRGLMFPDPMGCGT 113
Db
QY      121 LV 122
      114 LV 115

RESULT 2
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95;
AC Q9UL95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -.
DR HSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
SQ
Query Match 63.9%; Score 420.5; DB 4; Length 125;
Best Local Similarity 65.6%; Pred. No. 1.3e-37;
Matches 80; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

QY      1 QVOLLQSAADVKKPGASVKSCKASGYTFTSYDINMWROATGQGLEMMGNINPNSGNAGF 60
      1 EVOLVESGAEVKKPGASVKSCKASGYTFTGYMHVWROAPGQGLEMMGNINPNSGCTNY 60
Db
QY      61 AOKFKRLTLTRDTSTSTAYMELRLESEDTAVYYCARCOTLLIFGAPAYDSMGCGT 120
      61 AOKFKQAVTMTKDTSTSTAYMELSRLESDTAVYYCARSGCGGT-AAAAGDAFPMWCGT 119
Db
QY      121 LV 122
      120 MV 121

RESULT 3
Q9UL92 PRELIMINARY; PRT; 124 AA.
ID Q9UL92;
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSP; P01772; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
SQ
Query Match 63.2%; Score 416; DB 4; Length 124;
Best Local Similarity 66.1%; Pred. No. 3.9e-37;
Matches 82; Conservative 16; Mismatches 20; Indels 6; Gaps 2;

QY      1 QVOLLQSAADVKKPGASVKSCKASGYTFTSYDINMWROATGQGLEMMGNINPNSGNAGF 60
      1 EVOLVESGAEVKKPGASVKSCKASGYTFTSYMHVWROAPGQGLEMMGNINPNSGCTSY 60
Db
QY      61 AOKFKRLTLTRDTSTSTAYMELRLESEDTAVYYCARCOTLLIFGAPY--YDSMGQ 118
      61 AOKFKQAVTMTKDTSTSTAYMELSRLESDTAVYYCARG---LYVVVPAAFSPFDYWGQ 116
Db
QY      119 GTLV 122
      117 GTLV 120

RESULT 4
Q8WY24 PRELIMINARY; PRT; 497 AA.
ID Q8WY24;
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMC6 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Gao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SMC6, a Ig-like gene which is
   down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT SEQUENCE 497 AA; 53665 MW; F24D08DFA5A6355 CRC64;
SQ
Query Match 62.4%; Score 410.5; DB 4; Length 497;
Best Local Similarity 65.6%; Pred. No. 8e-36;
Matches 80; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY      1 QVOLLQSAADVKKPGASVKSCKASGYTFTSYDINMWROATGQGLEMMGNINPNSGNAGF 60
      20 QEOLDSGAEVKKPGASVKSCKASGYTFTAYDINMWROAPGQGLEMMGNINPOTGNTTF 79

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 29.7319 Seconds
(without alignments)
1058.876 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 658
Sequence: 1 QVQLQSAADYKKGASVKV.....LLWFGPAPYDSWGQSTLV 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioid:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	428.5	65.1	119	4 Q9UL94	Q9UL94 homo sapien
2	420.5	63.9	125	4 Q9UL95	Q9UL95 homo sapien
3	416	63.2	124	4 Q9UL92	Q9UL92 homo sapien
4	410.5	62.4	497	4 Q8WY24	Q8WY24 homo sapien
5	409	62.2	159	4 Q96GSO	Q96GSO homo sapien
6	394	59.9	500	4 Q9BRV0	Q9BRV0 homo sapien
7	381.5	58.0	147	11 Q92S53	Q92S53 mus musculu
8	381	57.9	116	4 Q9UL89	Q9UL89 homo sapien
9	374.5	56.9	119	5 Q9GY22	Q9GY22 schistocoma
10	373.5	56.8	614	4 Q96GA6	Q96GA6 homo sapien
11	367.5	55.9	157	4 Q95978	Q95978 homo sapien
12	361.5	54.9	489	11 Q8VCK4	Q8VCK4 mus musculu
13	360.5	54.8	120	11 Q920E8	Q920E8 mus musculu
14	359	54.6	463	11 Q99LC4	Q99LC4 mus musculu
15	358.5	54.5	473	11 Q9D8L4	Q9D8L4 mus musculu
16	356.5	54.2	481	11 Q91WT1	Q91WT1 mus musculu

17	356	54.1	145	11 Q924Q7	Q924Q7 mus musculu
18	351.5	53.4	146	11 Q924R8	Q924R8 mus musculu
19	351	53.3	241	11 Q921A6	Q921A6 mus musculu
20	351	53.3	613	11 Q8VCX7	Q8VCX7 mus musculu
21	349.5	53.1	150	4 Q9Y298	Q9Y298 homo sapien
22	348.5	53.0	117	11 Q90XF0	Q90XF0 mus musculu
23	347.5	52.8	146	11 Q924Q8	Q924Q8 mus musculu
24	346	52.6	147	11 Q924Q5	Q924Q5 mus musculu
25	345.5	52.5	117	11 Q9QX69	Q9QX69 mus musculu
26	344	52.3	145	11 Q924Q6	Q924Q6 mus musculu
27	344	52.3	145	11 Q924R1	Q924R1 mus musculu
28	343.5	52.2	480	11 Q8K0Z4	Q8K0Z4 mus musculu
29	343	52.1	143	11 Q91V67	Q91V67 mus musculu
30	343	52.1	143	11 Q924R0	Q924R0 mus musculu
31	343	52.0	145	11 Q924Q9	Q924Q9 mus musculu
32	342	52.0	488	11 Q91WR1	Q91WR1 mus musculu
33	341	51.8	143	11 Q924Q0	Q924Q0 mus musculu
34	341	51.8	143	11 Q924P9	Q924P9 mus musculu
35	341	51.8	278	11 Q921K1	Q921K1 mus musculu
36	340.5	51.7	140	11 Q924R2	Q924R2 mus musculu
37	340.5	51.7	144	11 Q924P5	Q924P5 mus musculu
38	339.5	51.6	168	11 Q8VDC9	Q8VDC9 mus musculu
39	339	51.5	137	11 Q924R6	Q924R6 mus musculu
40	339	51.5	145	11 Q924R3	Q924R3 mus musculu
41	339	51.5	145	11 Q924R4	Q924R4 mus musculu
42	339	51.5	473	11 Q99L25	Q99L25 mus musculu
43	339	51.5	496	4 Q96DK0	Q96DK0 homo sapien
44	338.5	51.4	142	11 Q924Q1	Q924Q1 mus musculu
45	337	51.2	118	11 Q921C4	Q921C4 mus musculu

ALIGNMENTS

RESULT 1

ID Q9UL94 PRELIMINARY; PRT: 119 AA.

AC Q9UL94; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RNA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035020; AAD56256.1; -.

DR HSSP; P01810; 2FBJ.

DR InterPro; IPR007110; IG_1like.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; IG_1.

DR SMART; SM00406; IGV_1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 119

SEQUENCE 119 AA; 13205 MW; 13B64F5345FA16E CRC64;

Query Match 65.1%; Score 428.5; DB 4; Length 119;

Best Local Similarity 65.6%; Pred. No. 1.6e-38;

Matches 80; Conservative 16; Mismatches 19; Indels 7; Gaps 1;

1 QVQLQSAADYKKGASVKVCTASGTFITSYDINWVROAGCGLEWGMGNPNPSSGNAGF 60

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RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A93708; GYMS11.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC65ED0BF CRC64;

Query Match 51.1%; Score 336.5; DB 1; Length 121;
Best Local Similarity 50.8%; Pred. No. 2.8e-29;
Matches 61; Conservative 23; Mismatches 31; Indels 5; Gaps 1;

Qy 1 OVQLQSADVKKPGASVYVSGTASGYFTSYDINMVRQATGQGLEWGMGNPNSGNAGF 60
Db 1 EAOLQOSGAELVRPGTSVKISCAAGYFTTNWIGWKEPGRGLEWIDDIIPGGGFTNY 60

Qy 61 AQKFKGRLLTRDSTSTAYMELRLRLESEDTAVVYVCARCDTLLIFGPAPYDSSGQGT 120
Db 61 NNLMKSKATLTIDTSSSTAYIQLSSLTSDSAIYHCARG-----IYNSSPFDSSGQGT 115

RESULT 15
HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Peckind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00539; AAA38172.1; -.
DR PIR: A02038; G2MS43.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19

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FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5081BF44B8BC9 CRC64;

Query Match 50.6%; Score 333; DB 1; Length 137;
Best Local Similarity 54.2%; Pred. No. 7.8e-29;
Matches 65; Conservative 17; Mismatches 30; Indels 8; Gaps 1;

Qy 1 OVQLQSADVKKPGASVYVSGTASGYFTSYDINMVRQATGQGLEWGMGNPNSGNAGF 60
Db 20 OVQLQDPGAEFVYKPGASVYVSGTASGYFTSYLMMVNRQATGQGLEWIDDIIPGGGFTNY 79

Qy 61 AQKFKGRLLTRDSTSTAYMELRLRLESEDTAVVYVCARCDTLLIFGPAPYDSSGQGT 120
Db 80 NEHFRSKATLTIDKPSSTAYIQLSSLTSDSAIYHCARG-----YRLGRYFDYWGQGT 131

Search completed: December 30, 2003, 10:55:53
Job time : 7.54102 secs

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QY 61 AOKFKGRLLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 120
 DB 61 AOKFKGRLLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 112
 QY 121 LV 122
 DB 113 LV 114

RESULT 12

HVS2_MOUSE
 ID HVS2_MOUSE STANDARD; PRT; 117 AA.
 AC P06327;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region VH58 A1/A4 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8509340; PubMed=2578321;
 RA Yancopoulos G.D., Alt F.W.;
 RT "Developmentally controlled and tissue-specific expression of
 RL Cell 40:271-281 (1985).
 CC -----
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DR EMBL: M13787; AAA38499.1; -
 DR PIR: A02029; HYMSA1.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR007110; IG_LIKE.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 19 IG HEAVY CHAIN V REGION VH58 A1/A4.
 FT DOMAIN 20 117 FRAMEWORK-1.
 FT DOMAIN 50 49 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 54 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12971 MW; 880BC13885DDFC9D CRC64;

Query Match 51.8%; Score 341; DB 1; Length 117;
 Best Local Similarity 63.3%; Pred. No. 9e-30;
 Matches 62; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLDLSADYKPKGASVKSCTASGYIFTSYDINVRQATGGLGEMGMNPNNSGNAF 60
 DB 20 QVQLDLSADYKPKGASVKSCTASGYIFTSYDINVRQATGGLGEMGMNPNNSGNAF 79
 QY 61 AOKFKGRLLTRDSTSTAYMELRLRLESEDTAVVYCAR 98
 DB 80 NEKFKGKATLTVKSSATYMQLSLTSENSAVYFCAR 117

RESULT 13

HVS0_MOUSE
 ID HVS0_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region AC38 15.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84182519; PubMed=6201362;
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
 RT "A V region determinant (idiotope) expressed at high frequency in B
 RT lymphocytes is encoded by a large set of antibody structural genes."
 RL EMBL J.31517-523 (1984).
 DR PIR: A02037; MEMS15.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR007110; IG_LIKE.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 99 105 D SEGMENT.
 FT DOMAIN 106 120 J SEGMENT.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON TER 120 120
 SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 51.5%; Score 339; DB 1; Length 120;
 Best Local Similarity 53.3%; Pred. No. 1.5e-29;
 Matches 65; Conservative 18; Mismatches 33; Indels 6; Gaps 1;

QY 1 QVQLDLSADYKPKGASVKSCTASGYIFTSYDINVRQATGGLGEMGMNPNNSGNAF 60
 DB 1 QVQLDLSADYKPKGASVKSCTASGYIFTSYDINVRQATGGLGEMGMNPNNSGNAF 60
 QY 61 AOKFKGRLLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 120
 DB 61 NEKFKGKATLTVKSSATYMQLSLTSENSAVYFCARCDTTLIIFGPAPYDSWGCGT 114
 QY 121 LV 122
 DB 115 TV 116

RESULT 14

HV01_MOUSE
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 RT region of immunoglobulin heavy chain MPC11."
 RL Nucleic Acids Res. 8:3591-3601 (1980).
 RN [2]
 RP REVISIONS.
 RA Zakut R., Cohen J., Givol D.;

RA Kehry M.R., Fuhman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424(1982).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN HAS ALSO BEEN DETERMINED.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP: P01789; MEMS4E.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 KM Immunoglobulin V region; Glycoprotein.
 FT DOMAIN 1 116
 FT DISULFID 22 96
 FT CARBOHYD 55 55
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE47E41 CRC64;
 Query Match 52.7%; Score 346.5; DB 1; Length 117;
 Best Local Similarity 55.7%; Pred. No. 2.3e-30;
 Matches 68; Conservative 17; Mismatches 28; Indels 9; Gaps 2;
 QY 1 QVOLLQSAADVKKPGASVKSCTASGYIFTSYDINWVRQATGGLEMGMMNPNSGNAGF 60
 DB 1 EVQLQSGPELVKPGASVSKSCASGYTFDYMKWKVQSHGKSLKLEIGINPNNGTSTY 60
 QY 61 AQKFKRLTLTRDTSTSTAYMELRLRLESEDTAVYVCARCDTLLIWFGPAPYYDSMGQT 120
 DB 61 NQKFKKATLTVDKSSSTAYMQLSLTPEFAVYCARSD-----GYDWMFYWG 111
 QY 121 LV 122
 DB 112 TV 113
 RESULT 10
 HV48_MOUSE STANDARD; PRT; 138 AA.
 ID HV48_MOUSE STANDARD; PRT; 138 AA.
 AC P03980;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region TEPC 1017 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=64248078; PubMed=6429663;
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
 RA Tucker P.W.;
 RT "Illegitimate recombination generates a class switch from C mu to C
 RT delta in an Igd-secreting plasmacytoma.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 138
 FT DOMAIN 21 49
 IG HEAVY CHAIN V REGION TEPC 1017.
 FRAMEWORK-1.

FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DOMAIN 118 127
 FT DOMAIN 128 138
 FT DISULFID 41 115
 FT NON TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C69078BE CRC64;
 Query Match 52.4%; Score 344.5; DB 1; Length 138;
 Best Local Similarity 55.2%; Pred. No. 4.6e-30;
 Matches 69; Conservative 17; Mismatches 26; Indels 13; Gaps 2;
 QY 1 QVOLLQSAADVKKPGASVKSCTASGYIFTSYDINWVRQATGGLEMGMMNPNSGNAGF 60
 DB 20 QVQLQPGAEVLVPGASVQLSCASGHTFTNTHHWKQKPGGLEIGIGINPNDGRSNV 79
 QY 61 AQKFKRLTLTRDTSTSTAYMELRLRLESEDTAVYVCARCDTLLIWFGPAPYYD---SWG 117
 DB 80 NQKFKKATLTVDKSSSTAYMQLSLTPEFAVYCARSD-----GYDWMFYWG 129
 QY 118 QGTLV 122
 DB 130 QGTLV 134
 RESULT 11
 HV00_MOUSE STANDARD; PRT; 114 AA.
 ID HV00_MOUSE STANDARD; PRT; 114 AA.
 AC P01741;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-FEB-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region (Anti-arsenate antibody).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=79195438; PubMed=109536;
 RA Capra J.D., Nisonoff A.;
 RT "Structural studies on induced antibodies with defined idiotypic
 RT specificities. VII. The complete amino acid sequence of the heavy
 RT chain bearing a cross-reactive idiotype.";
 RL J. Immunol. 123:279-284(1979).
 CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
 CC REGION SEQUENCE.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02022; GIMSA.
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 106
 FT DISULFID 114 114
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12555 MW; 99D8F0B6A9F4BE CRC64;
 Query Match 52.3%; Score 344; DB 1; Length 114;
 Best Local Similarity 55.7%; Pred. No. 4.2e-30;
 Matches 68; Conservative 23; Mismatches 23; Indels 8; Gaps 2;
 QY 1 QVOLLQSAADVKKPGASVKSCTASGYIFTSYDINWVRQATGGLEMGMMNPNSGNAGF 60
 DB 1 EVQLQSGAEVLVPGASVSKSCASGYTFSSYELVWVQAPQGLDLGIYSSSSAYPNV 60

FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA: 15419 MW: 1857DD4FD0C9F465 CRC64;

Query Match 54.1%; Score 356; DB 1; Length 139;
Best Local Similarity 57.5%; Pred. No. 2.7e-31;
Matches 69; Conservative 20; Mismatches 25; Indels 6; Gaps 2;

QY 1 OVQLQASADYKKPGASVYVSCASGYFTSYDINMWAOATGQGLEMMGNPNNGNAGF 60
DB 20 OVQLQAPAEVLVKGASVYKLSCKASGYFTSYDINMWAOATGQGLEMMGNPNNGNAGF 79
QY 61 AOKFKRLTLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLTIWFGPAPYDSWGCGT 120
DB 80 NEKFKSKATLTVDKSSATYMLRLSLTSEDSAVVYCARVD-----YGC-SSYFDVWGCGT 133

RESULT 7

HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Slekewitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J. 3:517-523(1984).
DR PIR; A02040; MMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA: 12934 MW: 94F7BEE4C762A018 CRC64;

Query Match 53.5%; Score 352; DB 1; Length 118;
Best Local Similarity 56.6%; Pred. No. 6e-31;
Matches 69; Conservative 17; Mismatches 28; Indels 8; Gaps 2;

QY 1 OVQLQASADYKKPGASVYVSCASGYFTSYDINMWAOATGQGLEMMGNPNNGNAGF 60
DB 1 EVQLQSGPELVKPGASVKISCKASGYFTDYYMHWKSHGSKLEWIGDINPNNGCTSY 60
QY 61 AOKFKRLTLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLTIWFGPAPYDSWGCGT 120
DB 61 NOKFKSKATLTVDKSSATYMLRLSLTSEDSAVVYCARVD-----GYGIDP-FDVWGCT 112
QY 121 LV 122
RX

DB 113 TV 114

RESULT 8

HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
WHICH OCCUR IN THE D AND J SEGMENTS.
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR; A26242; MMSJ5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA: 13024 MW: 292E2AF4BE447E41 CRC64;

Query Match 52.8%; Score 347.5; DB 1; Length 117;
Best Local Similarity 55.7%; Pred. No. 1.8e-30;
Matches 68; Conservative 17; Mismatches 28; Indels 9; Gaps 2;

QY 1 OVQLQASADYKKPGASVYVSCASGYFTSYDINMWAOATGQGLEMMGNPNNGNAGF 60
DB 1 EVQLQSGPELVKPGASVYKLSCKASGYFTDYYMHWKSHGSKLEWIGDINPNNGCTSY 60
QY 61 AOKFKRLTLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLTIWFGPAPYDSWGCGT 120
DB 61 NOKFKSKATLTVDKSSATYMLRLSLTSEDSAVVYCARVD-----RYW-----YFDVWGAGT 111

QY 121 LV 122
DB 112 TV 113

RESULT 9

HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M0PC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8311846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marek-Rothstein A.,
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region, Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 56.8%; Score 373.5; DB 1; Length 120;
Best Local Similarity 58.0%; Pred. No. 3e-33;
Matches 69; Conservative 22; Mismatches 23; Indels 5; Gaps 1;

QY 2 VQLQGSADYKPKGASVYKSCASGYITFTSYDINWVRQATGGLGEMWGMNPNNSGNAGFA 61
DB 1 VQLQGSAGELVRASSVYKMSCKASGYFTSYGINWVRQPGGLEWIGYINPGNGTKYN 60
QY 62 QKFKGRLTLTRDTSTAYMELRLSEEDTAVYVCARCDTLLIFGPAFYDSMGCGT 120
DB 61 EKFKGKTLTLVDKSSSTAYMQLRSLTSEDSAVYFCARSH-----YVGGSYDFDYGCGT 114

RESULT 5
HVO2_MOUSE STANDARD; PRT; 140 AA.
ID HVO2_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Bates P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: J00493; AAA38128.1; -.
CC PIR: A94264; HWM5G7.
CC

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DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region, Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DASCE8 CRC64;

Query Match 55.1%; Score 362.5; DB 1; Length 140;
Best Local Similarity 56.7%; Pred. No. 5.4e-32;
Matches 68; Conservative 22; Mismatches 25; Indels 5; Gaps 1;

QY 1 QVQLQSADYKPKGASVYKSCASGYITFTSYDINWVRQATGGLGEMWGMNPNNSGNAGF 60
DB 20 EVQLQGSAGELVRASSVYKMSCKASGYFTSYGINWVRQPGGLEWIGYINPGNGTKYN 79
QY 61 AOKFKGRLTLTRDTSTAYMELRLSEEDTAVYVCARCDTLLIFGPAFYDSMGCGT 120
DB 80 NEKFKGKTLTLVDKSSSTAYMQLRSLTSEDSAVYFCARSH-----YVGGSYDFDYGCGT 134

RESULT 6
HVO7_MOUSE STANDARD; PRT; 139 AA.
ID HVO7_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/16e-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reih M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
CC (NPB ANTIBODIES).
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: J00529; AAA38170.1; -.
CC PIR: A90809; MMS18.
CC PDB: 1A6U; 27-MAY-98.
CC PDB: 1A6W; 15-JUL-98.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.

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QY      61 A Q F K R L T I T R D S T S T A M E L R R L E E D T A V Y Y C A R   98
        ||| : | : | | | | | | | | | | : | | | | |
Db      80 A Q F G R V S T R D P S I S T A M E L S R L R S D D T V Y Y C A R  117
```

RESULT 2	
HV1B_HUMAN	
ID	STANDARD;
HV1B_HUMAN	PRT; 117 AA

DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V-I region Hg3 precursor.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;

RX MEDLINE=83144028; PubMed=6298778;

RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
RL
CC -1: SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC entities requires a license agreement (See <http://www.isb-sb.ch/announce>
CC or send an email to license@isb-sb.ch).

DR EMBL; J00240; AAA52988.1; -
DR PIR; A02024; HVHUNG.

DR HSSP; POL172; ZFB4.
DR GO; GO:000576; C:extracellular; NAS

DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.

DR	InterPro; IPR007110; Ig-like
DR	InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v
DR Pfam; PF00047; Ig_1.

```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
```

Accession	Protein	Length	Signal
KM	Immunoglobulin V region; Signal.	19	
FT	SIGNAL	1	

FT	CHAIN	20	117	IG HEAVY
FT	DOMAIN	20	117	IG-LIKE

FT	20	12946	MM.	3D3E02ECC60CD1EE7	CBC6C4
NON TER	117				
SEQUENCE	117	AB.			

Query Match	59.3%	Score 390;	DB 1;	Length 117;
Best Local Similarity	74.5%	Pred. No. 4.9e-35;		
Matches 7;	Conservative 14;	Mismatches 0;	Gaps 0	

[illegible]

```

Oy      61 AQAQFKGALTTRDSTSTAYMELRLSESDTAYYYCAR 98
        |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      80 AQAQFGKVTMRDSTSTAYMELSSLRSDTAYYYCAR 117

```

RESULT 3		
HVIC_HUMAN	STANDARD;	PRT; 147 AA
ID HVIC_HUMAN		
AC P01744		
DT 21-JUL-1986	(Rel. 01, Created)	
DT 16-OCT-2001	(Rel. 40, Last sequence update)	

DT 15-SEP-2003 (Rel. 42, last annotation update)
DE 1g heavy chain V-I region ND precursor (Fragmente).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Carniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 111

RN
RP
RX
RA
MEDLINE=83065234; PubMed=6815656;
Kenten J H., Molgaard H V., Houghton M., Derbyshire R.B., Viney J.
[1]
SEQUENCE FROM N.A.

RA Bell L.O., Gould H.U.?
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).
[2]

RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and develop-
PL

CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN

CC -1- SMILARITY: Contains 1 immunoglobulin-like domain
HSP: P01789; IMCP
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.

```
DR InterPro: IPR003006; Ig_MHC.  
DR InterPro: IPR003596; Ig_v.
```

DR PFam; PF00047; Ig; 1.
DR SMART: SM00406; IGV: 1.
DR

DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal: Pyrrolidone carboxylic acid.

NAME	NUMBER	DATE	TIME	LOCATION	REMARKS
FT	1	19			
FT	20	147			
FT	20	147			

FT	20	IG-LIKE.
MOD	20	DYBOLITONE CARBOXYLIC ACID
DOMAIN	131	
CHAIN	17	
FT	20	IG-HVARY CHAIN & 2 MODULON

FT	MODRES	20	20	FINRODIDONE CARBONATE
FT	DISULFID	41	115	
FT	DISULFID	21	21	T 2 V (IN BEE 2)

FT	21	1 - 2 V (IN REF. 2) .
CONFLICT	21	1H -> HI (IN REF. 2) .
FT	53	CV (IN REF. 2)
CONFLICT	53	WC (IN REF. 2)

FT	CONFLICT	67	68	VG - 5 GV (IN REF. 2)
FT	CONFLICT	125	125	MISSING (IN REF. 2).

FT	NON TER	147	147
SEQUENCE	147 AA;	16491 MW;	948F9F72A5366C20 CFE

Query Match 58.5%; Score 385; DB 1; Length 147

Best Local Similarity 56.2%; Pred. No. 2.2e-34;
Matches 73; Conservative 19; Mismatches 24; Indels 14; Gaps 3.

Qy 1 QVOLLQSADYVKKPGASVKSVCSTASGYIFTSYDINWVRQTGCGLEMMCHNPNNSGNAGF 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
20 OTOLVOSGEVRKPGASVRSCKSGSYTFDSYLHMIROAPGHGEGEMVGGINPNSGGTNY 79

```

61 AOKFGRLLITRDITSTAYAMELRRIESEDPAVYVCARDOTLLIINGPAPY-----113
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
80 APRFGCRVMTTRDAFSFSTAYMDLRSLRSDSDAVFYCAKSDP---FW---SDYYNFDQSYT 133
Db

```

Qy	114	-DSWGQGLV	122
	134	LDVWGQGLV	143
Db			

RESULT 4	STANDARD.	DPT.
HV03_MOUSE		120 AA
TS - HV03_MOUSE		

DT 21-JUL-1986 (rel. 01, create)
 DT 21-JUL-1986 (rel. 01, last sequence update)
 DT 15-SEP-2003 (rel. 42, last annotation update)
 DE 1g heavy chain V region 36-65.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.54102 Seconds
(without alignment)

877.119 Million cell updates/sec

Title: US-09-674-752-40

Sequence: 1 QVQLQSADVKKPKGASVY.....LLWFGPAPYYDSWGQGLTV 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	392	59.6	117	1	HVIG_HUMAN
2	390	59.3	117	1	HV1B_HUMAN
3	385	58.5	147	1	HVIC_HUMAN
4	373.5	56.8	120	1	HV03_MOUSE
5	362.5	55.1	140	1	HV02_MOUSE
6	356	54.1	139	1	HV07_MOUSE
7	352	53.5	118	1	HV51_MOUSE
8	347.5	52.8	117	1	HV13_MOUSE
9	346.5	52.7	117	1	HV12_MOUSE
10	344.5	52.4	138	1	HV48_MOUSE
11	344	52.3	114	1	HV00_MOUSE
12	341	51.8	117	1	HV02_MOUSE
13	339	51.5	120	1	HV50_MOUSE
14	336.5	51.1	121	1	HV01_MOUSE
15	333	50.6	137	1	HV11_MOUSE
16	329	50.0	117	1	HV09_MOUSE
17	323	49.1	117	1	HV14_MOUSE
18	322	48.9	117	1	HV1A_HUMAN
19	319.5	48.6	125	1	HV1F_HUMAN
20	316	48.0	117	1	HV06_MOUSE
21	315.5	47.9	136	1	HV15_MOUSE
22	315	47.9	117	1	HV04_MOUSE
23	307	46.7	117	1	HV10_MOUSE
24	307	46.7	117	1	HV49_MOUSE
25	303	46.0	117	1	HV05_MOUSE
26	301	45.7	120	1	HV1H_HUMAN
27	300.5	45.7	119	1	HV31_HUMAN
28	299	45.4	119	1	HV37_MOUSE
29	296.5	45.1	121	1	HV3J_HUMAN
30	294	44.7	119	1	HV38_MOUSE
31	293	44.5	117	1	HV3O_HUMAN
32	291.5	44.3	120	1	HV3E_HUMAN
33	291	44.2	119	1	HV40_MOUSE

34	290	44.1	122	1	HV3G_HUMAN	P01768	homo sapien
35	290	44.1	122	1	HV3H_HUMAN	P01769	homo sapien
36	290	43.9	136	1	HV16_MOUSE	P01783	mus musculus
37	289	43.9	120	1	HV3U_HUMAN	P01782	homo sapien
38	284	43.2	114	1	HV3B_HUMAN	P01772	homo sapien
39	282	42.9	126	1	HV3K_HUMAN	P01772	homo sapien
40	281	42.7	114	1	HV01_CANFA	P01784	canis fam1
41	280.5	42.6	115	1	HV3D_HUMAN	P01765	homo sapien
42	278	42.2	119	1	HV3P_HUMAN	P01777	homo sapien
43	278	42.2	124	1	HV1E_HUMAN	P01761	homo sapien
44	276.5	42.0	117	1	HV42_MOUSE	P01812	mus musculus
45	275	41.8	119	1	HV3M_HUMAN	P01774	homo sapien

ALIGNMENTS

```
RESULT 1
HVIG_HUMAN          STANDARD;          PRT;          117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zeng S.Q.,
RA Ono H., Fukushima S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
heavy-chain locus.";
RL EMBL J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: X07448; -; NOT_ANNOTATED_CDS.
DR PIR: S00476; HVH035.
DR HSSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS00835; IG_LIKE_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL          1
FT CHAIN           20 117
FT DOMAIN          20 >117
FT NON_TER        117 117
SQ SEQUENCE       117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
Query Match          59.6%; Score 392; DB 1; Length 117;
Best Local Similarity 75.5%; Pred. No. 3e-35;
Matches 74; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
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C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 465.5; DB 2; Length 127;
Best Local Similarity 71.9%; Pred. No. 1.7e-37;
Matches 92; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

QY 1 QVQLQSAADYVKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60
DB 1 QVQWVSGAEVKKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNSSGNTGY 60
QY 61 AOKFKGRLLTRDTSSTAYMELRLSESDTAIVYCARCDTLLIWFPAPIYDSMGQGT 114
DB 61 AOKFKGRVMTMTNTSISTAYMELSLRSEDTAIVFCARA-----LSIGVAIRGYVALD 115

QY 115 SWGCGTIV 122
DB 116 VMGCGTTV 123

RESULT 3

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596

R:Clainier, A.M.; Gauchier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31596

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <CUI>

A:Cross-references: EMBL:214166; NID:g30996; PIDN:CAA78535.1; PID:g30997

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 452; DB 2; Length 132;
Best Local Similarity 71.3%; Pred. No. 3.4e-36;
Matches 87; Conservative 12; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVQLQSAADYVKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60
DB 20 QVQLVSGAEVKKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNSSGNTGY 79
QY 61 AOKFKGRLLTRDTSSTAYMELRLSESDTAIVYCARCDTLLIWFPAPIYDSMGQGT 120
DB 80 AOKFKGRVMTMTNTSISTAYMELSLRSEDTAIVYLAKE-----AP---AWGCGT 125

QY 121 LV 122
DB 126 MV 127

RESULT 4

Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26918

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

A:Title: The repertoire of human germline VH sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:212317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 449; DB 2; Length 98;
Best Local Similarity 84.7%; Pred. No. 4.9e-36;
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQSAADYVKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNSSGNTGY 60
QY 61 AOKFKGRLLTRDTSSTAYMELRLSESDTAIVYCAR 98
DB 61 AOKFKGRVMTMTNTSISTAYMELSLRSEDTAIVYCAR 98

RESULT 5

S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human

C:Species: Homo sapiens (man)

C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999

C:Accession: S49530

R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A:Description: Molecular characterization of natural human anti-Sm autoantibodies.

A:Reference number: S48797

A:Accession: S49530

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <MAH>

A:Cross-references: EMBL:246348; NID:g560839; PIDN:CAA66467.1; PID:g560840

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 447; DB 2; Length 135;
Best Local Similarity 69.7%; Pred. No. 1e-35;
Matches 85; Conservative 11; Mismatches 16; Indels 10; Gaps 1;

QY 1 QVQLQSAADYVKPKGASVKSCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60
DB 20 QVQLVSGAEVKKPKGASVKSCTASGYFTGYMHMVRQATGCGLEMMGMNPNSSGNTGY 79
QY 61 AOKFKGRLLTRDTSSTAYMELRLSESDTAIVYCARCDTLLIWFPAPIYDSMGQGT 120
DB 80 AOKFKGRVMTMTNTSISTAYMELSLRSDTAIVYCARITG-----YTWGCGT 129

QY 121 LV 122
DB 130 LV 131

RESULT 6

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defios, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23623

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <OLB>

A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 443; DB 2; Length 171;
Best Local Similarity 65.6%; Pred. No. 3.2e-35;
Matches 84; Conservative 15; Mismatches 17; Indels 12; Gaps 2;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 11.6946 Seconds

(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-40

Sequence: 1 QVQLVDSADVKPKGASVKV.....LLMFAPYDSWGQGLV 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	72.5	136	2 S31600	Ig heavy chain V r
2	465.5	70.7	127	2 S34014	Ig heavy chain V r
3	452	68.7	132	2 S31596	Ig heavy chain V r
4	449	68.2	98	2 S26918	Ig heavy chain V r
5	447	67.9	135	2 S49530	Ig heavy chain V r
6	443	67.3	171	2 S23623	Ig heavy chain V r
7	442	67.2	110	2 PH1670	Ig heavy chain V r
8	441	67.0	118	2 S36265	Ig heavy chain V r
9	436.5	66.3	123	2 D33548	Ig heavy chain V-1
10	431.5	65.6	122	2 S36271	Ig heavy chain V r
11	430.5	65.4	129	2 S46393	Ig heavy chain V r
12	429.5	65.3	129	2 S36260	Ig heavy chain V r
13	421.5	64.1	129	2 A33548	Ig heavy chain V-1
14	420	63.8	124	2 S19665	Ig heavy chain V r
15	417.5	63.4	121	2 S20783	Ig heavy chain V r
16	416.5	63.3	142	2 S19245	Ig heavy chain pre
17	414	62.9	98	2 S26938	Ig heavy chain V r
18	414	62.9	117	2 S31680	Ig heavy chain V r
19	414	62.9	117	2 S18551	Ig heavy chain V r
20	413.5	62.8	142	2 A32483	Ig heavy chain V r
21	410.5	62.4	109	2 PH1668	Ig heavy chain V r
22	408.5	62.1	148	2 S29257	Ig heavy chain V r
23	407.5	61.9	160	2 PH0105	anti-PR2 erythrocy
24	406	61.7	98	2 S26912	Ig heavy chain V r
25	406	61.7	132	2 S46394	Ig heavy chain V r
26	405	61.6	116	2 PH0959	Ig heavy chain V r
27	402.5	61.2	125	2 PH0957	Ig heavy chain V r
28	401	60.9	104	2 S69899	Ig heavy chain V r
29	401	60.9	114	2 PH1667	Ig heavy chain V r

30	400	60.8	120	2 PH0962	Ig heavy chain V r
31	399	60.6	98	2 S26919	Ig heavy chain V r
32	398.5	60.6	126	2 I44151	Ig heavy chain V r
33	398	60.5	110	2 PH1669	Ig heavy chain V r
34	397.5	60.4	125	2 S68170	Ig heavy chain V r
35	397	60.3	128	2 PH0952	Ig heavy chain V r
36	397	60.3	132	2 PH0954	Ig heavy chain V r
37	395.5	60.1	111	2 S26792	Ig heavy chain V r
38	395	60.0	98	2 S26920	Ig heavy chain V r
39	394	59.9	118	2 PH1666	Ig heavy chain V r
40	393.5	59.8	133	2 C33548	Ig heavy chain V-1
41	393.5	59.8	627	2 S14683	Ig mu chain precu
42	393	59.7	117	2 S18553	Ig heavy chain V r
43	393	59.7	122	2 PH0958	Ig heavy chain V r
44	392	59.6	117	1 HVH035	Ig heavy chain pre
45	392	59.6	136	2 PH0960	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S31600
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31600

R:Clisnlier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31600

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.5% Score 477; DB 2; Length 136;

Best Local Similarity 74.6% Pred. No. 1.4e-38;

Matches 91; Conservative 9; Mismatches 12; Indels 10; Gaps 2;

Qy	1	QVQLVDSADVKPKGASVKVCTASGYIFTSYDINVRQATGQGLEWMGMNPNQNA	60
Db	20	QVQLVDSADVKPKGASVKVCTASGYIFTSYDINVRQATGQGLEWMGMNPNQNA	79
Qy	61	AQRFKGRITRTSTSTAMERLSEEDTAVYCCARCDTLLIMFGPAPYDSWGQGT	120
Db	80	AQRFKGRITRTSTSTAMERLSEEDTAVYCCARCDTLLIMFGPAPYDSWGQGT	129
Qy	121	LV 122	
Db	130	WV 131	

RESULT 2

S34014
Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C:Accession: S34014; S30535

R:Marlette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; WUID:93209281; PMID:7681398

A:Accession: S34014

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127 <MAR>

A:Cross-references: EMBL:Z18321

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION NUMBER: US/08/526,136
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
TYPE: amino acid
STRADEDNESS: N/A
TOPOLOGY: N/A
US-08-526-136-13

Query Match 32.8%; Score 44; DB 3; Length 466;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 GCGAYEDVWSGEYP 16
||| | | | |
Db 42 GCGAYPOVPSGYP 55

Search completed: December 30, 2003, 11:05:34
Job time : 3.41883 secs

Query Match 33.2%; Score 44.5; DB 4; Length 105;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 DGGGAYEDVWSGEYP 16
||||| : : : : :
6 DGGGGG--IMGGWMP 18

RESULT 11
US-09-252-991A-19413

; Sequence 19413, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19413
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19413

Query Match 33.2%; Score 44.5; DB 4; Length 217;
Best Local Similarity 38.5%; Pred. No. 54;
Matches 10; Conservative 3; Mismatches 6; Indels 7; Gaps 1;

QY 3 GGGAYEDVWSGEY-----PEYYAM 21
||||| : : : : :
53 GGGSVRDMLGHPPLTWHRHPEYAL 78

RESULT 12

US-09-343-011B-1
; Sequence 1, Application US/09343011B
; Patent No. 6300473
; GENERAL INFORMATION:
; APPLICANT: Stephanie Richard
; TITLE OF INVENTION: SLIM-1 AND SLIM-2; NOVEL
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343.011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-343-011B-1

Query Match 33.2%; Score 44.5; DB 4; Length 349;
Best Local Similarity 36.7%; Pred. No. 93;
Matches 11; Conservative 2; Mismatches 6; Indels 11; Gaps 2;

QY 1 DGGGAYEDVWSGEY-----PEY 19
||||| : : : : :
274 DGYGGEYDQTYEAYDNSYVTPQSVPEY 303

RESULT 13
US-09-157-370-1
; Sequence 1, Application US/09157370A

; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Stefan
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-157-370-1

Query Match 32.8%; Score 44; DB 3; Length 117;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAYEDVW 11
||||| : : : : :
DB 98 GGGGGEYFDYW 107

RESULT 14

US-09-328-352-5411
; Sequence 5411, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5411
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5411

Query Match 32.8%; Score 44; DB 4; Length 229;
Best Local Similarity 57.1%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGAYEDVWSGEYP 16
||||| : : : : :
DB 57 GGGSVRDMLGHP 70

RESULT 15

US-08-526-136-13
; Sequence 13, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

```

;
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,846
; FILING DATE: 09-FEB-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 9-027015
; FILING DATE: 10-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-024045
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 053466/0225
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-020-846-68

Query Match 33.6%; Score 45; DB 4; Length 421;
Best Local Similarity 62.5%; Pred. No. 98;
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Oy 1 DGG--GGAYEDVWSGE 14
Db 82 DGGCGGAYDIGSGE 97

RESULT 10
US-09-205-258-745
; Sequence 745, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 745
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-745
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/ LENGTH: 285
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-7483

Query Match      33.6%; Score 45; DB 4; Length 285;
Best Local Similarity 42.9%; Pred. No. 62;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCGAYEDVWSGEYPEYAMDV 23
DB      68 GHGRSSQVWDGHDMDHYADDV 88

RESULT 6
US-09-252-991A-31155
; Sequence 31155, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31155
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31155

Query Match      33.6%; Score 45; DB 4; Length 338;
Best Local Similarity 42.9%; Pred. No. 76;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCGAYEDVWSGEYPEYAMDV 23
DB      121 GHGRSSQVWDGHDMDHYADDV 141

RESULT 7
US-09-020-846-69
; Sequence 69, Application US/09020846
; Patent No. 6322965
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kenjiro
; APPLICANT: KASHIMAKUMA, Tomiko
; APPLICANT: CHIBA, Yukie
; APPLICANT: YAGI, Shintaro
; APPLICANT: HASEGAWA, Akira
; TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,846
; FILING DATE: 09-FEB-1998
; CLASSIFICATION: 424
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 9-027015
/ FILING DATE: 10-FEB-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 8-024045
/ FILING DATE: 09-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wegner, Harold C.
/ REGISTRATION NUMBER: 25,258
/ REFERENCE/DOCKET NUMBER: 053466/0225
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 672-5300
/ TELEFAX: (202) 672-5399
/ INFORMATION FOR SEQ ID NO: 69:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 396 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-020-846-69

Query Match      33.6%; Score 45; DB 4; Length 396;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY      1 DGG--GAYEDVWSGE 14
DB      67 DGGCAGAYDVIGSGE 82

RESULT 8
US-09-252-991A-30606
; Sequence 30606, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30606
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30606

Query Match      33.6%; Score 45; DB 4; Length 410;
Best Local Similarity 34.5%; Pred. No. 95;
Matches 10; Conservative 5; Mismatches 8; Indels 6; Gaps 1;

QY      1 DGGGAYE-----DVWSGEYPEYAMDV 23
DB      337 DGDGDHDMPLWLCVWGTGSGFLYKLDL 365

RESULT 9
US-09-020-846-68
; Sequence 68, Application US/09020846
; Patent No. 6322965
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kenjiro
; APPLICANT: KASHIMAKUMA, Tomiko
; APPLICANT: CHIBA, Yukie
; APPLICANT: YAGI, Shintaro
; APPLICANT: HASEGAWA, Akira
; TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29606

Query Match 34.3% Score 46; DB 4; Length 1287;
Best Local Similarity 42.1%; Pred. No. 2,6e+02;
Matches 8; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GGGAYEDVMSGEYPEYVA 20
Db 326 GGGATTGCGWDTGTFKAYS 344

RESULT 3
US-07-882-329-2
Sequence 2, Application US/07882329

Patent No. 5108765

GENERAL INFORMATION:

APPLICANT: Ozaki, Eiichi

APPLICANT: Sakimae, Akihiro

APPLICANT: Numazawa, Ryozo

TITLE OF INVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT

TITLE OF INVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT

TITLE OF INVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE

TITLE OF INVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID

TITLE OF INVENTION: TRANSFORMANTS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/882,329

FILING DATE: 19920513

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7005-046-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Pseudomonas putida

STRAIN: MR-2068 (FERM BP-3846)

US-07-882-329-2

Query Match

Best Local Similarity 33.6%; Score 45; DB 1; Length 276;

Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GGGAYEDVMSGEYPEYVA 23
Db 59 GGGSSQVWDGDMHDYADV 79

RESULT 4
US-08-183-213-2

Sequence 2, Application US/08183213
Patent No. 5482847

GENERAL INFORMATION:

APPLICANT: Ozaki, Eiichi

APPLICANT: Sakimae, Akihiro

APPLICANT: Numazawa, Ryozo

TITLE OF INVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT

TITLE OF INVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT

TITLE OF INVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE

TITLE OF INVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID

TITLE OF INVENTION: TRANSFORMANTS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/183,213

FILING DATE: 14-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 07/882,329

FILING DATE: 13-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7005-046-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Pseudomonas putida

STRAIN: MR-2068 (FERM BP-3846)

US-08-183-213-2

Query Match

Best Local Similarity 33.6%; Score 45; DB 1; Length 276;

Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GGGAYEDVMSGEYPEYVA 23
Db 59 GGGSSQVWDGDMHDYADV 79

RESULT 5
US-09-328-352-7483

Sequence 7483, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7483

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 2.3355 Seconds
(Without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-30

Perfect score: 134
Sequence: 1 DGGGAYEDVSGEYPEYAMDV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCtUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	46	34.3	659 4 US-09-562-737-12	Sequence 12, Appl
2	46	34.3	1287 4 US-09-252-991A-29606	Sequence 29606, A
3	45	33.6	276 1 US-07-882-329-2	Sequence 2, Appl1
4	45	33.6	276 1 US-08-183-213-2	Sequence 2, Appl1
5	45	33.6	285 4 US-09-328-352-7483	Sequence 7483, Ap
6	45	33.6	338 4 US-09-252-991A-31155	Sequence 31155, A
7	45	33.6	396 4 US-09-020-846-69	Sequence 69, Appl
8	45	33.6	410 4 US-09-252-991A-30606	Sequence 30606, A
9	45	33.6	421 4 US-09-020-846-68	Sequence 68, Appl
10	44.5	33.2	105 4 US-09-205-258-745	Sequence 745, A
11	44.5	33.2	217 4 US-09-252-991A-19413	Sequence 19413, A
12	44.5	33.2	349 4 US-09-343-0118-1	Sequence 1, Appl1
13	44	32.8	117 3 US-09-157-370-1	Sequence 1, Appl1
14	44	32.8	229 4 US-09-328-352-5411	Sequence 5411, Ap
15	44	32.8	466 3 US-08-526-136-13	Sequence 13, Appl
16	44	32.8	659 4 US-09-562-737-13	Sequence 13, Appl
17	44	32.8	1220 3 US-08-930-996A-2	Sequence 2, Appl1
18	43.5	32.5	473 4 US-08-914-375C-71	Sequence 71, Appl
19	43.5	32.5	476 4 US-08-914-375C-69	Sequence 69, Appl
20	43.5	32.5	499 4 US-09-252-991A-25819	Sequence 25819, A
21	43.5	32.5	548 3 US-08-688-988-41	Sequence 41, Appl
22	43	32.1	16 1 US-08-133-011-130	Sequence 130, App
23	43	32.1	16 3 US-08-907-739-130	Sequence 130, App
24	43	32.1	16 4 US-09-729-597-130	Sequence 130, App
25	43	32.1	70 1 US-08-315-695-3	Sequence 3, Appl1
26	43	32.1	197 1 US-08-044-621D-29	Sequence 29, Appl
27	43	32.1	197 1 US-08-709-912-9	Sequence 9, Appl1

28	43	32.1	197 2 US-09-047-370-9	Sequence 9, Appl1
29	43	32.1	217 4 US-09-229-583A-6	Sequence 6, Appl1
30	43	32.1	261 2 US-07-857-224B-59	Sequence 59, Appl
31	43	32.1	270 2 US-08-859-201-4	Sequence 4, Appl1
32	43	32.1	275 2 US-08-701-191A-36	Sequence 36, Appl
33	43	32.1	299 4 US-09-205-258-265	Sequence 265, App
34	43	32.1	314 2 US-08-859-201-8	Sequence 8, Appl1
35	43	32.1	461 4 US-09-134-001C-3316	Sequence 3316, Ap
36	43	32.1	462 1 US-08-458-023B-2	Sequence 2, Appl1
37	43	32.1	463 3 US-09-111-556A-2	Sequence 2, Appl1
38	43	32.1	463 3 US-08-360-758-2	Sequence 2, Appl1
39	43	32.1	485 4 US-09-107-532A-4797	Sequence 4797, Ap
40	43	32.1	603 4 US-09-396-149-8	Sequence 8, Appl1
41	43	32.1	659 4 US-09-562-737-11	Sequence 11, Appl
42	43	32.1	660 3 US-08-819-177-1	Sequence 1, Appl1
43	43	32.1	714 2 US-08-859-201-2	Sequence 2, Appl1
44	43	32.1	800 4 US-09-175-928-10	Sequence 10, Appl
45	42.5	31.7	817 4 US-09-252-991A-25598	Sequence 25598, A

ALIGNMENTS

RESULT 1
US-09-562-737-12
Sequence 12, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Hertz, Joachim
TITLE OF INVENTION: LdL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562, 737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 659
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-12

Query Match 34.3%; Score 46; DB 4; Length 659;
Best local Similarity 34.6%; Pred. No. 1.2e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 10; Gaps 1;

Qy 8 EDVWSEY-----PEYAMDV 23
Db 517 EDWYGAYNRTGARHVPAYVAIEI 542

RESULT 2
US-09-252-991A-29606
Sequence 29606, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29606
LENGTH: 1287
TYPE: PRT

QY 6 AYEDVMSGEPEYAMDV 23
DB 102 AYYDILTYLYYYMDV 119

RESULT 14

US-10-062-254-246
; Sequence 246, Application US/10062254
; Publication No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgente, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 246
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Zea mays
US-10-062-254-246

Query Match 36.6%; Score 49; DB 14; Length 389;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 11; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 DGGGGAVED--VMSGEPEYAY 20
DB 359 NSGCGFGRCDFWSPQYAY 380

RESULT 15
US-09-840-459-77
; Sequence 77, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FaalSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77

Query Match 36.2%; Score 48.5; DB 10; Length 128;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 9 DVMSCGEPEYAMDV 23
DB 104 DFWSGXY-YTGMMDV 117

Search completed: December 30, 2003, 11:45:23
Job time : 4.93258 secs

Db 99 GAYYDILTGYP--YGM DV 115

RESULT 10

US-09-880-748-1695
; Sequence 1695, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1695
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1695

Query Match 38.8%; Score 52; DB 11; Length 252;
Best Local Similarity 57.9%; Pred. No. 21;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 5 GAYEDVWSGEYPEYAMD V 23
Db 99 GAYYDILTGYP--YGM DV 115

RESULT 11

US-09-880-748-1698
; Sequence 1698, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1698
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1698

Query Match 38.8%; Score 52; DB 11; Length 252;
Best Local Similarity 57.9%; Pred. No. 21;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 5 GAYEDVWSGEYPEYAMD V 23

Db 99 GAYYDILTGYP--YGM DV 115

RESULT 12

US-09-880-748-2172
; Sequence 2172, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2172
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2172

Query Match 37.3%; Score 50; DB 11; Length 21;
Best Local Similarity 55.6%; Pred. No. 3.1;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 6 AYEDVWSGEYPEYAMD V 23
Db 4 AYDILTGYYLXYYYMD V 21

RESULT 13

US-09-880-748-839
; Sequence 839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 839
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-839

Query Match 37.3%; Score 50; DB 11; Length 256;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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1      RESULT 6
2      US-09-880-748-926
3      ; Sequence 926, Application US/09880748
4      ; Publication No. US20030059937A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT : Ruben et al.
7      ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
8      ; FILE REFERENCE: PPS523
9      ; CURRENT APPLICATION NUMBER: US/09/880,748
10     ; CURRENT FILING DATE: 2001-06-15
11     ; PRIOR APPLICATION NUMBER: 60/212,210
12     ; PRIOR FILING DATE: 2000-06-15
13     ; PRIOR APPLICATION NUMBER: 60/240,816
14     ; PRIOR FILING DATE: 2000-10-17
15     ; PRIOR APPLICATION NUMBER: 60/276,248
16     ; PRIOR FILING DATE: 2001-03-16
17     ; PRIOR APPLICATION NUMBER: 60/277,379
18     ; PRIOR FILING DATE: 2001-03-21
19     ; PRIOR APPLICATION NUMBER: 60/293,499
20     ; PRIOR FILING DATE: 2001-05-25
21     ; NUMBER OF SEQ ID NOS: 3239
22     ; SOFTWARE: PatentIn Ver. 2.0
23     ; SEQ ID NO 926
24     ; LENGTH: 249
25     ; TYPE: PRT
26     ; ORGANISM: Homo sapiens
27     ; US-09-880-748-926

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[illegible]

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RESULT 7
US-09-880-748-1394
; Sequence 1394, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: p5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1394
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1394

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Query Match      38.8%  Score 52;  DB 11;  Length 252;
Best Local Similarity 50.0%;  Pred. NO. 21;
Matches 9;  Conservative 3;  Mismatches 6;  Indels 0;  Gaps 0.

QY      6 AYEDVWSGGEYPEYYAMDV 23
      :|:|:|:|:|
      101 SYVDILTGYVHHVYGMVD 118

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```

RESULT 8
US-09-880-748-1646
; Sequence 1646, Application US/09880748
; Publication No. US20030058937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1646

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Query Match	38.8%	Score 52	DB 11	Length 252
Best Local Similarity	57.9%	Pred. No. 21		
Matches 11, Conservative	2	Mismatches 4	Indels 2	Gaps 1
QY	5	GAYEDVMSGEIPEYYAMDV	23	
		:	:	
Db	102	GAYYDILTGYYP--YGMDDV	118	

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RESULT 9
US-09-880-748--1674
; Sequence 1674, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880.748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,459
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver..2.0
; SEQ ID NO 1674
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748--1674

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```

Query Match      38.8%  Score 52;  DB 11;  Length 252;
Beet Local Similarity  57.9%  Pred. No. 21;
Matches 11;  Conservative  2;  Mismatches  4;  Indels  2;  Gaps  1;

OY      5 GATEDVMSGGEYEPYAMDV 23
||||| : : ||| | |||

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US-09-880-748-1777

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/ Sequence 1777, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1777
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1777
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Query Match

Best Local Similarity 41.4%; Score 55.5; DB 11; Length 253;
Pred. No. 7;
Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

2 GGGCAEDVWSGEPYAMDV 23

Db 99 GDFG DY-DILTGYYPVYGM DV 119

RESULT 3

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US-09-880-748-2860
/ Sequence 2860, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2860
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-2860
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Query Match

Best Local Similarity 38.8%; Score 52; DB 11; Length 17;
Pred. No. 1.3;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

5 GAYEDVWSGEPYAMDV 23

Db 1 GAYYDILTYYP--YGM DV 17

RESULT 4

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US-09-880-748-2743
/ Sequence 2743, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2743
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-2743
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Query Match

Best Local Similarity 38.8%; Score 52; DB 11; Length 20;
Pred. No. 1.6;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

6 AYEDVWSGEPYAMDV 23

Db 3 SYDYDILTYGYVHYGM DV 20

RESULT 5

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US-09-880-748-918
/ Sequence 918, Application US/09880748
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 918
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-918
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Query Match

Best Local Similarity 38.8%; Score 52; DB 11; Length 249;
Pred. No. 21;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

5 GAYEDVWSGEPYAMDV 23

Db 99 GAYYDILTYYP--YGM DV 115

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 4.93258 Seconds

(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-30

Perfect score: 134
Sequence: 1 DGGGAYEDVWSGEPEYVAMDV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	52	38.8	17	11	US-09-880-748-2860
4	52	38.8	20	11	US-09-880-748-2743
5	52	38.8	249	11	US-09-880-748-918
6	52	38.8	249	11	US-09-880-748-926
7	52	38.8	252	11	US-09-880-748-1394
8	52	38.8	252	11	US-09-880-748-1546
9	52	38.8	252	11	US-09-880-748-1674
10	52	38.8	252	11	US-09-880-748-1695
11	52	38.8	252	11	US-09-880-748-1698
12	50	37.3	21	11	US-09-880-748-2172
13	50	37.3	256	11	US-09-880-748-839
14	49	36.6	389	14	US-10-062-254-246
15	48.5	36.2	128	10	US-09-840-459-77

16	48.5	36.2	128	10	US-09-840-459-79	Sequence 79, App1
17	48.5	36.2	477	12	US-10-169-493-8940	Sequence 8940, App
18	47.5	35.4	22	11	US-09-880-748-2761	Sequence 2761, App
19	47.5	35.4	253	11	US-09-880-748-938	Sequence 938, App
20	47	35.1	19	11	US-09-880-748-2987	Sequence 2987, App
21	47	35.1	254	11	US-09-880-748-1625	Sequence 1625, App
22	46.5	34.7	552	9	US-09-815-028-2	Sequence 2, App1
23	46.5	34.7	552	12	US-10-137-870-196	Sequence 196, App
24	46.5	34.7	552	12	US-10-140-018-196	Sequence 196, App
25	46.5	34.7	552	12	US-10-140-021-196	Sequence 196, App
26	46.5	34.7	552	12	US-10-140-021-196	Sequence 196, App
27	46.5	34.7	552	12	US-10-140-274-196	Sequence 196, App
28	46.5	34.7	552	12	US-10-140-807-196	Sequence 196, App
29	46.5	34.7	552	12	US-10-140-807-196	Sequence 196, App
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31	46.5	34.7	552	12	US-10-140-922-196	Sequence 196, App
32	46.5	34.7	552	12	US-10-140-928-196	Sequence 196, App
33	46.5	34.7	552	12	US-10-141-698-196	Sequence 196, App
34	46.5	34.7	552	12	US-10-141-702-196	Sequence 196, App
35	46.5	34.7	552	12	US-10-141-704-196	Sequence 196, App
36	46.5	34.7	552	12	US-10-142-421-196	Sequence 196, App
37	46.5	34.7	552	12	US-10-142-433-196	Sequence 196, App
38	46.5	34.7	552	12	US-10-142-767-196	Sequence 196, App
39	46.5	34.7	552	12	US-10-143-033-196	Sequence 196, App
40	46.5	34.7	552	12	US-10-144-994-196	Sequence 196, App
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44	46.5	34.7	552	12	US-10-145-746-196	Sequence 196, App
45	46.5	34.7	552	12	US-10-145-823-196	Sequence 196, App

ALIGNMENTS

RESULT 1
US-09-880-748-3082
Sequence 3082, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3082
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-3082
Query Match 41.4%, Score 55.5, DB 11, Length 21,
Best Local Similarity 54.5%, Pred. No. 0.56,
Matches 12, Conservative 2, Mismatches 7, Indels 1, Gaps 1,

Qy 2 DGGGAYEDVWSGEPEYVAMDV 23
Db 1 GDFPDY-DILGTGYTVYGMADV 21

RESULT 2

XX AC ABP45684;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human Blys binding scFv SEQ ID 1695.
 XX
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 XX Homo sapiens.
 XX OS
 XX PN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US19110.
 XX PR 16-JUN-2000; 2000US-212210P.
 XX PR 17-OCT-2000; 2000US-240816P.
 XX PR 16-MAR-2001; 2001US-276248P.
 XX PR 21-MAR-2001; 2001US-277379P.
 XX PR 25-MAY-2001; 2001US-293499P.
 XX
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 XX DR WPI; 2002-114799/15.
 XX
 XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 XX PS Claim 1; Page 2425-2426; 3148pp; English.
 XX
 XX CC This invention describes novel antibodies that immunospecifically bind to
 XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 XX tumour necrosis factor (TNF) super family and induces B cell
 XX proliferation and differentiation. The antibodies of the invention have
 XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX antineumatic and antiAIDS activity and can be used in vaccines to
 XX inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX and so may be used to detect and quantitate the presence of Blys in
 XX biological samples and may be used in this way to diagnose disease
 XX associated with aberrant expression of Blys. They may also be
 XX administered to treat diseases associated with aberrant Blys expression
 XX and activity such as cancer, immune, and autoimmune disorders and
 XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX the antibodies and fragments of the antibodies described in the method
 XX of the invention.
 XX
 XX SQ Sequence 252 AA;
 XX
 XX Query Match 38.8%; Score 52; DB 23; Length 252;
 XX Best Local Similarity 57.9%; Pred. No. 22;
 XX Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
 XX
 XX QY 5 GAYEDVMSGEYEPYAMDV 23
 XX |||||:|:|:|:|:|:|
 XX DB 99 GAYYDILTGYP--YGM DV 115
 XX
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 XX ID ABP45687 standard; Protein; 252 AA.
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AC ABP45687;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human Blys binding scFv SEQ ID 1698.
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 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 XX Homo sapiens.
 XX OS
 XX PN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US19110.
 XX PR 16-JUN-2000; 2000US-212210P.
 XX PR 17-OCT-2000; 2000US-240816P.
 XX PR 16-MAR-2001; 2001US-276248P.
 XX PR 21-MAR-2001; 2001US-277379P.
 XX PR 25-MAY-2001; 2001US-293499P.
 XX
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 XX DR WPI; 2002-114799/15.
 XX
 XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 XX PS Claim 1; Page 2428-2429; 3148pp; English.
 XX
 XX CC This invention describes novel antibodies that immunospecifically bind to
 XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 XX tumour necrosis factor (TNF) super family and induces B cell
 XX proliferation and differentiation. The antibodies of the invention have
 XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX antineumatic and antiAIDS activity and can be used in vaccines to
 XX inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX and so may be used to detect and quantitate the presence of Blys in
 XX biological samples and may be used in this way to diagnose disease
 XX associated with aberrant expression of Blys. They may also be
 XX administered to treat diseases associated with aberrant Blys expression
 XX and activity such as cancer, immune, and autoimmune disorders and
 XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX the antibodies and fragments of the antibodies described in the method
 XX of the invention.
 XX
 XX SQ Sequence 252 AA;
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 XX Query Match 38.8%; Score 52; DB 23; Length 252;
 XX Best Local Similarity 57.9%; Pred. No. 22;
 XX Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
 XX
 XX QY 5 GAYEDVMSGEYEPYAMDV 23
 XX |||||:|:|:|:|:|:|
 XX DB 99 GAYYDILTGYP--YGM DV 115
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 XX Search completed: December 30, 2003, 10:54:33
 XX Job time : 8.4822 secs

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 ID ABP45635 standard; Protein; 252 AA.
 AC ABP45635;
 DT 19-AUG-2002 (first entry)
 DE Human BlyS binding scFv SEQ ID 1646.
 XX
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US19110.
 XX
 XX 16-JUN-2000; 2000US-212210P.
 XX 17-OCT-2000; 2000US-240816P.
 XX 16-MAR-2001; 2001US-276248P.
 XX 21-MAR-2001; 2001US-277379P.
 XX 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 XX
 XX Claim 1; Page 2367-2368; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 XX B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 XX tumour necrosis factor (TNF) super family and induces B cell
 XX proliferation and differentiation. The antibodies of the invention have
 XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX antirheumatic and antiAIDS activity and can be used in vaccines to
 XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 XX and so may be used to detect and quantitate the presence of BlyS in
 XX biological samples and may be used in this way to diagnose disease
 XX associated with aberrant expression of BlyS. They may also be
 XX administered to treat diseases associated with aberrant BlyS expression
 XX and activity such as cancer, immune, and autoimmune disorders and
 XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX the antibodies and fragments of the antibodies described in the method
 XX of the invention.
 XX
 XX
 XX Sequence 252 AA;
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 XX
 XX Query Match 38.8%; Score 52; DB 23; Length 252;
 XX Best Local Similarity 57.9%; Pred. No. 22;
 XX Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
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 XX 5 GAYEDVWSGEYPERYAMDV 23
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 XX Db 102 GAYYDILTGYP--YGMVDV 118

ID ABP45663 standard; Protein; 252 AA.
 AC ABP45663;
 DT 19-AUG-2002 (first entry)
 DE Human BlyS binding scFv SEQ ID 1674.
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 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.
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 XX 15-JUN-2001; 2001WO-US19110.
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 XX 16-JUN-2000; 2000US-212210P.
 XX 17-OCT-2000; 2000US-240816P.
 XX 16-MAR-2001; 2001US-276248P.
 XX 21-MAR-2001; 2001US-277379P.
 XX 25-MAY-2001; 2001US-293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 XX
 XX Claim 1; Page 2400-2401; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 XX B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 XX tumour necrosis factor (TNF) super family and induces B cell
 XX proliferation and differentiation. The antibodies of the invention have
 XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX antirheumatic and antiAIDS activity and can be used in vaccines to
 XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 XX and so may be used to detect and quantitate the presence of BlyS in
 XX biological samples and may be used in this way to diagnose disease
 XX associated with aberrant expression of BlyS. They may also be
 XX administered to treat diseases associated with aberrant BlyS expression
 XX and activity such as cancer, immune, and autoimmune disorders and
 XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX the antibodies and fragments of the antibodies described in the method
 XX of the invention.
 XX
 XX
 XX Sequence 252 AA;
 XX
 XX
 XX Query Match 38.8%; Score 52; DB 23; Length 252;
 XX Best Local Similarity 57.9%; Pred. No. 22;
 XX Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
 XX
 XX 5 GAYEDVWSGEYPERYAMDV 23
 XX ||| : : |||
 XX Db 99 GAYYDILTGYP--YGMVDV 115

RESULT 13
 ABP45663

RESULT 14
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 ID ABP45664 standard; Protein; 252 AA.

RESULT 10
ABP44915
ID ABP44915 standard; Protein; 249 AA.
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AC ABP44915;
XX
DT 19-AUG-2002 (first entry)
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DE Human Blys binding scFv SEQ ID 926.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 1507-1508; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
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SO Sequence 249 AA;
XX
Query Match 38.8%; Score 52; DB 23; Length 249;
Best Local Similarity 57.9%; Pred. No. 22;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
QY 5 AYEDVWSGEYPRYAMDV 23
DB 99 GAYVDILTGYPP--YGMDDV 115

RESULT 11
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ID ABP45383 standard; Protein; 252 AA.
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AC ABP45383;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1394.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2066-2067; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SO Sequence 252 AA;
XX
Query Match 38.8%; Score 52; DB 23; Length 252;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 6 AYEDVWSGEYPRYAMDV 23
DB 101 SYVDILTGYVHYGMDDV 118

RESULT 12

Db 1 GAYYDILTGYP--YGMV 17

RESULT 8
ABP46732
ID ABP46732 standard; peptide: 20 AA.
XX
AC ABP46732;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv VH CDR3 SEQ ID 2743.
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 2; Page 3042; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 20 AA;
Query Match 38.8%; Score 52; DB 23; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEYYAMDV 23
: : : : :
Db 3 SYVDILGTGYVHHYGMV 20

RESULT 9
ABP44907
ID ABP44907 standard; Protein; 249 AA.
XX
AC ABP44907;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 918.
XX
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 1497-1498; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 249 AA;
Query Match 38.8%; Score 52; DB 23; Length 249;
Best Local Similarity 57.9%; Pred. No. 22;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 5 GAYEDVWSGEYPEYYAMDV 23
: : : : :
Db 99 GAYYDILTGYP--YGMV 115

OY 2 GCGAYEDVMSGEYPEYAMDV 23
Db 1 GDFGDY-DILTGYPVYGMVDV 21

RESULT 6
ID ABP45766 standard; Protein; 253 AA.

XX ABP45766;

XX 19-AUG-2002 (first entry)

DE Human Blys binding scfv SEQ ID 1777.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for

XX the diagnosis and treatment of cancers and immune disorders -

XX Claim 1; Page 2522-2523; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.

XX Sequence 253 AA;

XX Query Match 41.4%; Score 55.5; DB 23; Length 253;
XX Best Local Similarity 54.5%; Pred. No. 7.2;
XX Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

OY 2 GCGAYEDVMSGEYPEYAMDV 23

Db 99 GDFGDY-DILTGYPVYGMVDV 119

RESULT 7
ID ABP46849 standard; peptide; 17 AA.

XX ABP46849;

XX 19-AUG-2002 (first entry)

DE Human Blys binding scfv VH CDR3 SEQ ID 2860.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for

XX the diagnosis and treatment of cancers and immune disorders -

XX Claim 2; Page 3066; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.

XX Sequence 17 AA;

XX Query Match 38.8%; Score 52; DB 23; Length 17;
XX Best Local Similarity 57.9%; Pred. No. 1.1;
XX Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 5 GAYEDVMSGEYPEYAMDV 23

XX DE Human gene 22-encoded secreted protein fragment, SEQ ID NO:236.
 XX KW Human: secreted protein; proliferative disorder; cancer;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiodysplasia; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;
 KW endocrine disorder; infection; wound healing; uinary;
 KW cell culture; chemotaxis; food additive; expression;
 KW binding partner identification.
 XX KW Homo sapiens.
 XX OS
 XX PN MO200132910-A2.
 XX PD 10-MAY-2001.
 XX PF 25-OCT-2000; 2000MO-US29362.
 XX PR 29-OCT-1999; 99US-0162240.
 XX PR 30-JUN-2000; 2000US-0215131.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Komatoullis GA, Birse CE, Ni J, Sopet DR,
 XX DR WPI; 2001-335835/35.
 XX PT Novel 27 isolated human secreted proteins and polynucleotides encoding
 PT them useful for treating, diagnosing, preventing Alzheimer's disease,
 PT Parkinson's disease, AIDS, rheumatoid arthritis, asthma
 XX PS Disclosure; Page 62; 594pp; English.
 XX CC AAH19170-AAH19250 represent cDNAs corresponding to 27 human secreted
 CC protein genes, and AAG62156-AAG62235 represent the proteins they encode.
 CC AAG62236-AAG62293 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of:
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC brain disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiodysplasia, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.
 XX SO Sequence 129 AA;

Query Match 44.4%; Score 59.5; DB 22; Length 129;
 Best Local Similarity 50.0%; Pred. No. 0.92;
 Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

OY 1 DGGGG---AYEDVWSGEYPTIAM 21
 Db 26 DGGGAPSWAPBEDAMWGHKYLEM 49
 RESULT 5
 ABP47071
 ID ABP47071 standard; peptide; 21 AA.
 XX AC ABP47071;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human Blys binding scFv VH CDR3 SEQ ID 3082.
 XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX PN MO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001MO-US19110.
 XX PR 16-JUN-2000; 2000US-212210P.
 XX PR 17-OCT-2000; 2000US-240816P.
 XX PR 16-MAR-2001; 2001US-276248P.
 XX PR 21-MAR-2001; 2001US-277379P.
 XX PR 25-MAY-2001; 2001US-293499P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX DR WPI; 2002-114799/15.
 XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX PS Claim 2; Page 3111-3112; 3148pp; English.
 XX CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX SO Sequence 21 AA;

Query Match 41.4%; Score 55.5; DB 23; Length 21;
 Best Local Similarity 54.5%; Pred. No. 0.43;
 Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

XX Example 4; Fig 4C; 61p; English.
 XX This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specifically which has
 CC hemostatic activity. (I) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents the human
 CC anti-factor VIII antibody VH IT-2 protein CDR3 fragment which is used
 CC in the method of the invention.
 XX
 SQ Sequence 23 AA;
 Query Match 100.0%; Score 134; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 3.9e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DGGGAYEDVMSGEYPEYAMDV 23
 1 DGGGAYEDVMSGEYPEYAMDV 23
 Db 1 DGGGAYEDVMSGEYPEYAMDV 23
 RESULT 2
 AAY50950
 ID AAY50950 standard; Protein; 132 AA.
 XX
 AC AAY50950;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human anti-factor VIII antibody VH clone IT-2 encoded protein.
 XX
 KW Human; heavy chain; antibody; factor VIII; hemostatic;
 XX hemophilia A; VH gene.
 XX
 OS Homo sapiens.
 XX
 PN WO958680-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-NL00285.
 XX
 PR 08-MAY-1998; 98EP-0201543.
 XX
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
 XX
 PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
 DR WPI; 2000-053102/04.
 XX
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for
 PT treatment of hemophilia A patients with these antibodies -
 XX
 XX Example 4; Fig 4A; 61p; English.
 XX This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specificity which has the
 CC hemostatic activity. (I) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents the human
 CC anti-factor VIII antibody clone IT-2 protein which is used in the method
 CC of the invention.
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 134; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DGGGAYEDVMSGEYPEYAMDV 23
 1 DGGGAYEDVMSGEYPEYAMDV 121
 Db 99 DGGGAYEDVMSGEYPEYAMDV 121
 RESULT 4
 AAG62284
 ID AAG62284 standard; Protein; 129 AA.
 XX
 AC AAG62284;
 XX
 DT 18-JUL-2001 (first entry)

Query Match 100.0%; Score 134; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DGGGAYEDVMSGEYPEYAMDV 23
 99 DGGGAYEDVMSGEYPEYAMDV 121
 Db 99 DGGGAYEDVMSGEYPEYAMDV 121
 RESULT 3
 AAY50953
 ID AAY50953 standard; Protein; 132 AA.
 XX
 AC AAY50953;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human anti-factor VIII antibody VH protein VH IT-2.
 XX
 KW Human; heavy chain; antibody; factor VIII; hemostatic;
 XX hemophilia A; VH protein.
 XX
 OS Homo sapiens.
 XX
 PN WO958680-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-NL00285.
 XX
 PR 08-MAY-1998; 98EP-0201543.
 XX
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
 XX
 PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
 DR WPI; 2000-053102/04.
 XX
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for
 PT treatment of hemophilia A patients with these antibodies -
 XX
 XX Example 4; Fig 4B; 61p; English.
 XX This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specificity which has
 CC hemostatic activity. (I) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them
 CC are useful in compositions for neutralizing factor VIII inhibiting
 CC antibodies in hemophilia A patients. This sequence represents the human
 CC anti-factor VIII antibody VH IT-2 protein which is used in the method
 CC of the invention.
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 134; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DGGGAYEDVMSGEYPEYAMDV 23
 99 DGGGAYEDVMSGEYPEYAMDV 121
 Db 99 DGGGAYEDVMSGEYPEYAMDV 121
 RESULT 4
 AAG62284
 ID AAG62284 standard; Protein; 129 AA.
 XX
 AC AAG62284;
 XX
 DT 18-JUL-2001 (first entry)

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 7.39886 Seconds
(without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-30
Perfect score: 134
Sequence: 1 DGGCGAYEDVWSEGEPEPYAMDV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	23	21	AA150957 Human anti-factor
2	134	100.0	132	21	AA150950 Human anti-factor
3	134	100.0	132	21	AA150953 Human anti-factor
4	59.5	44.4	129	22	AA62284 Human gene 22-enco
5	55.5	41.4	21	23	ABP47071 Human Blys binding
6	55.5	41.4	253	23	ABP45766 Human Blys binding
7	52	38.8	17	23	ABP46849 Human Blys binding
8	52	38.8	20	23	ABP46732 Human Blys binding
9	52	38.8	249	23	ABP44907 Human Blys binding

10	52	38.8	249	23	ABP44915 Human Blys binding
11	52	38.8	252	23	ABP45383 Human Blys binding
12	52	38.8	252	23	ABP45635 Human Blys binding
13	52	38.8	252	23	ABP45663 Human Blys binding
14	52	38.8	252	23	ABP45684 Human Blys binding
15	52	38.8	252	23	ABP45687 Human Blys binding
16	50.5	37.7	475	24	ABJ36921 Anti-CD40 monoclon
17	50	37.3	21	23	ABP46161 Human Blys binding
18	50	37.3	44	23	ABG31313 Anti-CD40 monoclon
19	50	37.3	151	24	ABJ36933 Human Blys binding
20	50	37.3	256	23	ABP44828 Human ORF198 prot
21	49	36.6	123	23	ABP34925 Human heavy chain
22	48.5	36.2	128	22	AAE07014 Human heavy chain
23	48	35.8	124	22	ABG09454 Human polypeptide
24	48	35.8	304	22	AA442096 H. pylori lactofer
25	48	35.8	528	23	ABB07347 Human Blys binding
26	47.5	35.4	22	23	ABP46750 Human Blys binding
27	47.5	35.4	253	23	ABP44927 Human Blys binding
28	47	35.1	19	23	ABP46976 Human Blys binding
29	47	35.1	108	21	AA41476 Human ORFX ORF1240
30	47	35.1	158	23	ABP31473 Human ORF446 prote
31	47	35.1	254	23	ABP45614 Human Blys binding
32	47	35.1	331	21	AA613982 Arabidopsis thalia
33	47	35.1	331	21	AA650644 Arabidopsis thalia
34	47	35.1	333	21	AA613981 Arabidopsis thalia
35	47	35.1	333	21	AA650643 Arabidopsis thalia
36	47	35.1	383	23	AAU72500 Arabidopsis thalia
37	47	35.1	401	21	AA613980 Arabidopsis thalia
38	47	35.1	401	21	AA650642 Arabidopsis thalia
39	47	35.1	1579	23	ABB91088 Hericidially activ
40	46.5	34.7	305	22	ABG25421 Novel human diagno
41	46.5	34.7	357	21	ABP42978 Human ORFX ORF2742
42	46.5	34.7	552	22	AAU09026 Human novel glycos
43	46.5	34.7	552	22	AAU12269 Human PRO4994 poly
44	46.5	34.7	552	22	AAU06620 Human protein protel
45	46.5	34.7	552	23	ABB97254 Novel human protei

ALIGNMENTS

RESULT 1	AA150957 standard; Protein; 23 AA.
AA150957	
XX	AA150957;
AC	23-MAR-2000 (first entry)
XX	
DT	Human anti-factor VIII antibody VH protein VH IT-3 CDR3 fragment.
XX	
DE	Human; heavy chain; antibody; factor VIII; hemostatic;
XX	hemophilia A; VH protein.
KW	
OS	Homo sapiens.
XX	
PN	WO9958680-A2.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-NL00285.
XX	
PR	06-MAY-1998; 98BP-0201543.
XX	
PA	(SANC-) STICHTING SANQUIN BLOEDVOORZIENING.
XX	
PI	Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX	WPI; 2000-053102/04.
DR	
XX	New polynucleotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -

Oy 121 MYTSS 126
 |||||
 Db 138 TTVSS 143

RESULT 2

OSMUK1 PRELIMINARY; PRT; 613 AA.

AC OSMUK1 08MUK1
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tonsil;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 72.0%; Score 479; DB 4; Length 613;
 Best Local Similarity 71.4%; Pred. No. 2.5e-40;
 Matches 90; Conservative 16; Mismatches 14; Indels 6; Gaps 1;

Oy 1 OVQLVSGGGLVOPGKSLRLSCAAGFTFGDYAIHWYRQAPGEGLEWVSGVTWSTTIGF 60
 |||||
 Db 20 OVQLVESGGGVOPGKSLRLSCAAGFTFGDYAIHWYRQAPGEGLEWVSGVTWSTTIGF 79
 |||||
 Oy 61 ADVKGRFTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGAFAFDIWGOT 120
 |||||
 Db 80 ADVKGRFTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGAFAFDIWGOT 133
 |||||
 Oy 121 MYTSS 126
 |||||
 Db 134 MYTSS 139

RESULT 3

OSMUK1 PRELIMINARY; PRT; 118 AA.

AC OSMUK1 08MUK1
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RL EMBL; AF035023; AAD56259.1; -

DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 69.0%; Score 459; DB 4; Length 118;
 Best Local Similarity 73.2%; Pred. No. 3.5e-39;
 Matches 93; Conservative 12; Mismatches 10; Indels 12; Gaps 2;

Oy 1 OVQLVSGGGLVOPGKSLRLSCAAGFTFGDYAIHWYRQAPGEGLEWVSGVTWSTTIGF 60
 |||||
 Db 1 EVQLVESGGGVOPGKSLRLSCAAGFTFGDYAIHWYRQAPGEGLEWVSGVTWSTTIGF 60
 |||||
 Oy 61 ADVKGRFTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGAFAFDIWGOT 118
 |||||
 Db 61 ADVKGRFTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGAFAFDIWGOT 110
 |||||
 Oy 119 GTMYTSS 125
 |||||
 Db 111 GTMYTSS 117

RESULT 4

OSMUK1 PRELIMINARY; PRT; 121 AA.

AC OSMUK1 08MUK1
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 68.8%; Score 457.5; DB 4; Length 121;
 Best Local Similarity 73.0%; Pred. No. 5.1e-39;
 Matches 92; Conservative 13; Mismatches 16; Indels 5; Gaps 2;

Oy 1 OVQLVSGGGLVOPGKSLRLSCAAGFTFGDYAIHWYRQAPGEGLEWVSGVTWSTTIGF 60
 |||||
 Db 1 EVQLVESGGGVOPGKSLRLSCAAGFTFGDYAIHWYRQAPGEGLEWVSGVTWSTTIGF 60
 |||||
 Oy 61 ADVKGRFTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGAFAFDIWGOT 120
 |||||
 Db 61 ADVKGRFTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGAFAFDIWGOT 115
 |||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 30.7067 Seconds
(without alignments)
1058.876 Million cell updates/sec

Title: US-09-674-752-43

Sequence: 1 QVQLVQSGGGLVQPGKSLRL.....RRGVAAPDIWGQGTMTVYSS 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvivirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	75.5	573	4	Q8WU38
2	479	72.0	613	4	Q8WU38
3	459	69.0	118	4	Q8WU38
4	457.5	68.8	121	4	Q9UL91
5	456	68.6	112	4	Q9UL71
6	450	67.7	471	4	Q9HCC1
7	446.5	67.1	597	4	Q8TC77
8	443.5	66.7	116	4	Q9UL93
9	439.5	66.1	499	4	Q8NSK4
10	437.5	65.8	113	4	Q9UL90
11	427	64.2	147	4	Q9Y509
12	420	63.2	122	4	Q9UL84
13	419.5	63.1	493	4	Q8NCL6
14	419	63.0	118	4	Q9UL72
15	417	62.7	494	4	Q96K68
16	415	62.4	473	11	Q91205

17	409.5	61.6	104	4	Q9UL87	Q9UL87	mus	sapien
18	397	59.7	487	11	Q9YKA4	Q9YKA4	mus	muscult
19	384.5	57.8	119	11	Q920E7	Q920E7	mus	muscult
20	381.5	57.4	131	4	Q9UL88	Q9UL88	mus	sapien
21	381.5	57.4	479	11	Q91WP5	Q91WP5	mus	muscult
22	378	56.8	469	11	Q8R3V9	Q8R3V9	mus	muscult
23	376	56.5	95	4	Q9UL86	Q9UL86	mus	sapien
24	374.5	56.3	486	11	Q91207	Q91207	mus	muscult
25	371	55.8	484	11	Q8VEA0	Q8VEA0	mus	muscult
26	365	54.9	298	11	Q9QYF0	Q9QYF0	mus	muscult
27	358.5	53.9	521	4	Q8N4Y9	Q8N4Y9	mus	sapien
28	351.5	52.9	480	11	Q91XE1	Q91XE1	mus	muscult
29	342	51.4	437	11	Q9R1A4	Q9R1A4	mus	muscult
30	339.5	51.1	112	4	Q9UGP3	Q9UGP3	mus	sapien
31	337	50.7	124	4	Q9UL92	Q9UL92	mus	sapien
32	333	50.1	124	6	Q9N0M4	Q9N0M4	orycto	laque
33	330	49.6	124	6	Q9N0M6	Q9N0M6	orycto	laque
34	330	49.6	482	11	Q91X92	Q91X92	mus	muscult
35	327.5	49.2	614	4	Q96GA6	Q96GA6	mus	sapien
36	325.5	48.9	125	4	Q9UL95	Q9UL95	mus	muscult
37	325.5	48.9	484	11	Q9UL96	Q9UL96	mus	muscult
38	319	48.0	121	11	Q99NG4	Q99NG4	mus	muscult
39	313	47.1	159	4	Q96OS0	Q96OS0	mus	sapien
40	313	47.1	500	4	Q9BRV0	Q9BRV0	mus	sapien
41	310.5	46.7	142	11	Q924Q1	Q924Q1	mus	muscult
42	308.5	46.4	119	4	Q9UL94	Q9UL94	mus	sapien
43	304	45.7	241	11	Q921A6	Q921A6	mus	muscult
44	303.5	45.6	150	4	Q9Y298	Q9Y298	mus	sapien
45	302.5	45.5	146	11	Q924R8	Q924R8	mus	muscult

ALIGNMENTS

RESULT 1

ID Q8WU38 PRELIMINARY; PRT: 573 AA.

```
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC021276; AAH21276.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 2.
DR PROSITE: PSS0290; IG_MHC; 2.
KW Hypothetical protein.
SQ
SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
```

Query Match 75.5%; Score 502; DB 4; Length 573;

Best Local Similarity 76.2%; Pred. No. 16-42; Matches 96; Conservative 12; Mismatches 16; Indels 2; Gaps 1;

```
QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDIAIHVRQAPAEGLRWVGSGTTIGF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGLVQPGKSLRLSCAASGFTFDVAHMTVRQAPKGLIEWSGISWNSGSI 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ASVYGRFTISRDNAKNSLYLWNLSLRAPDTALYYCALPYINSSYRRQVAAPDIWGQGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ADSVGRFTISRDNAKNSLYLWNLSLRAPDTALYYCALH--GSGSYIGYYGMDWGQGT 137
```

DR Pfam: PF00047; Ig, 1.
 DR SMART; SM00406; IgV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 108
 FT NON_TER 115 115 IG-LIKE.
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 59.0%; Score 392.5; DB 1; Length 115;
 Best Local Similarity 61.1%; Pred. No. 9.5e-34;
 Matches 77; Conservative 19; Mismatches 19; Indels 11; Gaps 3;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTTGDYAIHWVROAPRGELWVGSGVTMSGTTIGF 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYVMWVROAPGKGLZMWGAIZGLSYSSZY 60
 QY 61 ADSVGRFTISRDNKNSLYLVNSSLRAEDTALYYCALPYINSSNVRGVAFDIWGOST 120
 DB 61 ADSVGRFTISRDNKNSLYLVNSSLRAEDTALYYCALPYINSSNVRGVAFDIWGOST 109
 QY 121 MYTVSS 126
 DB 110 LVTSS 115

RESULT 14
 ID HVJL_HUMAN STANDARD; PRT; 119 AA.
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgM1 immunoglobulin. IV. Streptococcal
 RT IgM1 protease, digestion, Fab and Fc fragments, and the complete
 RT amino acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874(1979).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02056; A1HBR.
 DR HSSP: P01772; 2F84.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig, 1.
 DR SMART; SM00406; IgV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 58.1%; Score 386.5; DB 1; Length 119;
 Best Local Similarity 59.2%; Pred. No. 4.1e-33;
 Matches 74; Conservative 21; Mismatches 23; Indels 7; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTTGDYAIHWVROAPRGELWVGSGVTMSGTTIGF 60
 DB 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFTSYVMWVROAPGKGLZMWGAIZGLSYSSZY 60

QY 61 ADSVGRFTISRDNKNSLYLVNSSLRAEDTALYYCALPYINSSNVRGVAFDIWGOST 120
 DB 61 ADSVGRFTISRDNKNSLYLVNSSLRAEDTALYYCALPYINSSNVRGVAFDIWGOST 113
 QY 121 MYTVSS 125
 DB 114 LVTSS 118

RESULT 15
 ID HVJL_CANFA STANDARD; PRT; 114 AA.
 AC P01784;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region GOM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242268; PubMed=407924;
 RA Waseeman R.L., Capra U.D.;
 RT "Primary structure of the variable regions of two canine
 RT immunoglobulin heavy chains.";
 RT Biochemistry 16:3160-3168(1977).
 RL -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02067; AVDGSM.
 DR HSSP: P01772; 2F84.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig, 1.
 DR SMART; SM00406; IgV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112
 FT NON_TER 114 114 IG-LIKE.
 SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;

Query Match 57.4%; Score 382; DB 1; Length 114;
 Best Local Similarity 61.9%; Pred. No. 1.1e-32;
 Matches 78; Conservative 17; Mismatches 19; Indels 12; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTTGDYAIHWVROAPRGELWVGSGVTMSGTTIGF 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYVMWVROAPGKGLZMWGAIZGLSYSSZY 60
 QY 61 ADSVGRFTISRDNKNSLYLVNSSLRAEDTALYYCALPYINSSNVRGVAFDIWGOST 120
 DB 61 ADSVGRFTISRDNKNSLYLVNSSLRAEDTALYYCALPYINSSNVRGVAFDIWGOST 108
 QY 121 MYTVSS 126
 DB 109 LVTSS 114

Search completed: December 30, 2003, 10:55:53
 Job time : 6.75548 secs

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=81101090; PubMed=6450418;
RA Matchyessens G., Rabbits T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region."
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.1sb-sib.ch/announce/
or send an email to license@sib-ch).

```

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RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT 1A2 immunoglobulin of the A2m (2) allotype."
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPIC, C
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02050; A2HUBV.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FM Immunoglobulin V region.
FM DOMAIN 1 111 IG-LIKE.
FM NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match
Best Local Similarity 60.3%; Score 394.5; DB 1; Length 115;
Matches 76; Conservative 24; Mismatches 15; Indels 11; Gaps 2;

QY 1 QVQLVSGGGLVQPGKSLRLSCAASGFFPDYAIHWYRQAPGEGLEWVSQVTTSGTTIGF 60
DB 1 EVQLVSGGGLVQPGKSLRLSCAASGFFPSYAMSWVQAPOKGLEWVSAISGSGSTYY 59
QY 61 ADVSKGRFTISRDNKNSLYLVNNSLRAPDTALYYCALPYINSSNYRGVAAPDIWQGT 120
DB 60 ADVSKGRFTISRDNKNTLYLVNNSLRAPDTALYYCA-----RDIAAARLFQKGT 109
QY 121 MVTYSS 126
DB 110 TTYTSS 115

RESULT 13
HV3D HUMAN STANDARD; PRT; 115 AA.
ID HV3D HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=7805528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain."
RL J. Biol. Chem. 252:7192-7199(1977).
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMOGATRY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
IDENTICAL.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02048; H3H0T4.
DR HSSP; P01772; 2F94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.

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RP SEQUENCE OF 17-136.
RX MEDLINE=7100368; PubMed=401950;
RA Adeyugo K., Milestein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; J00522; AAD15290.1; -.
DR PIR; J09809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
KM NON_TER 1
FT SIGNAL 1
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT CONFLICT 136 136 Y -> W (IN REF. 2).
SQ NON_TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 61.5%; Score 409; DB 1; Length 136;
Best Local Similarity 62.0%; Pred. No. 2,3e-35;
Matches 80; Conservative 16; Mismatches 19; Indels 14; Gaps 2;

QY 2 VOLVSGGGIVOPGKSLRSCAASGFTFGDYAIHWVROAPGEGLEWVSGVTWSGTTIGFA 61
DB 18 VOLVESGGGIVOPGSRKLSCAASGFTFSFGHWRQAPGKLEWVAIYSSGSLHYA 77
QY 62 DSVYKGFRTISRDNAKNSLYVYNSLRADPALTYYCA-----LPYINSNRRGAAADING 117
DB 78 DTVYKGFRTISRDNPKNLTFLQMTSLRSEDTAMYYCARMGNYPRY-----ANDYWG 127
QY 118 OGTMVTYSS 126
DB 128 QGTSVTYSS 136

RESULT 10
HV3K HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SBP-2003 (Rel. 42, Last annotation update)
DR Ig heavy chain V-II region KOL.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6864994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.",
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

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RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguerat M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GIMUTL.
DR PDB; 2PR4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
KM DOMAIN 1 112
FT MOD_RES 1 1 IG-LIKE.
FT DISULFID 22 96 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 59.8%; Score 398; DB 1; Length 126;
Best Local Similarity 59.3%; Pred. No. 2,8e-34;
Matches 80; Conservative 18; Mismatches 19; Indels 18; Gaps 2;

QY 1 OVOLVSGGGIVOPGKSLRSCAASGFTFGDYAIHWVROAPGEGLEWVSGVTWSGTTIGF 60
DB 1 OVOLVESGGGIVOPGSRKLSGSSGFTFSYAMTWROAPGKLEWVAIIMDDGSDQHY 60
QY 61 ADSVYKGFRTISRDNAKNSLYVYNSLRADPALTYYCALPYINSNRRGVAAF----- 113
DB 61 ADSVYKGFRTISRDNSKNTLFLQMTSLRPRDTGVYFCA-----RDGHHGFCSSASCF 111
QY 114 --DIWGGTMVTYSS 126
DB 112 GPDYWGQGTPTVYSS 126

RESULT 11
HV3C HUMAN STANDARD; PRT; 117 AA.
AC P01764;

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QY 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAPFIWGQGT 120
 DB 61 AASVKGRFTISRBSKBTMYLBNMSLRADPTALYYCA-----RSGIALGSAVAGTDYWGQGT 116
 QY 121 MVTVSS 126
 DB 117 LVTIVSS 122

RESULT 7

HV3B_HUMAN STANDARD; PRT; 114 AA.
 ID HV3B_HUMAN
 AC P01763;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RX MEDLINE=83273707; PubMed=6410398;
 RP Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 (protein WEA) with antibody activity against 3,4-pyruvylated
 galactose in Klebsiella polysaccharides K30 and K33."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WALDENSTROM'S MACROGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02046; M3HUME.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD RES 1 114
 FT NON TER 114 114
 SO SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 62.3%; Score 414; DB 1; Length 114;
 Best Local Similarity 65.1%; Pred. No. 5, 6e-36;
 Matches 82; Conservative 18; Mismatches 14; Indels 12; Gaps 1;

QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGDVAIHWRAPGEGLEWVSQGTIGF 60
 DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGDVAIHWRAPGEGLEWVSQGTIGF 60
 QY 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAPFIWGQGT 120
 DB 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAPFIWGQGT 120
 QY 121 MVTVSS 126
 DB 109 LVTIVSS 114

RESULT 8
 HV3A_HUMAN STANDARD; PRT; 122 AA.
 ID HV3A_HUMAN
 AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RX MEDLINE=76023781; PubMed=809331;
 RP Kretzlin H., Altevogt P., Ruban E., Kortt A., Starosck K.,
 RA Hilschmann N.;
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
 RT structure of the complete IgA-molecule."
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02045; A1HUTR.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 108
 FT MOD RES 1 1
 FT NON TER 122 122
 SO SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 62.0%; Score 412; DB 1; Length 122;
 Best Local Similarity 59.5%; Pred. No. 9, 8e-36;
 Matches 75; Conservative 24; Mismatches 23; Indels 4; Gaps 1;

QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGDVAIHWRAPGEGLEWVSQGTIGF 60
 DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGDVAIHWRAPGEGLEWVSQGTIGF 60
 QY 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAPFIWGQGT 120
 DB 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAPFIWGQGT 120
 QY 121 MVTVSS 126
 DB 117 LVTIVSS 122

RESULT 9

HV16_MOUSE STANDARD; PRT; 136 AA.
 ID HV16_MOUSE
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NC NCB1_Taxid=10090;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paekind M., Reth M., Imantsht-Karl T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 RN [2]

SO	SEQUENCE	116 AA;	12730 MW;	26C7CA99AAAAA1282 CRC64;
PT	NON TER	116	116	IG-LIKE.
FT	DOMAIN	1	112	
KM	Immunoglobulin V region.			
KM	IMMUNOGLOBULIN V REGION.			
DR	PROSITE; PS50835; IG LIKE; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	Pfam; PF00047; IGV; 1.			
DR	InterPro; IPR003066; IG_MHC.			
DR	InterPro; IPR003066; IG_LIKE.			
DR	InterPro; IPR007110; IG-LIKE.			
DR	GO; GO:0006955; P:Immune response; NAS.			
DR	GO; GO:0003823; P:antigen binding activity; NAS.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	HSP; P01272; 2PB4.			
DR	PIR; A02064; M3HUGL.			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	MACROGLOBULIN.			
CC	-1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S			
RL	Submitted (JUN-1975) to the PIR data bank.			
RA	Hilsechmann N.;			
RP	REVISION TO 28-33.			
RT	MacFarlane S., Barikol H.V., Horn J., Bettram J., Hilsechmann N.;			
RT	"The primary structure of a monoclonal IgM-immunoglobulin			
RT	(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-			
RT	type), subunit H II.1. Architecture of the complete IgM-molecule.";			
RL	Hope-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).			
RM	[2]			

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Query Match      63.8%; Score 424; DB 1; Length 116;
Best Local Similarity 65.9%; Pred. No. 5,3e-37;
Matches 83; Conservative 12; Mismatches 21; Indels 10; Gaps 1.

QY      1 QVQLVQSGGGLVPQPKSLRLSCAASGFFTFGGVAIHMHVARQAPEGLEWYSGVTWGTTIGF 60
Dd      1 EVQLVESGGDLVQPGRSRLRSCAASGFDFBBLGMWTWVRQAPOKGLEWYANI KZBSZZBY 60
        |||
QY      61 ADSVKGRFTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSIRRGCAAFDIWGCT 120
Dd      61 VDSVKGRFTISRDNANKSLYLQMNSLRVEDTALYYCA-----KGWGDDYWGCT 110
        |||
QY      121 MTIVSS 126
Dd      111 LTVST 116

RESULT 5
HVJ3 HUMAN
ID ID HVJ3 HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-IIJ region HTL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mamalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=79124695; PubMed=420800;
RX Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
   cryoimmunoglobulin Igg H1.";
RL Biochemistry 18:553-560(1979).
CC -I- MYCELIANEUS: THIS CHAIN WAS ISOLATED FROM AN IGCI MYELOMA
   PROTEIN.
CC CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02054; GIHUTL.
DR HSP; P01772; ZPB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPRO07110; Ig-like.
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DR	InterPro: IPR003006; IG_MHC.
DR	InterPro: IPR003596; IG_v.
DR	Pfam: PF000047; Ig_v.1.
DR	SMART: SM00406; IGV.1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT	DOMAIN 1 112 IG-LIKE.
FT	MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT	NON_TER 121 121
SO	SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CAC64;

Query Match	Best Local Similarity	63.5%; Score 422.5; DB 1; Length 121;
		63.8%, Pred. No. 8e-37;
Matches	81; Conservative	21; Mismatches 18; Indels 7; Gaps 2
Oy	1 QVQLVQSGGGLVPQGSKLRISCAASGFTFGDYAIHWYRQAPEGLEWVGVTWGSGTTIGF	60
Dd	1 QVKLVQAQGGGVAGGRSLRLSCIASGFTFSNYGMHWYQAQEGKGLEWVAIVMNSRTTY	60
Oy	61 ADSYKGRFTISRDAKNSLYIMNLSLAEDTALYYCAL-PIINSNTNRKGAAPIDWOG	119
Dd	61 GDYSYKGRFTISRDNKSRYLMZMNLSLRTEDTAIVYAACAPDILTA-----FSPDYWGOG	114
Oy	120 TMTVTSS 126	
Dd	115 VLVTVSS 121	

RESULT 6			
ID	HW3H_HUMAN	STANDARD	PRT: 122 AA.
AC	P01769		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Ig heavy chain V-II region GA.		
OS	Homo sapiens (Human)		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=74175307; PubMed=4208843;		
RA	Florent G., Lehman D., Putnam F.W.;		
RT	"The switch point in mu heavy chains of human IgM immunoglobulins.";		
RL	Biochemistry 13(12):2462-2498(1974).		
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S		
CC	MACROGLOBULIN.		
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.		
DR	PIR; A02052; M3HUGA.		
DR	HSP; P01772; 2PB4.		
DR	GO; GO:0005576; C:extracellular; NAS.		
DR	GO; GO:0003823; F:antigen binding activity; NAS.		
DR	GO; GO:0006955; P:immune response; NAS.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_V.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGv; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin V region; Pyrrolidone carboxylic acid.		
FT	DOMAIN 1		
FT	MOD_RES 112		
FT	MOD_RES 11		
FT	NON_TER 122		
FT	SEQUENCE 122 AA; 13166 MW; 74E5E6959B84100A CRC64;		
QY	Query Match	63.0%; Score 419; DB 1; Length 122;	
DB	Best Local Similarity	61.1%; Pred. No. 1.8e-36;	
DB	Matches 77; Conservative 24; Mismatches 21; Indels 4; Gaps 1;		

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RESULT 2
HV3U_HUMAN          STANDARD;          PRT;          120 AA.
ID   P01782;
AC   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region DOB.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80020921; PubMed=114209;
RA   Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT   "Amino acid sequence of the heavy-chain variable region of the
RL   crystallizable human myeloma protein Dob."
RL   Biochemistry 18:4068-4080(1979).
[2]
RN   [2]
RP   CRYSTALLIZATION.
RX   MEDLINE=80020920; PubMed=114208;
RA   Steiner L.A.; Lopes A.D.;
RT   "The crystallizable human myeloma protein Dob has a hinge-region
RT   deletion."
RL   Biochemistry 18:4054-4067(1979).
CC   -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
CC   HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
CC   DISULFIDE BONDS.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90431; GIH0DB.
DR   HSSP; P01772; 2F84.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_Like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN 1 112 IG-LIKE.
FT   NON TER 120 120
SQ   SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 65.7%; Score 437; DB 1; Length 120;
Best Local Similarity 65.1%; Pred. No. 2.5e-38;
Matches 82; Conservative 18; Mismatches 20; Indels 6; Gaps 1;

QY 1 OVQLVSGGGLVQPGSLRLSCAAGFTGPDVAIHVRQAPGSGLEWVGVTWSTTIGF 60
DB 1 EVQLVSGGDLVQPGSLRLSCAAGFTFPEYFHHWLRQPGSGLEWVGVTITWNGSGLV 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALVYCALPYINSSNYRGAAPFDIWGQT 120
DB 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALVYCALPYINSSNYRGAAPFDIWGQT 120
QY 121 MVTSS 126
DB 115 LVTSS 120

RESULT 3
HV3I_HUMAN          STANDARD;          PRT;          119 AA.
ID   P01770;
AC   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region NIB.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OX   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponsing H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure."
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
[2]
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreher L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges."
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG01 MYELOMA
CC   PROTEIN.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A91668; GIH0NT.
DR   HSSP; P01772; 2F84.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_Like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN 1 112 IG-LIKE.
FT   MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID 22 96
FT   NON TER 119 119
SQ   SEQUENCE 119 AA; 13242 MW; C96935A655E1658 CRC64;

Query Match 64.0%; Score 425.5; DB 1; Length 119;
Best Local Similarity 66.7%; Pred. No. 3.8e-37;
Matches 84; Conservative 14; Mismatches 21; Indels 7; Gaps 1;

QY 1 OVQLVSGGGLVQPGSLRLSCAAGFTGPDVAIHVRQAPGSGLEWVGVTWSTTIGF 60
DB 1 OVQLVSGGGLVQPGSLRLSCAAGFTFRTTIVWDAPGSGLEWVANSYGBBIGHY 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALVYCALPYINSSNYRGAAPFDIWGQT 120
DB 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALVYCA-----RIQTAEPFAWGQT 113
QY 121 MVTSS 126
DB 114 LVTSS 119

RESULT 4
HV3T_HUMAN          STANDARD;          PRT;          116 AA.
ID   P01781;
AC   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-III region GAL.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.75548 Seconds
(Without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-43

Sequence: 1 QVQLVSGGGLVPGKSLRL.....RRGVAFDIWGQITVTVSS 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	66.8	122	1	HV3G_HUMAN
2	437	65.7	120	1	HV3U_HUMAN
3	425.5	64.0	119	1	HV3I_HUMAN
4	424	63.8	116	1	HV3T_HUMAN
5	422.5	63.5	121	1	HV3J_HUMAN
6	419	63.0	122	1	HV3H_HUMAN
7	414	62.3	114	1	HV3B_HUMAN
8	412	62.0	122	1	HV3A_HUMAN
9	409	61.5	126	1	HV3K_MOUSE
10	398	59.8	136	1	HV3L_MOUSE
11	396	59.5	117	1	HV3C_HUMAN
12	392.5	59.0	115	1	HV3F_HUMAN
13	392.5	59.0	115	1	HV3D_HUMAN
14	386.5	58.1	119	1	HV3L_HUMAN
15	382	57.4	114	1	HV01_CANFA
16	379	57.0	119	1	HV3M_HUMAN
17	379	57.0	122	1	HV20_MOUSE
18	378.5	56.9	120	1	HV3E_HUMAN
19	377.5	56.8	116	1	HV3R_HUMAN
20	377	56.7	119	1	HV38_MOUSE
21	376	56.5	119	1	HV37_MOUSE
22	373	56.1	119	1	HV40_MOUSE
23	372.5	56.0	123	1	HV18_MOUSE
24	372	55.9	117	1	HV3O_HUMAN
25	369	55.5	122	1	HV21_MOUSE
26	368.5	55.4	123	1	HV19_MOUSE
27	367.5	55.3	116	1	HV05_CARAU
28	367	55.2	119	1	HV3N_HUMAN
29	365.5	55.0	123	1	HV22_MOUSE
30	365.5	55.0	123	1	HV23_MOUSE
31	363.5	54.7	117	1	HV02_CANFA
32	362	54.4	111	1	HV35_MOUSE
33	360.5	54.2	115	1	HV32_MOUSE

34	360	54.1	119	1	HV3P_HUMAN	P01777 homo sapien
35	358.5	53.9	113	1	HV30_MOUSE	P01799 mus musculu
36	358.5	53.9	117	1	HV41_MOUSE	P01811 mus musculu
37	356	53.5	98	1	HV57_MOUSE	P01828 mus musculu
38	355.5	53.5	113	1	HV34_MOUSE	P01803 mus musculu
39	354.5	53.3	117	1	HV17_MOUSE	P01786 mus musculu
40	354.5	53.3	123	1	HV24_MOUSE	P01793 mus musculu
41	354.5	53.3	142	1	HV01_RAT	P01805 fatus norv
42	353.5	53.2	113	1	HV02_MOUSE	P01796 mus musculu
43	353.5	53.0	118	1	HV39_MOUSE	P01809 mus musculu
44	352.5	53.0	115	1	HV33_MOUSE	P01802 mus musculu
45	350.5	52.7	123	1	HV25_MOUSE	P01794 mus musculu

ALIGNMENTS

RESULT 1
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP
RX MEDLINE=61013859; Pubmed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RL location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUM.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_Like; 1.
KW Immunoglobulin V region; Pyroglutone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 1 PYROGLUTONE CARBOXYLIC ACID.
FT NON TER 122
SQ SEQUENCE 122 AA; A42D0F17D252P1C2 CRC64;

Query Match 66.8%; Score 444; DB 1; Length 122;
Best Local Similarity 65.1%; Pred. No. 4.8e-39; Indels 4; Gaps 1;
Matches 82; Conservative 23; Mismatches 17;

QY 1 QVQLVSGGGLVPGKSLRLCAASGFTFGDVAIHWRQAPGSGLEWVSGVTSGTTIGF 60
DB 1 QVQLVSGGGLVPGKSLRLCAASGFTFGDVAIHWRQAPGSGLEWVSGVTSGTTIGF 60
QY 61 ADSVKGFTISRNMAKNSLYLTVNSLRAEPTALTYCALPTINSNTRRGVAADINGGCT 120
DB 61 ADSVKGFTISRNMAKNSLYLTVNSLRAEPTALTYCALPTINSNTRRGVAADINGGCT 120
QY 121 MVTVSS 126
DB 117 LVTVSS 122


```
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102506
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-102506

Query Match          80.9%; Score 503; DB 22; Length 118;
Best Local Similarity 82.4%; Pred. No. 1e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

QY 2 VOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKYYA 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VOLVESGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKGLEWVAVISYDGSNKYYA 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 DSVKGRFAISRDNKNTLYLQNMSLTIETDPAVYYCAKDLIESNIAELMGCGTLVTSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCADDYGDYALLDYWGCGTLVTSS 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
PCT-US03-05128-18
; Sequence 18, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034M01
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-05128-18

Query Match          80.9%; Score 503; DB 1; Length 120;
Best Local Similarity 80.0%; Pred. No. 1e-42;
Matches 96; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKGLEWVAVISYDGSNKYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADVKGRFAISRDNKNTLYLQNMSLTIETDPAVYYCAKDLIESNIAELMGCGTLVTSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCADDYGDYALLDYWGCGTLVTSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-371-942-18
; Sequence 18, Application US/10371942
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Reneus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
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; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-18

Query Match          80.9%; Score 503; DB 29; Length 120;
Best Local Similarity 80.0%; Pred. No. 1e-42;
Matches 96; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKGLEWVAVISYDGSNKYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADVKGRFAISRDNKNTLYLQNMSLTIETDPAVYYCAKDLIESNIAELMGCGTLVTSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCADDYGDYALLDYWGCGTLVTSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-791-537-19813
; Sequence 19813, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19813
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-19813

Query Match          80.8%; Score 502.5; DB 22; Length 132;
Best Local Similarity 81.7%; Pred. No. 1.3e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 QVOLVSGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKGLEWVAVISYDGSNKYY 75
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADVKGRFAISRDNKNTLYLQNMSLTIETDPAVYYCAKDLIESNIAELMGCGTLVTSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 ADVKGRFTISRDNKNTLYLQNMGLRAEDTAVYYCAKDLF---YFDDYWGCGTLVTSS 132
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-09-791-537-31924
; Sequence 31924, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31924
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31924

Query Match          80.7%; Score 502; DB 22; Length 118;
Best Local Similarity 80.8%; Pred. No. 1.3e-42;
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US-09-791-106428
; Sequence 106428, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106428
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-106428

Query Match      81.6%; Score 507.5; DB 22; Length 125;
Best Local Similarity 80.0%; Pred. No. 3.8e-43;
Matches 100; Conservative 7; Mismatches 13; Indels 5; Gaps 1;

Cy 1 EVOLVESGGGLVQPGKSLRLSCGVSGLTFSSYGMMHWRAQAPGAGLEWVAVISYDGNKYY 60
Db 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMMHWRAQAPGKLEWVAVISYDGSNKYY 60

Cy 61 ADSVGRPAISRDNAKNTLYIQMNSLTIEDTAIVYCAADLIENIAEA-----LWGQGLT 115
Db 61 ADSVGRFTISRDNKNTLYIQMNSLRADTAIVYCAADPKRAIAAIPNPFDPGQGLT 120

Cy 116 TVVSS 120
Db 121 TVVSS 125

RESULT 7
US-09-791-537-68722
; Sequence 68722, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68722
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-68722

Query Match      81.5%; Score 507; DB 22; Length 118;
Best Local Similarity 80.8%; Pred. No. 4e-43;
Matches 97; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

Cy 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWRAQAPGAGLEWVAVISYDGNKYY 60
Db 1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMMHWRAQAPGKLEWVAVISYDGSNKYY 60

Cy 61 ADSVGRPAISRDNAKNTLYIQMNSLTIEDTAIVYCAADLIENIAEAALWGQGLT 120
Db 61 ADSVGRFTISRDNKNTLYIQMNSLRADTAIVYCAKERVGVWN--WGQGLTVVSS 118

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; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102505
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-102505

Query Match      81.4%; Score 506.5; DB 22; Length 119;
Best Local Similarity 83.2%; Pred. No. 4.6e-43;
Matches 99; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Cy 2 VQLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWRAQAPGAGLEWVAVISYDGNKYYA 61
Db 1 VQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMMHWRAQAPGKLEWVAVISYDGSNKYYA 60

Cy 62 DSVGRPAISRDNAKNTLYIQMNSLTIEDTAIVYCAADLIENIAEAALWGQGLT 120
Db 61 DSVGRFTISRDNKNTLYIQMNSLRADTAIVYCAADLGQWSSD--WGQGLTVVSS 118

RESULT 9
US-09-791-537-31283
; Sequence 31283, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31283
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31283

Query Match      81.4%; Score 506; DB 22; Length 125;
Best Local Similarity 81.5%; Pred. No. 5.4e-43;
Matches 101; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

Cy 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWRAQAPGAGLEWVAVISYDGNKYY 60
Db 1 EVOLVESGGGVVQPGKSLRLSCAASGFTFSSYGMMHWRAQAPGKLEWVAVISYDGSNKYY 60

Cy 61 ADSVGRPAISRDNAKNTLYIQMNSLTIEDTAIVYCAAD--LIENIAEAAL--WGQGLTV 116
Db 61 ADSVGRFTISRDNKNTLYIQMNSLRADTAIVYCAADLYVYSSGYSIDYWGQGLTV 120

Cy 117 TVSS 120
Db 121 TVSS 124

RESULT 10
US-09-791-537-102506
; Sequence 102506, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph

```

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60
DB 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60

QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120
DB 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120

RESULT 2
US-09-674-752-46
; Sequence 46; Application US/09674752
; GENERAL INFORMATION:
; APPLICANT: Vooorberg, Johannes
; TITLE OF INVENTION: Method For Diagnosis and Treatment of Haemophilia A Patients With
; FILE REFERENCE: Sequence Nos 1-59 for 294-86 PCT/US
; CURRENT APPLICATION NUMBER: US/09/674,752
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00285
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: EP 98201543.0
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-752-46

Query Match 100.0%; Score 622; DB 20; Length 120;
Best Local Similarity 100.0%; Pred. No. 8.6e-55;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60
DB 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60

QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120
DB 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120

RESULT 3
US-09-791-537-87993
; Sequence 87993; Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87993
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-87993

Query Match 83.3%; Score 518; DB 22; Length 121;
Best Local Similarity 81.7%; Pred. No. 3.2e-44;
Matches 98; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60
DB 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60

QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120
DB 61 ADVKGRFRTISRDNKNTLYLQNNSLRAEDTAVYFCADFGAGGCGYELTWGQTLTVSS 120

RESULT 4
US-09-791-537-31853
; Sequence 31853; Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31853
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31853

Query Match 81.8%; Score 509; DB 22; Length 121;
Best Local Similarity 80.8%; Pred. No. 2.6e-43;
Matches 97; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60
DB 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60

QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120
DB 61 ADVKGRFRTISRDNKNTLYLQNNSLRAEDTAVYFCADFGAGGCGYELTWGQTLTVSS 120

RESULT 5
US-09-791-537-69157
; Sequence 69157; Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69157
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-69157

Query Match 81.8%; Score 508.5; DB 22; Length 117;
Best Local Similarity 82.5%; Pred. No. 2.8e-43;
Matches 99; Conservative 7; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60
DB 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWVROAPGAGLEWAVISYDGNDKYY 60

QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIETDAVYYCAKDLESNIABALMGQTLTVSS 120
DB 61 ADVKGRFRTISRDNKNTLYLQNNSLRAEDTAVYFCADFGAGGCGYELTWGQTLTVSS 117

RESULT 6

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:54:45 ; Search time 191.162 Seconds
(without alignments)
571.193 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622
Sequence: 1 EVQLVESGGGLVQPGKSLRL.....IESNIAELALWGQTLTVVSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
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16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
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29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	100.0	120	US-09-674-752-36	Sequence 36, App1

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	622	100.0	120	20	US-09-674-752-46	Sequence 46, App1	518	83.3	121	22	US-09-791-537-87993	Sequence 87993, A	509	81.8	121	22	US-09-791-537-31853	Sequence 31853, A	508.5	81.8	117	22	US-09-791-537-69157	Sequence 69157, A	507.5	81.5	125	22	US-09-791-537-106428	Sequence 106428, A	507	81.6	125	22	US-09-791-537-68722	Sequence 68722, A	506.5	81.4	119	22	US-09-791-537-102505	Sequence 102505, A	506	81.4	125	22	US-09-791-537-31283	Sequence 31283, A	503	80.9	118	22	US-09-791-537-102506	Sequence 102506, A	503	80.9	120	1	PCT-US03-05128-18	Sequence 18, App1	502.5	80.8	132	22	US-09-791-537-119813	Sequence 119813, A	502	80.7	118	22	US-09-791-537-31924	Sequence 31924, A	502	80.7	122	22	US-09-791-537-69145	Sequence 69145, A	502	80.6	128	22	US-09-791-537-63340	Sequence 63340, A	501.5	80.6	119	22	US-09-791-537-80297	Sequence 80297, A	501.5	80.6	120	22	US-09-791-537-63269	Sequence 63269, A	501.5	80.6	121	1	PCT-US03-05128-54	Sequence 54, App1	501.5	80.6	121	1	PCT-US03-05128-62	Sequence 62, App1	501.5	80.6	121	29	US-10-371-942-54	Sequence 54, App1	501.5	80.6	121	29	US-10-371-942-62	Sequence 62, App1	501.5	80.6	123	22	US-09-791-537-69270	Sequence 69270, A	501.5	80.6	123	28	US-10-269-711-7	Sequence 7, App1	501.5	80.6	123	32	US-10-269-711-7	Sequence 7, App1	501.5	80.6	123	32	US-09-000-802-11	Sequence 11, App1	501.5	80.6	120	22	US-09-791-537-69606	Sequence 69606, A	501	80.5	122	1	PCT-US02-36107-114	Sequence 114, App	501	80.5	122	28	US-10-292-088-114	Sequence 114, App	501	80.5	126	22	US-09-791-537-106426	Sequence 106426, A	501	80.5	138	22	US-09-791-537-102461	Sequence 102461, A	501	80.5	227	1	PCT-US02-33556-76	Sequence 76, App1	501	80.5	227	25	US-09-972-656-76	Sequence 76, App1	501	80.5	241	1	PCT-US03-09625-100	Sequence 100, App	500.5	80.5	121	22	US-09-791-537-106429	Sequence 106429, A	500.5	80.5	123	28	US-10-269-711-43	Sequence 43, App1	500.5	80.5	123	32	US-09-791-537-116121	Sequence 116121, A	500.5	80.5	133	22	US-09-791-537-71741	Sequence 71741, A	500	80.4	130	22	US-09-791-537-31907	Sequence 31907, A	500	80.4	130	22	US-09-791-537-116626	Sequence 116626, A	500	80.4	133	22	US-09-791-537-11717	Sequence 11717, App	500	80.4	232	22	US-09-791-537-128053	Sequence 128053, A	499.5	80.3	135	22	US-09-791-537-96305	Sequence 96305, A	499.5	80.3	138	18	US-09-403-107-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-09-674-752-36
Sequence 36, Application US/09674752
GENERAL INFORMATION:
APPLICANT: Vooberg, Johannes
TITLE OF INVENTION: Method For Diagnosis and Treatment of Haemophilia A Patients With
FILE REFERENCE: Sequence Nos 1-59 for 294-86 PCT/US
CURRENT APPLICATION NUMBER: US/09/674,752
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: PCT/US99/00285
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: EP 98201543.0
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-09-674-752-36
Query Match 100.0%; Score 622; DB 20; Length 120;
Best Local Similarity 100.0%; Pred. No. 8.6e-55;


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Qy      1 EVOLVESGGGLVQPGKSLRLSCVDSGIEFTSSVGMHVRQAPGAGLEWVAIVSYDGNKTY 60
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Db      1 QVQLVDSGGGVQPGKSLRLSCAASGFTSSVGMHVRQAPGKLEWVAIVSYDGSIKYY 60
Qy      61 ADSVKGKRFATSRDNNKNTLYIQMNSLTIEDTAVYYCAKDLIESNIAEALWGCGTLVTSS 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61 ADSVKGKRFATSRDNNKNTLYIQMNSLAEEDTAVYYCARD--AAVTAEGWGKGLVTSS 117
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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Search completed: December 30, 2003, 11:45:24
 Job time : 25.7352 secs

;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: ABGENIX.051A
;; CURRENT APPLICATION NUMBER: US/10/041,860
;; CURRENT FILING DATE: 2002-01-07
;; NUMBER OF SEQ ID NOS: 377
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 33
;; LENGTH: 127
;; TYPE: PRF
;; ORGANISM: homo sapiens
US-10-041-860-33

Query Match 79.3%; Score 493.5; DB 12; Length 127;
Best Local Similarity 74.8%; Pred. No. 2.8e-40;
Matches 95; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMHWVQAPAGLEWVAIVSYDGNKDY 60
DB 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYGMHWVQAPGKLEWVAIIWYDGNKDY 60
QY 61 ADVKGRFAISRDNKNTLYLQMSLTIEDTAVYYCAK-----DLIESNIAELMGQG 113
DB 61 ADVKGRFVSRDNRKNTLYLQMSLRADTAVYYCARGYYDSDYLYYYGMDVWGQG 120
QY 114 TLVTVSS 120
DB 121 TTVTVSS 127

RESULT 13

US-10-041-860-211
;; Sequence 211, Application US/10041860
;; Publication No. US20030157109A1
;; GENERAL INFORMATION:
;; APPLICANT: Corvalan, Jose R.F.
;; APPLICANT: Jia, Xiao-Chi
;; APPLICANT: Peng, Xiao
;; APPLICANT: Yang, Xiao-Dong
;; APPLICANT: Chen, Francine
;; APPLICANT: Gazit, Gadi
;; APPLICANT: Weber, Richard
;; APPLICANT: Bezabeh, Binyam
;; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
;; FILE REFERENCE: THEREOF
;; CURRENT APPLICATION NUMBER: US/10/041,860
;; CURRENT FILING DATE: 2002-01-07
;; NUMBER OF SEQ ID NOS: 377
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 211
;; LENGTH: 127
;; TYPE: PRF
;; ORGANISM: homo sapiens
US-10-041-860-211

Query Match 79.3%; Score 493.5; DB 12; Length 127;
Best Local Similarity 74.8%; Pred. No. 2.8e-40;
Matches 95; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMHWVQAPAGLEWVAIVSYDGNKDY 60
DB 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYGMHWVQAPGKLEWVAIIWYDGNKDY 60
QY 61 ADVKGRFAISRDNKNTLYLQMSLTIEDTAVYYCAK-----DLIESNIAELMGQG 113
DB 61 ADVKGRFVSRDNRKNTLYLQMSLRADTAVYYCARGYYDSDYLYYYGMDVWGQG 120
QY 114 TLVTVSS 120
DB 121 TTVTVSS 127

RESULT 14

US-10-041-860-331

;; Sequence 331, Application US/10041860
;; Publication No. US20030157109A1
;; GENERAL INFORMATION:
;; APPLICANT: Corvalan, Jose R.F.
;; APPLICANT: Jia, Xiao-Chi
;; APPLICANT: Peng, Xiao
;; APPLICANT: Yang, Xiao-Dong
;; APPLICANT: Chen, Francine
;; APPLICANT: Gazit, Gadi
;; APPLICANT: Weber, Richard
;; APPLICANT: Bezabeh, Binyam
;; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
;; FILE REFERENCE: THEREOF
;; CURRENT APPLICATION NUMBER: US/10/041,860
;; CURRENT FILING DATE: 2002-01-07
;; NUMBER OF SEQ ID NOS: 377
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 331
;; LENGTH: 127
;; TYPE: PRF
;; ORGANISM: homo sapiens
US-10-041-860-331

Query Match 79.3%; Score 493.5; DB 12; Length 127;
Best Local Similarity 74.8%; Pred. No. 2.8e-40;
Matches 95; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMHWVQAPAGLEWVAIVSYDGNKDY 60
DB 1 QVQLVESGGGVQPGSRSLRSCAASGFTFSYGMHWVQAPGKLEWVAIIWYDGNKDY 60
QY 61 ADVKGRFAISRDNKNTLYLQMSLTIEDTAVYYCAK-----DLIESNIAELMGQG 113
DB 61 ADVKGRFVSRDNRKNTLYLQMSLRADTAVYYCARGYYDSDYLYYYGMDVWGQG 120
QY 114 TLVTVSS 120
DB 121 TTVTVSS 127

RESULT 15

US-09-880-748-1912
;; Sequence 1912, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1912
;; LENGTH: 240
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-09-880-748-1912

Query Match 79.3%; Score 493.5; DB 11; Length 240;
Best Local Similarity 79.2%; Pred. No. 5.6e-40;
Matches 95; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

```
APPLICANT: Es van, Helmut
APPLICANT: Havena, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID
TITLE OF INVENTION: TRANSPORTER
FILE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/10/235,175
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: US/09/315,926
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: EP 99201593.3
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 80
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Description of Artificial Sequence: phage
LOCATION: (1)..(248)
OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-10-235-175-80
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Query Match 79.6%; Score 495; DB 12; Length 248;
Best Local Similarity 78.3%; Pred. No. 4.2e-40;
Matches 94; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
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Db 23 QVQLVDSGGGVQPGSRSLRLSCASGFTFSSYGMHWVRQAAGGLEWVAIVSYDGNKYY 82
Qy 61 ADSVKGRAISRDNKNTLYLQWNSLTIEDTAVVYCAKDLIESNIAEALMGOGTLVTSS 120
Db 83 ADSVKGRTISRDNKNTLYLQWNSLRAEDTAVVYCAKGIYTKSRPFYWGOGTLVTSS 142
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RESULT 10
US-09-880-748-512
Sequence 512, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 512
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-512
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Query Match 79.6%; Score 495; DB 11; Length 249;
Best Local Similarity 77.0%; Pred. No. 4.2e-40;
Matches 97; Conservative 7; Mismatches 16; Indels 6; Gaps 1;
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Qy 1 EVQLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGHWVRQAAGGLEWVAIVSYDGNKYY 60
Db 1 QVQLVDSGGGVQPGSRSLRLSCASGFTFSSYGMHWVRQAAGGLEWVAIVSYDGNKYY 60
Qy 61 ADSVKGRAISRDNKNTLYLQWNSLTIEDTAVVYCAKDLIESNIAEALMGOGT 114
Db 61 ADSVKGRTISRDNKNTLYLQWNSLRAEDTAVVYCAKGIYTKSRPFYWGOGT 120
Qy 115 LVTYSS 120
Db 121 MVTYSS 126
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```
RESULT 11
US-09-880-748-1109
Sequence 1109, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1109
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1109
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Query Match 79.4%; Score 494; DB 11; Length 249;
Best Local Similarity 76.2%; Pred. No. 5.2e-40;
Matches 96; Conservative 10; Mismatches 14; Indels 6; Gaps 2;
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Qy 1 EVQLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGHWVRQAAGGLEWVAIVSYDGNKYY 60
Db 1 QVQLVDSGGGVQPGSRSLRLSCASGFTFSSYGMHWVRQAAGGLEWVAIVSYDGNKYY 60
Qy 61 ADSVKGRAISRDNKNTLYLQWNSLTIEDTAVVYCAKDLIESNIAEALMGOGT 114
Db 61 VDSVKGRTISRDNKNTLYLQWNSLRAEDTAVVYCAKGIYTKSRPFYWGOGT 120
Qy 115 LVTYSS 120
Db 121 MVTYSS 126
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```
RESULT 12
US-10-041-860-33
Sequence 33, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gad
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PGPFD AND USES
```


US-10-325-694-144
; Sequence 144, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 144
; LENGTH: 138
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-144

Query Match 80.3%; Score 499.5; DB 12; Length 138;
Best Local Similarity 77.2%; Pred. No. 8.1e-41;
Matches 98; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWVAVISYDNDKYY 60
DB 1 EVOLVESGGGVOPGSRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWVAVISYDGSNKYY 60
QY 61 ADVSKGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLIESN-----IABALWGG 113
DB 61 ADVSKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKDWGSGWPRYYGYGMDVWGQ 120
QY 114 TLVTVSS 120
DB 121 TTVTVSS 127

RESULT 3

US-10-269-805-21
; Sequence 21, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-21

Query Match 80.1%; Score 498.5; DB 15; Length 123;
Best Local Similarity 79.7%; Pred. No. 8.9e-41;
Matches 98; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWVAVISYDNDKYY 60
DB 1 EVOLVESGGGVOPGSRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWVAVISYDGSNKYY 60
QY 61 ADVSKGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAK---DLIESNIAEALWGGTLVT 117
DB 61 ADVSKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKGPVDPYGYDAIDYWGQGLTIVT 120
QY 118 VSS 120
DB 121 VSS 123

RESULT 4
US-09-880-748-1731
; Sequence 1731, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyts
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1731
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1731

Query Match 80.1%; Score 498.5; DB 11; Length 252;
Best Local Similarity 75.2%; Pred. No. 1.9e-40;
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWVAVISYDNDKYY 60
DB 1 EVOLVESGGGVOPGSRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWVAVISYDGSNKYY 60
QY 61 ADVSKGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLIE-----SNIABALW 111
DB 61 ADVSKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCARLREYDILTGYYYYGYMDVWG 120
QY 112 QGTLTVSS 120
DB 121 RGTTLTVSS 129

RESULT 5

US-09-791-153A-63
; Sequence 63, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deehpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 63
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-63

Query Match 80.0%; Score 497.5; DB 11; Length 113;
Best Local Similarity 80.8%; Pred. No. 1e-40;
Matches 97; Conservative 5; Mismatches 11; Indels 7; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 25.7352 Seconds
(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622
Sequence: 1 EVOLVESGGGLVQPGKSLRL.....IESNIAELMGQGLTVTSS 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	80.5	227	11	US-09-972-656-76 Sequence 76, App1
2	499.5	80.3	138	12	US-10-325-694-144 Sequence 14, App1
3	498.5	80.1	123	15	US-10-269-805-21 Sequence 21, App1
4	498.5	80.1	252	11	US-09-880-748-1731 Sequence 1731, App1
5	497.5	80.0	113	11	US-09-791-1534-63 Sequence 63, App1
6	496.5	79.8	138	12	US-10-325-694-150 Sequence 150, App1
7	495.5	79.7	119	12	US-10-010-729-7 Sequence 7, App1
8	495.5	79.7	252	11	US-09-880-748-1394 Sequence 1394, App1
9	495	79.6	248	12	US-10-235-175-80 Sequence 80, App1
10	495	79.6	249	11	US-09-880-748-512 Sequence 512, App1
11	494	79.4	249	11	US-09-880-748-1109 Sequence 1109, App1
12	493.5	79.3	127	12	US-10-041-860-33 Sequence 33, App1
13	493.5	79.3	127	12	US-10-041-860-211 Sequence 211, App1
14	493.5	79.3	127	12	US-10-041-860-331 Sequence 331, App1
15	493.5	79.3	240	11	US-09-880-748-1912 Sequence 1912, App1

16	493	79.3	248	11	US-09-880-748-1890 Sequence 1890, App1
17	491.5	79.0	109	12	US-10-309-764-1 Sequence 1, App1
18	491.5	79.0	123	15	US-10-269-805-1 Sequence 1, App1
19	491	78.9	122	15	US-10-269-805-39 Sequence 39, App1
20	490.5	78.9	119	12	US-10-120-377-76 Sequence 76, App1
21	490	78.8	241	11	US-09-880-748-1887 Sequence 1887, App1
22	490	78.8	241	11	US-09-880-748-1901 Sequence 1901, App1
23	490	78.8	247	11	US-09-880-748-1330 Sequence 1330, App1
24	490	78.8	249	11	US-09-880-748-1397 Sequence 1397, App1
25	490	78.8	249	11	US-09-880-748-1102 Sequence 1102, App1
26	490	78.8	249	11	US-09-880-748-1115 Sequence 1115, App1
27	489	78.6	249	11	US-09-880-748-1117 Sequence 1117, App1
28	489	78.6	252	11	US-09-880-748-1627 Sequence 1627, App1
29	488.5	78.5	238	11	US-09-880-748-1931 Sequence 1931, App1
30	488.5	78.5	451	15	US-10-153-182-17 Sequence 17, App1
31	488	78.5	118	12	US-10-120-377-78 Sequence 78, App1
32	488	78.5	247	11	US-09-880-748-924 Sequence 924, App1
33	488	78.5	252	11	US-09-880-748-1519 Sequence 1519, App1
34	488	78.5	254	11	US-09-880-748-977 Sequence 977, App1
35	487	78.3	249	11	US-09-880-748-911 Sequence 911, App1
36	487	78.3	249	11	US-09-880-748-1119 Sequence 1119, App1
37	487	78.3	249	11	US-09-880-748-1956 Sequence 1956, App1
38	486	78.1	122	15	US-10-269-805-53 Sequence 53, App1
39	486	78.1	251	11	US-09-880-748-952 Sequence 952, App1
40	486	78.1	251	11	US-09-880-748-982 Sequence 982, App1
41	486	78.1	254	11	US-09-880-748-981 Sequence 981, App1
42	486	78.1	254	11	US-09-880-748-1428 Sequence 1428, App1
43	485.5	78.1	123	15	US-10-243-265-2 Sequence 2, App1
44	485.5	78.1	241	11	US-09-880-748-2055 Sequence 2055, App1
45	485	78.0	122	10	US-09-144-886-68 Sequence 68, App1

ALIGNMENTS

RESULT 1
US-09-972-656-76
Sequence 76, Application US/09972656
Publication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 76
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-76

Query Match 80.5%, Score 501, DB 11, Length 227;
Best Local Similarity 77.4%, Pred. No. 1e-40;
Matches 96; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

QY	1	EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSGYGMHWQAQAGLEWVAIVSYDNDKYY	60
DB	1	OVOLVETGGVVGQGRSLRLSCASGFTSSYAMHWQAQAGLEWVAIVSYDNDKYY	60
QY	61	ADSVKGRPAISRDNKNTLYQNNSLTIEDTAVYYCAKOLI-----ESNIAELMGQGLTV	116
DB	61	ADSVKGRFTISRDNKNTLYQNNSLRAEDTAVYYCAADLVLTMTSRRAFDIWDGQTMV	120
QY	117	TVSS 120	
DB	121	TVSS 124	

RESULT 2

CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromultibodies have
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas.
 CC The present sequence is the left chain of a heteromultibody
 CC comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to
 CC human CH1 domain which bears at its C-terminus the human inflammatory
 CC cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus
 CC a heparin-binding sequence for ease of purification. HD70 scFv
 CC specifically recognises the human epithelial cell adhesion molecule
 CC (EPCAM) also called 17-1A antigen.
 CC
 SO Sequence 523 AA:
 Query Match 79.8%; Score 496.5; DB 21; Length 523;
 Best Local Similarity 76.4%; Pred. No. 4,7e-39;
 Matches 97; Conservative 8; Mismatches 15; Indels 7; Gaps 1;
 QY 1 EVQLVSGGGLVQPGKSLRLSCYDSGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 60
 DB 142 EVQLVSGGGLVQPGKSLRLSCAASGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 201
 QY 61 ADSVKGKPAISRDNKATLYLQNNSLTIETDAVYYCAKDLEISN-----IAEALMGOG 113
 DB 202 ADSVKGKFTISRDNKATLYLQNNSLRAEDTAVYYCAKDGMGSGRPYYTYGMDVWGOG 261
 QY 114 TLVTVSS 120
 DB 262 TLVTVSS 268
 RESULT 10
 ID AAY44995 standard; Protein; 524 AA.
 AC AAY44995;
 XX
 DT 23-MAY-2000 (first entry)
 DE HD70scFv-CK-interleukin 2.
 XX
 KM HD70: single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;
 KM B2CAM, epithelial cell adhesion molecule; inflammatory cytokine;
 KM IL-2; interleukin-2; CK-domain; kappa light chain constant domain;
 KM heteromultibody; multifunctional compound; immunoglobulin;
 KM cytostatic; immunostimulatory; antileukemia; diagnosis; prevention;
 KM antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
 KM leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
 XX
 OS Homo sapiens.
 PN W0200006605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PF 28-JUL-1999; 99WO-BP05416.
 XX
 PR 28-JUL-1998; 98EP-0114082.
 XX
 PA (MICR-) MICROMET GBS BIOMEDIZINISCHE FORSCHUNG.
 PI Kufer P, Dreier T, Baerle PA, Borschert K, Zettl F;
 DR WPI; 2000-195265/17.
 DR N-PSDB; AA250588.
 XX
 PT New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis
 XX
 PS Example 10; Fig 55B; 16pp; English.

XX
 CC The patent discloses heteromultibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secreted and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises, a CH1 domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises CL domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromultibodies have
 CC cytostatic, immunostimulatory, antileukemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas.
 CC The present sequence is the right chain of a heteromultibody
 CC comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to
 CC human CK domain (constant domain of immunoglobulin-kappa light chain)
 CC which bears at its C-terminus the human inflammatory cytokine
 CC interleukin-2 (IL-2). HD70 scFv specifically recognises the human
 CC epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.
 CC
 SO Sequence 524 AA:
 Query Match 79.8%; Score 496.5; DB 21; Length 524;
 Best Local Similarity 76.4%; Pred. No. 4,7e-39;
 Matches 97; Conservative 8; Mismatches 15; Indels 7; Gaps 1;
 QY 1 EVQLVSGGGLVQPGKSLRLSCYDSGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 60
 DB 142 EVQLVSGGGLVQPGKSLRLSCAASGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 201
 QY 61 ADSVKGKPAISRDNKATLYLQNNSLTIETDAVYYCAKDLEISN-----IAEALMGOG 113
 DB 202 ADSVKGKFTISRDNKATLYLQNNSLRAEDTAVYYCAKDGMGSGRPYYTYGMDVWGOG 261
 QY 114 TLVTVSS 120
 DB 262 TLVTVSS 268
 RESULT 11
 ID ABB07169 standard; Protein; 119 AA.
 AC ABB07169;
 XX
 DT 13-MAR-2002 (first entry)
 DE shlgM22 heavy chain variable region clone A sequence.
 XX
 KM Neuromodulatory; central nervous system; CNS; shlgM22; LYM 22; AKR4;
 KM edvH1GM M6119D10; edv H1GM CB2B68; CB21E12; CB21E5; vlnucide;
 KM antiParkinsonian; neuroprotective; nootropic; vulnerary.
 XX
 OS Homo sapiens.
 PN W0200185797-A1.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-MAY-2000; 2000MO-US14902.
 XX
 PR 10-MAY-2000; 2000US-0568351.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
 PI Rodriguez M, Miller DJ, Pease LR;
 DR WPI; 2002-066596/09.
 DR N-PSDB; ABA94216.
 XX

Matches	97;	Conservative	7;	Mismatches	15;	Indels	1;	Gaps	1;
QY	1	EVOLVESSGGLVQGRGRSLRLSCVDSGLTFSSYGNHMPVQAGAGLEWVAVSYSDNDKTY	60						
Db	1	QVQLVDSGGVAVQPPRSFRLRLSCASGFTFSSGGMHVAQAPKGLIEWVAIISYDSGRKY	60						
QY	61	ADSVKGRFAISRDNKNTLTYLQNNSLTIEDPAVYVYCAQDLIESNIAEALMGQGLVTVSS	120						
Db	61	ADSVKGRFTISRDNKNTLTYLQNNSLTIEDPAVYVYCAQGVTVGSPTLD-YMGQGLVTVSS	119						
RESULT 6									
AAW15522									
ID	AAW15522	standard; Protein; 115 AA.							
XX	AAW15522;								
AC									
XX									
DT	27-NOV-1997	(first entry)							
XX									
DE	Anti-TGF beta-2 scFv antibody 2A-H11 VH domain.								
XX									
XX	Transforming growth factor beta-2; TGF-beta-2; human;								
KM	antibody engineering; scFv; phage display; lung fibrosis;								
KM	arterial injury; proliferative retinopathy; retinal detachment;								
KM	adult respiratory distress syndrome; liver cirrhosis;								
KM	post myocardial infarction; post-angioplasty restenosis;								
KM	ectoderm; vascular disease; cataract; glaucoma; scarring;								
KM	glomerulonephritis; osteoporosis; immune disease; inflammation;								
KM	rheumatoid arthritis; macrophage deficiency disease;								
XX	macrophage pathogen infection; therapy.								
XX									
OS	Chimeric Homo sapiens;								
OS	Chimeric synthetic.								
XX									
FH	Key	Location/Qualifiers							
FT	Region	31..35							
FT		/label= CDR1							
FT		/note= "complementarity determining region 1"							
FT	Region	50..67							
FT		/label= CDR2							
FT		/note= "complementarity determining region 2"							
FT	Region	99..104							
FT		/label= CDR3							
FT		/note= "complementarity determining region 3"							
XX									
PN	GB2305921-A.								
XX									
PD	23-APR-1997.								
XX									
XX	07-OCT-1996;	96GB-002092							

Query Match	Best Local Similarity	79.8% Matches 97; Conservative	Score 496.5; Pred. No. 8.3e-40; 6; Mismatches 12;	DB 18; Indels 5; Gaps 1	Length 115;
Dd	1 EVOLVEGGGGLVPGGRSLRLSCVDSGLTFFSSYGMHWYQADGAGLEWYAVISYDGNDRXY	60			
Dd	1 EVOLVEGGGGLVPGGRSLRLSCVDSGLTFFSSYGMHWYQADGAGLEWYAVISYDGNDRXY	60			
Dd	61 ADVYKGRFTISRDNSKNTLYIQMDSLRAEDPAVYVYGGRTLESS-----LWGQGITLVTVSS	115			
RESULT 7					
AA171954					
ID	AA171954	standard; Protein; 127 AA.			
XX	AA171954;				
AC	AA171954;				
DT	04-AUG-1999	(first entry)			
DE	Human D4.5 heavy chain variable region.				
XX	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;				
KW	autoimmune disease; scFv-antibody; single-chain Fv.				
XX	Homo sapiens.				
OS					
PN	MO9925618-A1.				
PD	27-MAY-1999.				
XX					
PF	16-NOV-1998;	98WO-EP07313.			
XX					
PR	17-NOV-1997;	97EP-0120096.			
PA	(KUFEL) KUFER P.				
XX					
PI	Borchert K, Kufer P, Luttreuse R, Raum T, Zeitl F;				
XX					
DR	WPI, 1999-338004/28.				
XX	N-PSDB; AAX77236.				
XX					
PT	Phase display system for identification of binding site domains				
XX	retaining capacity to bind an epitope				
XX					
PS	Disclosure; Fig 3.1; 152pp; English.				
XX					
CC	The invention relates to a method of identifying binding site domains				
CC	(BSD) that retain the capacity of binding to a predetermined epitope when				
CC	positioned C-terminal of at least one further domain in a recombinant bi-				
CC	or multivalent polypeptide. The method comprises (a) testing a panel of				
CC	BSD displayed on the surface of a biological display system as part of a				
CC	fusion protein for binding to a predetermined epitope, where the fusion				

ID ABB45720 standard; Protein; 252 AA.
XX
AC ABB45720;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1731.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytotoxic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PE 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
XX
PR 17-OCT-2000; 2000US-240816P.
XX
PR 16-MAR-2001; 2001US-276248P.
XX
PR 21-MAR-2001; 2001US-277379P.
XX
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2468-2469; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antineumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABB43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
SQ Sequence 252 AA;
XX
Query Match 80.1%; Score 498.5; DB 23; Length 252;
Best Local Similarity 75.2%; Pred. No. 1.3e-39;
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 1;
XX
QY 1 EVQLVESGGGLVQPRSLRLSCVDSGLTPSSSGMMWRQAPAGLGVAVSYDSNDKRY 60
DB 1 OVQLVESGGGVQPRSLRLSCAASGFTSSSGMMWRQAPKGLGVAVSYDSNRY 60
XX
QY 61 ADSVGRFAISRDNANTLYLQMSLTIEDTAVVYCAKDLR-----SNIAELWG 111
DB 61 ADSVGRFTISRDNKNTLYLQMSLRADTAVVYCAKDRLEYDILGYTYTYGMDYWG 120

QY 112 QGLTVVSS 120
DB 121 RGLTVVSS 129
XX
RESULT 5
ID ABB07186 standard; Protein; 119 AA.
XX
AC ABB07186;
XX
DT 13-MAR-2002 (first entry)
XX
DE bHlgM22 heavy chain variable region clone B sequence.
XX
KW Neuromodulatory; central nervous system; CNS; bHlgM22; LYM 22; AKR4;
KW ebvHlgM M6119D10; ebv HlgM CB2bG8; CB21E12; CB21E7; MS119E5; vtrucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PR 30-MAY-2000; 2000WO-US14902.
XX
PR 10-MAY-2000; 2000US-0568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
XX
DR N-PSDB; ABA94243.
XX
PT Novel neuromodulatory agent (a human Igm monoclonal antibody),
XX promoting neurite outgrowth, regeneration, remyelination and
XX post-infectious encephalomyelitis -
XX
PS Claim 23; Fig 17; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system (CNS). (I) is capable of inducing remyelination,
XX promoting cellular proliferation of glial cells, and promoting Ca2+
XX signaling with oligodendrocytes. An humanised antibody to (I) can be
XX selected from antibody bHlgM22 (LYM 22), ebvHlgM M6119D10, ebv HlgM
XX CB2bG8, AKR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating
XX remyelination of CNS axons, stimulating proliferation of glial cells in
XX CNS axons, or treating demyelinating disease of CNS in a mammal in need
XX of such therapy. (I) is capable of binding to structures and cells within
XX CNS. (I) is preferably useful for treating a demyelinating disease of CNS
XX of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
XX (TMEV) or for treating a human being having multiple sclerosis, or a
XX human or domestic animal with a viral demyelinating disease, or a post-
XX neural disease of CNS. (I) is also useful for an in vitro method of
XX stimulating the proliferation of glial cells from mixed cell culture.
XX (I) is also useful for stimulating remyelination of CNS axons. The
XX antibodies are useful for preventing infection by a bacterium, virus or
XX like pathogen that causes demyelination or other neurodegenerative
XX condition in a subject. Methods where (I) is administered to a patient
XX are useful for treating multiple sclerosis, Parkinson's disease,
XX Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
XX demyelinating disease, CNS diseases, and other conditions in the CNS
XX where nerves are damaged as by trauma. The present sequence represents
XX the bHlgM22 heavy chain variable region clone B amino acid sequence.
XX
SQ Sequence 119 AA;
XX
Query Match 80.0%; Score 497.5; DB 23; Length 119;
Best Local Similarity 80.8%; Pred. No. 6.9e-40;

XX Example 8; Fig 9A; 61pp; English.

PS This invention describes a novel polynucleotide (I) (a

XX hybridizable polynucleotide) comprising a contiguous

CC coding for a human antibody with factor VIII specific;

CC hemostatic activity. (I) is useful as a primer or probe

CC presence of inhibitory antibodies directed against fac

CC polypeptides of the invention and the antibodies gene

CC are useful in compositions for neutralizing factor VII

CC antibodies in hemophilia A patients. This sequence rei

CC factor VIII antibody A3-C1 specific scFv protein B35 w

CC in the method of the invention.

XX

SO Sequence 120 AA;

Query Match 100.0%; Score 622; DB 21; Leng 20;

Best Local Similarity 100.0%; Pred. No. 9.5e-52;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWROAPGAGI VISYDGNKYY 60

DB 1 EVOLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWROAPGAGI VISYDGNKYY 60

QY 61 ADSVKGKFAISRDNKNTLYLQMNSLTIETDAVYYCAKDLIESN MGQGLTVTVSS 120

DB 61 ADSVKGKFAISRDNKNTLYLQMNSLTIETDAVYYCAKDLIESN MGQGLTVTVSS 120

RESULT 2

AAV50968

ID AAV50968 standard; Protein; 120 AA.

XX AAV50968;

AC 23-MAR-2000 (first entry)

DT 23-MAR-2000 (first entry)

XX Human FVIIII antibody heavy chain variable region B35 f

DE Human; heavy chain; antibody; factor VIII; hemostatic;

XX hemophilia A.

XX Homo sapiens.

OS WC0958680-A2.

PN 18-NOV-1999.

PD 07-MAY-1999; 99WO-NL00285.

PF 08-MAY-1998; 98EP-0201543.

PR (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

PI Voorberg JJ, Van Den Brink EW, Turenhout EAM;

XX WPI; 2000-053102/04.

DR N-PSDB; AAZ43865.

DR New polynucleotide, polypeptide and antibody useful f

PT presence of neutralizing antibodies against factor VII

XX treatment of hemophilia A patients with these antibod

XX Example 8; Fig 9D; 61pp; English.

XX This invention describes a novel polynucleotide (I) (

CC hybridizable polynucleotide) comprising a contiguous

CC coding for a human antibody with factor VIII specific;

CC hemostatic activity. (I) is useful as a primer or probe

CC presence of inhibitory antibodies directed against fac

CC polypeptides of the invention and the antibodies gene

CC are useful in compositions for neutralizing factor VII

CC antibodies in hemophilia A patients. This sequence rei

XX complements and

XX eotide sequence

XX which has

XX detecting the

XX VIII. The

XX from them

XX inhibiting

XX nts the human

XX is used

CC of the human factor VIII antibody heavy chain variable region protein B35

CC which is used in the method of the invention.

XX

SO Sequence 120 AA;

Query Match 100.0%; Score 622; DB 21; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.5e-52;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60

DB 1 EVOLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60

QY 61 ADSVKGKFAISRDNKNTLYLQMNSLTIETDAVYYCAKDLIESNIAEALMGQGLTVTVSS 120

DB 61 ADSVKGKFAISRDNKNTLYLQMNSLTIETDAVYYCAKDLIESNIAEALMGQGLTVTVSS 120

RESULT 3

AAV08598

ID AAV08598 standard; Protein; 223 AA.

XX AAV08598;

AC 05-AUG-1999 (first entry)

DT 05-AUG-1999 (first entry)

XX Anti-human TNF-alpha monoclonal antibody H-chain protein.

DE Anti-human TNF-alpha monoclonal antibody H-chain protein.

XX Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;

XX tumour necrosis factor; light chain; L chain.

XX Homo sapiens.

OS JP11127855-A.

PN 18-MAY-1999.

PD 27-OCT-1997; 97JP-0293994.

PF 27-OCT-1997; 97JP-0293994.

PR (NIHA) JAPAN ENERGY CORP.

XX WPI; 1999-350318/30.

DR N-PSDB; AAX77407.

DR Recombinant anti-human TNF-alpha human monoclonal antibody -

PT produced stably with a high purity, and in large amounts

XX Claim 3; Page 12-13; 22pp; Japanese.

XX This invention describes novel recombinant anti-human TNF-alpha human

CC monoclonal antibody consisting of a heavy (H) chain and a light (L)

CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody

CC can be produced stably in a high purity and in a large amount.

XX

SO Sequence 223 AA;

Query Match 82.6%; Score 514; DB 20; Length 223;

Best Local Similarity 81.7%; Pred. No. 3.8e-41;

Matches 98; Conservative 9; Mismatches 11; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60

DB 1 EVOLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60

QY 61 ADSVKGKFAISRDNKNTLYLQMNSLTIETDAVYYCAKDLIESNIAEALMGQGLTVTVSS 120

DB 61 ADSVKGKFAISRDNKNTLYLQMNSLTIETDAVYYCAKDLIESNIAEALMGQGLTVTVSS 118

RESULT 4

ABP45720

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 3f
(without alignment)
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updates/sec

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
5: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
6: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
7: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
8: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
9: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
10: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
11: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
12: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
13: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
14: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
15: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
16: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
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22: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
23: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA
24: /SIDSI1/gcgdata/geneseq/geneseqp-emb1/AA

Pred. No. is the number of results predicted by chance
score greater than or equal to the score of the result
and is derived by analysis of the total score distrib

SUMMARIES

Result No.	Score	Query Match	Length	ID
1	622	100.0	120	21 AAY50963
2	622	100.0	120	21 AAY50968
3	514	82.6	223	20 AAY08598
4	498.5	80.1	252	23 ABP45720
5	497.5	80.0	119	23 ABP45720
6	496.5	79.8	115	18 AAW15522
7	496.5	79.8	127	20 AAW19554
8	496.5	79.8	138	19 AAW80815
9	496.5	79.8	523	21 AAY44994

10	496.5	79.8	524	21 AAY44995	HD08scFv-CK-interf
11	495.5	79.7	119	23 ABP45715	gHlgM22 heavy chai
12	495.5	79.7	252	23 ABP45383	Human Blys binding
13	495	79.6	249	23 ABP4501	Human Blys binding
14	495	79.6	254	21 AAY56287	HCAT1 clone 25 ant
15	495	79.6	490	21 AAY56637	HCAT1 binding huma
16	494	79.4	113	22 AAU02537	Anti-adipocyte mon
17	494	79.4	120	22 AAU02501	Anti-adipocyte mon
18	494	79.4	249	23 ABP45098	Human Blys binding
19	493.5	79.3	117	18 AAW15523	Anti-TGF beta-2 sc
20	493.5	79.3	240	23 ABP45901	Human Blys binding
21	493	79.3	113	22 AAU02538	Anti-adipocyte mon
22	493	79.3	248	23 ABP45879	Human Blys binding
23	492.5	79.2	519	23 AAU81993	Human secreted pro
24	491.5	79.0	119	22 AAU02515	Anti-adipocyte mon
25	491	78.9	118	23 ABG30463	Human anti-CD40 mo
26	490.5	78.9	119	24 AAE82095	Human VEGF-2 hybr
27	490.5	78.9	120	15 AAE82064	Heavy chain variab
28	490	78.8	241	23 ABP45876	Human Blys binding
29	490	78.8	241	23 ABP45890	Human Blys binding
30	490	78.8	247	23 ABP45319	Human Blys binding
31	490	78.8	249	23 ABP44386	Human Blys binding
32	490	78.8	249	23 ABP45091	Human Blys binding
33	490	78.8	249	23 ABP45104	Human Blys binding
34	489.5	78.7	123	18 AAW15534	Anti-TGF beta-1 sc
35	489.5	78.7	192	14 AAR38161	Sequence of the he
36	489	78.6	249	23 ABP45106	Human Blys binding
37	489	78.6	252	23 ABP45616	Human Blys binding
38	488.5	78.5	125	23 AAO18437	Anti-GD2 antibody
39	488.5	78.5	238	23 ABP45920	Human Blys binding
40	488.5	78.5	451	21 AAY93734	The heavy chain of
41	488	78.5	118	24 AAE32097	Human VEGF-2 hybr
42	488	78.5	247	23 ABP44913	Human Blys binding
43	488	78.5	252	23 ABP45508	Human Blys binding
44	488	78.5	254	23 ABP44966	Human Blys binding
45	487	78.3	249	23 ABP44900	Human Blys binding

ALIGNMENTS

RESULT 1	
AA50963	
ID	AA50963 standard; Protein; 120 AA.
XX	
AC	AA50963;
XX	
DT	23-MAR-2000 (first entry)
XX	
DB	Human FVIII antibody A3-C1 scFv heavy chain protein B35.
XX	
KW	Human; heavy chain; antibody; factor VIII; hemostatic;
XX	
OS	hemophilia A; scFv; A3-C1.
XX	
OS	Homo sapiens.
XX	
PN	WO958680-A2.
XX	
PD	18-NOV-1999.
XX	
FP	07-MAY-1999; 99WO-NL00285.
XX	
PR	08-MAY-1998; 98EP-0201543.
XX	
PA	(SANO-) STRICHTING SANQUIN BLOEDVOORZIENING.
XX	
PI	Voorberg JJ, Van Den Brink EW, Turehout EAM;
DR	WPI; 2000-053102/04.
XX	
PT	New polyclonotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ database
 DR EMBL; AF307937; AAL09421.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 119
 SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 66.8%; Score 415.5; DB 11; Len 119;
 Best Local Similarity 70.0%; Pred. No. 4.5e-36;
 Matches 84; Conservative 10; Mismatches 25; Indel 1; Gaps 1;

QY 1 EVOLVESGGGLVQPGRLSLRSCVDSGLTFSSYGMHWVQAAPGAGL VVISYDGNKYY 60
 DB 1 EVOLVESGGGLVQPGSLKSLKSCAASGFTSSYGMHWVQTPDKRL VTSSGGSTYY 60
 QY 61 ADSVKGFAISRDNAAKNTLYLQMSLTIETDAVYYCAKDLIESNI :MGQGLVTVSS 120
 DB 61 PDSVKGFTISRDNAAKNTLYLQMSLSEDTAVYYCAHH-GDYDV :MGQGLVTVSA 119

RESULT 15

OBNCLE6 PRELIMINARY; PRT; 493 AA.
 AC OBNCLE6
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ90170.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=Mammary gland;
 RA Isogai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T.
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y.
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nag
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ database

DR EMBL; AK074651; BAC1114.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGC1; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 66.8%; Score 414.5; DB 4; Len 193;
 Best Local Similarity 66.7%; Pred. No. 3.7e-35;
 Matches 82; Conservative 10; Mismatches 26; Indel 5; Gaps 2;

QY 1 EVOLVESGGGLVQPGRLSLRSCVDSGLTFSSYGMHWVQAAPGAGL VVISYDGNKYY 60
 DB 20 QVQLVDSGGGLVLPQGLSLRSCAASGFRFRDYDMHWVQSPQEGIL ALIWDGDKTYY 79
 QY 61 ADSVKGFAISRDNAAKNTLYLQMSLTIETDAVYYCAKDLIESNI L---MGQGLVTV 117
 DB 80 SDSVKGRLTVSRDNYKNTLYLEMKSLGAEPTAVYYCARD--QGYV VPDHMGQGLVTV 137

QY 118 VSS 120
 DB 138 VSS 140

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
RX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases;
DR EMBL: BC021276; AAH21276.1; -
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 70.1%; Score 436; DB 4; Length
Best Local Similarity 71.8%; Pred. No. 2.4e-37;
Matches 89; Conservative 6; Mismatches 25; Indels 4; Gaps 1;

OY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWVRQAPGAGLE
DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTDDYAMHWVRQAPGKLE
OY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVYYCAQDLISNT-
DB 80 ADSVKGRTISRDNKNTLYLQMSLTIRADTALYYCAKSGSYIG
OY 117 TVSS 120
DB 140 TVSS 143

RESULT 12
O9UL72 PRELIMINARY; PRT; 118 AA.
AC O9UL72;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable res
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S
RT "Myosin-reactive autoantibodies in rheumatic carditis a
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AP035042; AAD56278.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 67.2%; Score 419; DB 4; Length
Best Local Similarity 72.5%; Pred. No. 2.4e-36;

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Matches 87; Conservative 7; Mismatches 24; Indels 2; Gaps 2;

OY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWVRQAPGAGLEWVAISYDNDKYY 60
DB 1 EVQLVESGGGLVQPGSRSLRLSCAASGFTVSSNVMHWVRQAPGKLESYSV-TYSGGSSTYY 59
OY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVYYCAQDLISNTAEALMGCGTLVTVSS 120
DB 60 ADSVKGRTISRDNKNTLYLQMSLTIRADTAFYYCARDRGEFLFD-YWGCGTLVTVSS 118

RESULT 13
O91205 PRELIMINARY; PRT; 473 AA.
AC O91205;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010327; AAH10327.1; -.
DR MGD: MGI:2144967; AU044919.
DR InterPro: IPR00345; CytC_heme_bind.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 66.9%; Score 416; DB 11; Length 473;
Best Local Similarity 69.2%; Pred. No. 2.4e-35;
Matches 83; Conservative 9; Mismatches 26; Indels 2; Gaps 1;

OY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLTFSYGMHWVRQAPGAGLEWVAISYDNDKYY 60
DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAIINSGSTTIYY 79
OY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVYYCAQDLISNTAEALMGCGTLVTVSS 120
DB 80 ADTVKGRFTISRDNKNTLYLQMSLTIRSEDTAMYYCAELWLR--DYMGCGTITVSS 137

RESULT 14
O920E7 PRELIMINARY; PRT; 119 AA.
AC O920E7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horatitz O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";

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DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; H
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ database;
DR EMBL; BC024289; AAH24289.1; -
DR InterPro; IPR003006; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match
Best Local Similarity 73.8%; Score 442; DB 4; Length 1;
Matches 90; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVOPGRLSLRSCVDSGLTFSSYGMHWVQAQAGL
DB 20 EVOLVESGGGLVOPGRLSLRSCVDSGLTFSSYGMHWVQAQAGL
QY 61 ADVKGRFAISRNKNTLYLQNSLTIEPTAVYYCAKDLSNIAEAL--MGOGTLVTV
DB 80 ADVKGRFRTSRNKNKSLYLQNSLRAEDTAVYYCARDLRLT
QY 119 SS 120
DB 140 SS 141

RESULT 9
Q9UL91 PRELIMINARY; PRT; 118 AA.
ID Q9UL91;
AC Q9UL91;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable re
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; H
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PSS00290; IG_MHC; 1.
FT NON_TER 1
FT TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

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Query Match
Best Local Similarity 70.4%; Score 438; DB 4; Length 118;
Matches 89; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVOPGRLSLRSCVDSGLTFSSYGMHWVQAQAGL
DB 1 EVOLVESGGGLVOPGRLSLRSCVDSGLTFSSYGMHWVQAQAGL
QY 61 ADVKGRFAISRNKNTLYLQNSLTIEPTAVYYCAKDLSNIAEAL--MGOGTLVTV
DB 80 ADVKGRFRTSRNKNKSLYLQNSLRAEDTAVYYCARDLRLT
QY 119 SS 120
DB 140 SS 141

RESULT 10
Q96K68 PRELIMINARY; PRT; 494 AA.
ID Q96K68;
AC Q96K68;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein Flj14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Mammary gland;
RA Isegai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
RA Magatsuna M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Nakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
RA Minomiya K., Iwayanagi T.;
RT "NEBO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ database.
DR EMBL; AK027379; BAB55072.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AB5A5E4C0E CRC64;

Query Match
Best Local Similarity 70.1%; Score 436; DB 4; Length 494;
Matches 87; Conservative 10; Mismatches 23; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVOPGRLSLRSCVDSGLTFSSYGMHWVQAQAGL
DB 20 EVOLVESGGGLVOPGRLSLRSCVDSGLTFSSYGMHWVQAQAGL
QY 61 ADVKGRFAISRNKNTLYLQNSLTIEPTAVYYCAKDLSNIAEAL--MGOGTLVTV
DB 80 ADVKGRFRTSRNKNKSLYLQNSLRAEDTAVYYCARDLRLT
QY 119 SS 120
DB 140 SS 141

RESULT 11
Q8WU38 PRELIMINARY; PRT; 573 AA.
ID Q8WU38;
AC Q8WU38;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

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AC Q9UL84:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable reg
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Euteria; Primates; Catarrhini; Hominidae; Ho
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis a
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D4136545B8 CRC64;

Query Match 72.7%; Score 452; DB 4; Length
Best Local Similarity 73.4%; Pred. No. 6.5e-40;
Matches 91; Conservative 9; Mismatches 18; Indels

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMMWVQAQGAEVVISDNDKYY 60
DB 1 EVQLVESGGGVQPGKSLRLSCAASGFTFSNYGMHWQAQPGKLEIATSDGSKYY 60
QY 61 ADVKGRFAISRDNKNTLYLQMSLTTEDTAVVYCAKDLIESNIAEALWGQGLTV 118
DB 61 ADVKGRFTISRDNKNTLYLQMSLTTEDTAVVYCAKDLIESNIAEALWGQGLTV 118
QY 117 TVSS 120
DB 119 TVSS 122

RESULT 6
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable reg
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Euteria; Primates; Catarrhini; Hominidae; Ho
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis a
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.

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DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 71.5%; Score 444.5; DB 4; Length 121;
Best Local Similarity 71.3%; Pred. No. 4e-39;
Matches 87; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMMWVQAQGAEVVISDNDKYY 60
DB 1 EVQLVESGGGVQPGKSLRLSCAASGFTFSNYGMHWQAQPGKLEIATSDGSKYY 60
QY 61 ADVKGRFAISRDNKNTLYLQMSLTTEDTAVVYCAKDLIESNIAEALWGQGLTV 118
DB 61 ADVKGRFTISRDNKNTLYLQMSLTTEDTAVVYCAKDLIESNIAEALWGQGLTV 118
QY 119 SS 120
DB 120 SS 121

RESULT 7
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9:
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=B-cell;
RA Struhsberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 71.2%; Score 444.5; DB 4; Length 597;
Best Local Similarity 71.2%; Pred. No. 3.3e-38;
Matches 89; Conservative 8; Mismatches 23; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMMWVQAQGAEVVISDNDKYY 60
DB 20 EVQLVESGGGVQPGKSLRLSCAASGFTFSNYGMHWQAQPGKLEIATSDGSKYY 79
QY 61 ADVKGRFAISRDNKNTLYLQMSLTTEDTAVVYCAKDLIESNIAEALWGQGLTV 115
DB 80 ADVKGRFTISRDNKNTLYLQMSLTTEDTAVVYCAKDLIESNIAEALWGQGLTV 139
QY 116 TVSS 120
DB 140 TVSS 144

RESULT 8
Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77:

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RESULT 2

09UL90 PRELIMINARY; PRT; 113 AA.

AC 09UL90; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable re (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia; Eutheria; Primates; Catarrhini; Homidae; H NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney ; Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis ; fetus.;"

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035024; AAD56260.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro: IPR007110; IG_1like.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 113

SO SEQUENCE 113 AA; 12437 MW; ED57EDD19086D07F CRC64;

Query Match 79.8%; Score 496.5; DB 4; Leng 113;
Best Local Similarity 80.8%; Pred. No. 1.2e-44;
Matches 97; Conservative 4; Mismatches 12; Inde 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGMHWROAPGAGL AVSYGNDKRY 60
DB 1 EVOLVESGGGVOPGSGSLRSLSCAASGTFSSYGMHWROAPGAGL AFIRYDGNKRY 60

QY 61 ADVYGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLESNI/ LMGQGLTVYSS 120
DB 61 ADVYGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKDL----- YMGQGLTVYSS 113

RESULT 3

09UL93 PRELIMINARY; PRT; 116 AA.

AC 09UL93; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable re (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia; Eutheria; Primates; Catarrhini; Homidae; H NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney ; Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis ; fetus.;"

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035021; AAD56257.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro: IPR007110; IG_1like.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 116

SO SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match 77.9%; Score 484.5; DB 4; Length 116;
Best Local Similarity 79.0%; Pred. No. 2.3e-43;
Matches 94; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 2 VOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGMHWROAPGAGLEAVAYISYDGNKRYA 61
DB 1 VOLVESGGGVOPGSGSLRSLSCAASGTFSSYGMHWROAPGAGLEAVAYISYDGNKRYA 60

QY 62 DSVYGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLESNI/ALMGQGLTVYSS 120
DB 61 DSVYGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKGS---GGIGIGYMGQGLTVYSS 116

RESULT 4

09Y509 PRELIMINARY; PRT; 147 AA.

AC 09Y509; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Vh3 protein (Fragment).

GN Vh3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96071149; PubMed=7475288;

RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C., Lichtenstein A.K., Berenson J.R.;

RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers.;"

RL Leukemia 9:1948-1953(1995).

DR EMBL; S80860; AAD14339.1; -.

DR HSSP; P01772; 2FB4.

DR InterPro: IPR007110; IG_1like.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 147

SO SEQUENCE 147 AA; 15768 MW; 8489FCMAA7BC925C CRC64;

Query Match 74.1%; Score 461; DB 4; Length 147;
Best Local Similarity 69.8%; Pred. No. 9.4e-41;
Matches 90; Conservative 13; Mismatches 14; Indels 12; Gaps 2;

QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGMHWROAPGAGLEAVAYISYDGNKRY 60
DB 1 EVOLVESGGGVOPGSGSLRSLSCAASGTFSTYGMHWROAPGAGLDVVALISYDGSIOY 60

QY 61 ADVYGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLESNI/ALMGQGLTVYSS 111
DB 61 ADVYGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKDL-----GNYFDSVGYVYAGIDYWG 117

QY 112 QGTLTVYSS 120
DB 118 QGTLTVYSS 126

RESULT 5

09UL84 PRELIMINARY; PRT; 122 AA.

GenCore version 5.1.6
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OM protein - protein search, using ew model

Run on: December 30, 2003, 10:46:19 ; Search time 29.45 Seconds
(without alignment)
1058.876 Million 1 updates/sec

Title: US-09-674-752-46

Perfect score: 622
Sequence: 1 EVOLVESGGGLVQPGSRURL.....IESNIAELMGQ...VTYSS 120

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues.

Total number of hits satisfying chosen parameters: 8305

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_ricent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance
score greater than or equal to the score of the result
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	82.5	613	4 Q8WUK1	01 homo sapien
2	496.5	79.8	113	4 Q9UL90	01 homo sapien
3	484.5	77.9	116	4 Q9UL93	01 homo sapien
4	461	74.1	147	4 Q9Y509	01 homo sapien
5	452	72.7	122	4 Q9UL84	01 homo sapien
6	444.5	71.5	121	4 Q9UL71	01 homo sapien
7	444.5	71.5	597	4 Q96B89	01 homo sapien
8	442	71.1	471	4 Q8RC77	01 homo sapien
9	438	70.4	118	4 Q9UL91	01 homo sapien
10	436	70.1	494	4 Q96K68	01 homo sapien
11	436	70.1	573	4 Q8WU38	01 homo sapien
12	418	67.2	118	4 Q9UL72	01 homo sapien
13	416	66.9	473	11 Q91205	01 mus musculu
14	415.5	66.8	119	11 Q920E7	01 mus musculu
15	414.5	66.6	493	4 Q8NCL6	01 mus musculu
16	412	66.2	112	4 Q9HCC1	01 homo sapien

17	409.5	65.8	499	4 Q8NSK4	08NSK4 homo sapien
18	398	64.0	95	4 Q9ULB6	Q9ULB6 homo sapien
19	396	63.7	487	11 Q99KA4	Q99KA4 mus musculu
20	385.5	62.0	479	11 Q91WP5	Q91WP5 mus musculu
21	372.5	59.9	486	11 Q91207	Q91207 mus musculu
22	370.5	59.6	131	4 Q9UL88	Q9UL88 homo sapien
23	365	58.7	469	11 Q8R3V9	Q8R3V9 mus musculu
24	354	56.9	298	11 Q9QYF0	Q9QYF0 mus musculu
25	348.5	56.0	480	11 Q91XE1	Q91XE1 mus musculu
26	348	55.9	484	11 Q8VEA0	Q8VEA0 mus musculu
27	341	54.8	124	6 Q9N0W4	Q9N0W4 oryctolagus
28	341	54.8	437	11 Q9R1A4	Q9R1A4 mus musculu
29	338	54.3	124	6 Q9N0W6	Q9N0W6 oryctolagus
30	337	54.2	124	4 Q9UL92	Q9UL92 homo sapien
31	336.5	53.1	521	4 Q8N4Y9	Q8N4Y9 homo sapien
32	331.5	53.3	104	4 Q9UL87	Q9UL87 homo sapien
33	321	51.6	121	11 Q99NG4	Q99NG4 mus musculu
34	319.5	51.4	125	4 Q9UL95	Q9UL95 homo sapien
35	318.5	51.2	484	11 Q991A6	Q991A6 mus musculu
36	315.5	50.7	112	4 Q9UGP3	Q9UGP3 homo sapien
37	313	50.3	145	11 Q924Q9	Q924Q9 mus musculu
38	312	50.2	139	11 Q924R5	Q924R5 mus musculu
39	305	49.0	145	11 Q924Q6	Q924Q6 mus musculu
40	305	49.0	145	11 Q924R3	Q924R3 mus musculu
41	305	49.0	145	11 Q924R4	Q924R4 mus musculu
42	303	48.7	145	11 Q924R4	Q924R4 mus musculu
43	302.5	48.6	146	11 Q924Q3	Q924Q3 mus musculu
44	302	48.6	159	4 Q96QSO	Q96QSO homo sapien
45	301	48.4	141	11 Q924Q4	Q924Q4 mus musculu

ALIGNMENTS

RESULT 1

Q8WUK1 PRELIMINARY; PRT; 613 AA.
ID Q8WUK1
AC Q8WUK1
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
DR EMBL; BC020240; AAH20240.1; -
DR EMBL; BC020240; AAH20240.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 82.5%; Score 513; DB 4; Length 613;
Best Local Similarity 81.7%; Pred. No. 2e-45;
Matches 98; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSRURLSCVDSGLTFSSYGMMWVRQAPQAGLEWVAIVSYDNDKRY 60
DB 20 QVQLVESGGGVQPGSRURLSCAASGFTFSYGMMWVRQAPQAGLEWVAIVSYDNDKRY 79
QY 61 ADSYKGRFAISRDAKNTLYIQMNSLTIEDPAVYYCAVDLIESNIAELMGQGLVTVSS 120
DB 80 ADSYKGRFTISRDSKNTLYIQMNSLTIEDPAVYYCAVDWSEGVETFDIMGQGLVTVSS 139

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AC P01774;
BT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
OS Ig heavy chain V-III region POM.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Ho
CC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the comp
RT of the heavy chain variable regions of two immunoglobul
RT anti-gamma globulins."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH
CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02057; M3HUPM.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KM DOMAIN
FT VARIANT 54 54 IG-LIKE.
FT N -> D (PROBABLY DUE TO DE
FT DURING ISOLATION).
FT /FTID=VAR_003966.
FT NON TER 119 119
FT SEQUENCE 119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;

Query Match 63.7%; Score 396; DB 1; Length 119;
Best Local Similarity 68.1%; Pred. No. 7,1e-35;
Matches 81; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGSRRLSCVDSGLTFSYGMHWVRQAPGAGLEWVA
DB 1 EVQLVESGGGLVQPGSRRLSCVDSGLTFSYGMHWVRQAPGAGLEWVA
QY 61 ADSVNGRFAISRDNKNTLYLQMSLTIEDTAIVYCAKDL--IESN
DB 61 ADSVNGRFTISRNDKNTLYLQMSLTIEDTAIVYCAKDL--IESN
DB 61 ADSVNGRFTISRNDKNTLYLQMSLTIEDTAIVYCAKDL--IESN

RESULT 15
HY3N_HUMAN
ID HY3N_HUMAN STANDARD; PRT; 119 AA.
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region IAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Ho
CC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the comp
RT of the heavy chain variable regions of two immunoglobul
RT anti-gamma globulins."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH
CC ANTI-GAMMA

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CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02058; M3HOLY.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KM DOMAIN
FT NON TER 119 119 IG-LIKE.
FT SEQUENCE 119 AA; 12858 MW; D6338098794DCF5E CRC64;

Query Match 62.9%; Score 391; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 2,4e-34;
Matches 79; Conservative 11; Mismatches 26; Indels 2; Gaps 1;

QY 2 VOLVESGGGLVQPGSRRLSCVDSGLTFSYGMHWVRQAPGAGLEWVA
DB 2 VOLVESGGGLVQPGSRRLSCVDSGLTFSYGMHWVRQAPGAGLEWVA
QY 62 DSVNGRFAISRDNKNTLYLQMSLTIEDTAIVYCAKDL--IESN
DB 62 DSVNGRFTISRNDKNTLYLQMSLTIEDTAIVYCAKDL--IESN
DB 62 DSVNGRFTISRNDKNTLYLQMSLTIEDTAIVYCAKDL--IESN

Search completed: December 30, 2003, 10:55:53
Job time : 6.43379 secs

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RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOC
 CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02046; M3HWR.
 DR HSSP: P01772; 2PB4.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Pyroglutamate carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD RES 1 114 PYRROLIDONE CARBOXYLIC ACI
 FT NON TER 114 114
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;
 Query Match 64.6%; Score 402; DB 1; Length 4;
 Best Local Similarity 65.8%; Pred. No. 1,6e-35; Indels 6; Gaps 1;
 Matches 79; Conservative 16; Mismatches 19;
 QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGMHWVROAPGAGLE /AVISYDNDKYY 60
 DB 1 QVQVDSGGGLVGVGSGSLRSLSCASGFTFSNDQNWVROAPGKLE /SFGSGSTIYY 60
 QY 61 ADVKGFPAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIA /LNGGGLTVTSS 120
 DB 61 ADVKGFRTISRDNSKSLYLQMSLRADTAVYYCARGLINL--- /MGGGLTVTSS 114
 Db 61 ADVKGFRTISRDNSKSLYLQMSLRADTAVYYCARGLINL--- /MGGGLTVTSS 114
 RESULT 12
 HV3F_HUMAN STANDARD; PRT; 115 AA.
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region BT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut. eostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hc
 OC NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=78137069; PubMed=416441;
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 RT Ig2 immunoglobulin of the A2m (2) allotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) LOTYPE, C
 CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02050; A2HUBU.
 DR HSSP: P01789; IMCP.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 111 IG-LIKE.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCFA CRC64;

Query Match 64.2%; Score 399.5; DB 1; Length 115;
 Best Local Similarity 65.8%; Pred. No. 2.9e-35;
 Matches 79; Conservative 14; Mismatches 22; Indels 5; Gaps 2;
 QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGMHWVROAPGAGLEWVAVISYDNDKYY 60
 DB 1 EVQVDTGGGLVOPGSGSLRSLSCASGFTFSNDSWVROAPGKALZWVSAI -YRGCTIYY 59
 QY 61 ADVKGFPAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIA /LNGGGLTVTSS 120
 DB 60 ADVKGFRTISRDNSKSLYLQMSLRADTAVYYCARL--- /AARLFKGKGLTVTSS 115
 Db 60 ADVKGFRTISRDNSKSLYLQMSLRADTAVYYCARL--- /AARLFKGKGLTVTSS 115
 RESULT 13
 HV02_CANFA STANDARD; PRT; 117 AA.
 AC P01785;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOO.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Pisipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP MEDLINE=80077682; PubMed=407924;
 RA Wasserman R.L., Capra J.D.;
 RT "Primary structure of the variable regions of two canine
 RT immunoglobulin heavy chains."
 RL Biochemistry 16:3160-3168(1977).
 RN [2]
 RP SEQUENCE OF 113-117.
 RX MEDLINE=80077682; PubMed=117299;
 RA McCumber L.J., Capra J.D.;
 RT "The complete amino-acid sequence of a canine mu chain."
 RL Mol. Immunol. 16:565-570(1979).
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A90403; MEDGMO.
 DR HSSP: P01772; 2PB4.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 IG-LIKE.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;
 Query Match 64.1%; Score 398.5; DB 1; Length 117;
 Best Local Similarity 70.2%; Pred. No. 3.8e-35;
 Matches 88; Conservative 9; Mismatches 22; Indels 5; Gaps 3;
 QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGMHWVROAPGAGLEWVAVISYDNDKYY 60
 DB 1 EVLVESGGDLVVRGSLRSLSCASGFTFSNDSWVROAPGELQVADISSSG -QTY 59
 QY 61 ADVKGFPAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIA /AALMGGLTVTSS 119
 DB 60 ADVKGFPAISRDNAKNTLYLQMSLRADTAVYYCA--- /TEGDIRIPRYGGLTVTSS 116
 QY 120 S 120
 Db 117 S 117
 RESULT 14
 HV3M_HUMAN STANDARD; PRT; 119 AA.
 ID HV3M_HUMAN

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DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=81101090; PubMed=6450418;
RA Mathysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.1ib-stb.ch/announce/
CC or send an email to license@lib-stb.ch).
CC
DR EMBL: J00236; AAA53516.1; -
DR EMBL: M35415; AAA58735.1; -
DR PIR: A02047; H3H026.
DR PDB: 1H0U; 23-DEC-99.
DR Genew: HGNC:5545; IGHV@.
DR GO: GO:0005576; C:cytoregulatory; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION /H26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
FT SEQUENCE 117 AA; 12562 MW; E826733F1A3CB0F1 CRC64;

Query Match
Best Local Similarity 65.1%; Score 405; DB 1; Length 7;
Matches 78; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGKSLRLSCVDSGLTSSSYGMHWROAPAGLEW AVISYDNDKYY 60
DB 20 EVQLVESGGGLVQPGKSLRLSCVDSGLTSSSYGMHWROAPAGLEW AVISYDNDKYY 79
QY 61 ADSVNGRAFSIRDNKNTLYIQMNSLTIEDTAIVYCAK 98
DB 80 GDSVNGRAFTSRDNTLYIQMNSLTIEDTAIVYCAK 117

RESULT 10
HY16_MOUSE STANDARD; PRT; 136 AA.
ID _HY16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paekind M., Rath M., Imanishi-Kari T., Jewsky K.,
RA Baltimore D.;

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RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP MEDLINE=77100368; PubMed=401950;
RA Aderugo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@lib-stb.ch).
CC
DR EMBL: J00522; AAD15290.1; -
DR PIR: E30809; G1M521.
DR PDB: 1IGC; 03-JUN-95.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 1
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 J4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON TER 136 136
FT SEQUENCE 136 AA; 15071 MW; 2276A98DBDF016 CRC64;

Query Match
Best Local Similarity 65.1%; Score 405; DB 1; Length 136;
Matches 82; Conservative 9; Mismatches 29; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGKSLRLSCVDSGLTSSSYGMHWROAPAGLEW AVISYDNDKYY 60
DB 17 DVQLVESGGGLVQPGKSLRLSCVDSGLTSSSYGMHWROAPAGLEW AVISYDNDKYY 76
QY 61 ADSVNGRAFSIRDNKNTLYIQMNSLTIEDTAIVYCAKDLIESNTAEALMGCGTLVTSS 120
DB 77 ADTVNGRAFTSRDNTLYIQMNSLTIEDTAIVYCAKMGVNYPYAMDYMGCGTSVTSS 136

RESULT 11
HY16_MOUSE STANDARD; PRT; 114 AA.
ID _HY16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=83273707; PubMed=6410398;
RA Goni F., Prangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAA1282 CRC64;

Query Match
Best Local Similarity 67.0%; Score 417; DB 1; Length 16;
Matches 83; Conservative 10; Mismatches 23; Indel 4; Gaps 1;

QY 1 EVQLVDSGGGLVQPGSRSLRSCVDSGLTFSSYGMHWVRQAPGAGLE /AVISYDGNDRKY 60
DB 1 EVQLVDSGGDLVQPGSRSLRSCAASGFBBLGWTWRQAPGKLE /ANIKZBSZBY 60

QY 61 ADVKGRFAISRDNAKNTLYLQNSLTIEDTAIVYYCAKDLIESNIA /LMGGCTLVTVSS 120
DB 61 VDSVGRFTISRDNKNSLYLQNSLVEDTALYYCARGGGDD - - YVGCGTLTVST 116

RESULT 7
HV3L_HUMAN STANDARD; PRT; 119 AA.
ID HV3L_HUMAN
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut eostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Ho 3.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgM1 immunoglobulin. IV. Cerepococcal
RT IgM1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain."
RL J. Biol. Chem. 254:2865-2874(1979).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02056; A1HUBR.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Glycoprotein; Pyroliidone carb ylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACI
FT DISULFD 22 96
FT CARBOHYD 28 28 N-LINKED (GLCNAc. . .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match
Best Local Similarity 67.0%; Score 416.5; DB 1; Length 119;
Matches 80; Conservative 12; Mismatches 26; Indel 1; Gaps 1;

QY 1 EVQLVDSGGGLVQPGSRSLRSCVDSGLTFSSYGMHWVRQAPGAGLE /AVISYDGNDRKY 60

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DB 1 EVQLVDSGGGVQAGTSRLRSLCTASAFNLSDYAMHWVRQAPGKGLZWVALLISGSSBTYY 60
QY 61 ADVKGRFAISRDNAKNTLYLQNSLTIEDTAIVYYCAKDLIESNIA /LMGGCTLVTVSS 119
DB 61 ADVKGRFTISRDNKNSLYLQNSLVEDTALYYCARGGGDD - - YVGCGTLTVST 118

RESULT 8
HV3U_HUMAN STANDARD; PRT; 120 AA.
ID HV3U_HUMAN
AC P01782;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80020921; PubMed=114209;
RA Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT "Amino acid sequence of the heavy-chain variable region of the
RT crystallizable human myeloma protein Dob."
RL Biochemistry 18:4068-4080(1979).
RN [2]
RP CRYSTALLIZATION.
RX MEDLINE=80020920; PubMed=114208;
RA Steiner L.A., Lopes A.D.;
RT "The crystallizable human myeloma protein Dob has a hinge-region
RT deletion."
RL Biochemistry 18:4054-4067(1979).
CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
CC HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
CC DISULFIDE BONDS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90431; G1HUBD.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DE307C4B2627 CRC64;

Query Match
Best Local Similarity 66.4%; Score 413; DB 1; Length 120;
Matches 82; Conservative 8; Mismatches 30; Indels 0; Gaps 0;

QY 1 EVQLVDSGGGLVQPGSRSLRSCVDSGLTFSSYGMHWVRQAPGAGLE /AVISYDGNDRKY 60
DB 1 EVQLVDSGGDLVQPGSRSLRSCAASGFBBLGWTWRQAPGKLE /ANIKZBSZBY 60

QY 61 ADVKGRFAISRDNAKNTLYLQNSLTIEDTAIVYYCAKDLIESNIA /LMGGCTLVTVSS 120
DB 61 ADVKGRFAISRDNAKNTLYLQNSLTIEDTAIVYYCAKDLIESNIA /LMGGCTLVTVSS 120

RESULT 9
HV3C_HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

```

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Pyridone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13166 MW; 745B6959E84100A CRC64;
 Query Match 70.9%; Score 441; DB 1; Length 172;
 Best Local Similarity 63.1%; Pred. No. 1.3e-39;
 Matches 77; Conservative 24; Mismatches 19; Indels 2; Gaps 1;
 QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMHWRAQAPGAGLEWVAISYQNDKRY 60
 DB 1 QVQLVSSGGGVAVZPQGRSLRLSCAASGFSFSTYAMHWVQAQPGKGLZWISVISYGBBZYY 60
 QY 61 ADSVKGRAISRDAKNTLYIQMNSLTIEDTAVVYCAKD-----LIESNI/EAALMGQGLTVT 118
 DB 61 AASVKGRTISRBSKNTLYEMNSLTAEHTAVVYCAASGIALGVAITDYMGZGLTVTI 120
 QY 119 SS 120
 DB 121 SS 122
 RESULT 5
 HV3K_HUMAN STANDARD; PRT; 126 AA.
 ID P01772;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies: Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=7441755;
 RA Marguaret M., Delsenhofer J., Huber R., Palm W.;
 RT "Cryoelectronographic refinement and atomic models of the intact
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02055; G1HUKL.
 DR PDB: 2FB4; 12-JUL-89.
 DR PDB: 2IG2; 12-JUL-89.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; 3D-structure; Pyridone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1 IG-LIKE.
 FT NON_TER 1 1 PYRROLIDONE CARBOXYLIC ACID
 FT DISULFID 22 96

FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT STRAND 29 31
 FT HELIX 34 39
 FT TURN 41 42
 FT TURN 45 51
 FT STRAND 53 54
 FT STRAND 58 60
 FT STRAND 62 64
 FT HELIX 65 65
 FT STRAND 66 67
 FT TURN 68 73
 FT STRAND 74 77
 FT STRAND 78 83
 FT STRAND 88 90
 FT STRAND 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 116
 FT STRAND 120 124
 FT NON_TER 126 126
 SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;
 Query Match 69.6%; Score 433; DB 1; Length 126;
 Best Local Similarity 68.3%; Pred. No. 9.6e-39;
 Matches 86; Conservative 12; Mismatches 22; Indels 6; Gaps 1;
 QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMHWRAQAPGAGLEWVAISYQNDKRY 60
 DB 1 QVQLVSSGGGVAVZPQGRSLRLSCSSGFSFSTYAMHWVQAQPGKGLZWIAITWDGSDQHY 60
 QY 61 ADSVKGRAISRDAKNTLYIQMNSLTIEDTAVVYCAKD-----LIESNI/EAALMGQGLTVT 114
 DB 61 ADSVKGRTISRBSKNTLYEMNSLTAEHTAVVYCAASGIALGVAITDYMGZGLTVTI 120
 QY 115 LVTVSS 120
 DB 121 PVTVSS 126
 RESULT 6
 HV3T_HUMAN STANDARD; PRT; 116 AA.
 ID P01781;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region GAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75059123; PubMed=4803843;
 RA Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;
 RT "The primary structure of a monoclonal IgM-immunoglobulin
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
 type), subgroup H III. Architecture of the complete IgM-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
 RN [2]
 RP REVISION TO 28-33.
 RA Hilschmann N.;
 RT Submitted (JUN-1975) to the PIR data bank.
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02064; M3HUGL.
 DR HSSP: P01772; 2FB4.

RESULT 2
HVJ1_HUMAN STANDARD; PRT; 119 AA.
ID HVJ1_HUMAN
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Postelting H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein N1e). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
[2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Draker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein N1e), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG G1 MYELOMA PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A9168; GIHUNI.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; Cxetracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPRO07110; IG-I like.
DR InterPro; IPRO03006; IG_MHC.
DR InterPro; IPRO03596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Pyrolydome carboxylic acid.
KM DOMAIN 1 112 IG-LIKE.
FT MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E55E165B CRC64;
Query Match 72.9%; Score 453.5; DB 1; Length 119;
Best Local Similarity 71.7%; Pred. No. 6.2e-41;
Matches 86; Conservative 17; Mismatches 16; Indels 1; Gaps 1
QY 1 EVOLVESGGLVQPGSRSLRSCVDSDGLTFSSGCMHWVRPAAGLEWVAIVISDGNKDY 60
DB 1 QVLTVQSGGGVVQGRSLRLSCASGFSTFSRYTIHWVRAPGKGLEWVAVMYSGBBKHY 60
QY 61 ADSVNGRFALISRDNAKNTLYLQNSLTITPDVAYVCAOKLIBSNIAMALMGCGTIVTSS 120
DB 61 ADSVNGRFITSHDSKNTLYLNMSLRPEDTAVYYCAR-IRDTAMFFAHMGSTLVTS 119
RESULT 3
HVJ3_HUMAN STANDARD; PRT; 121 AA.
ID HVJ3_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HIT.
OS Homo sapiens (Human).

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=79124695; PubMed=420800;
RA	Chiu Y.-Y., H., Lopez de Castro J.A., Poljak R.J.;
RT	"Amino acid sequence of the VH region of human myeloma
RL	cryoglobulinoglobulin IgG H1."
CC	Biochemistry 18:553-560(1979).
-I	MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGCI MYELOMA PROTEIN.
-I	SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A02054; GITHDL.
DR	HSSP; P01772; 2PB4.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; IG_1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KM	Immunoglobulin V region; Pyrolydione carboxylic acid.
FT	DOMAIN 1 112 IG-LIKE
MOD RES	1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON TER	121 121
SO	SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
Query Match	72.7%; Score 452.5; DB 1; Length 121;
Best Local Similarity	70.2%; Pred. No. 8.1e-41;
Matches	87; Conservative 14; Mismatches 16; Indels 7; Gaps 2
OY	1 EVQLVESGGGLVQGRSLRLSCVDSGLTFSSTSGMGHWQAQGAGLEWVAVISYDGNDRY 60
DB	1 QKLVNQAGSVQVQGRSLRLSCLASGFTFSSNYGMHWQAQKGLEWVAIVTNYSRRYY 60
OY	61 ADSVKGRPAISRDNAKNTLYQNNSLTIEDTAIVYCADLIENIAEEL---WGCGTLV 116
DB	61 GDSVYGRTTISRDSKRTLYVMZMNSLRTETDAVVYYCARD---PDILTAFSPDYWGCGTLV 117
OY	117 TVSS 120
DB	118 TVSS 121
RESULT 4	
HV3H_HUMAN	STANDARD; PRT; 122 AA.
AC	P01769;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V-I11 region GA.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RP	SEQUENCE.
RX	MEDLINE=74175307; PubMed=420843;
RA	Florent G., Lehman D., Putnam F.W.;
RT	"The switch point in mu heavy chains of human Igm immunoglobulins.";
RL	Biochemistry 13:2482-2498(1974).
-I	MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC	MACROGLOBULIN.
-I	SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A02052; M3HUGA.
DR	HSSP; P01772; 2PB4.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.43379 Seconds
(without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622
Sequence: 1 EVOLVESGGGLVQPGKSLRL.....IESNTAALMGQGLTVTVSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	76.7	122	1 HV3G_HUMAN	P01768 homo sapien
2	453.5	72.9	119	1 HV3I_HUMAN	P01770 homo sapien
3	452.5	72.7	121	1 HV3J_HUMAN	P01771 homo sapien
4	441	70.9	122	1 HV3H_HUMAN	P01769 homo sapien
5	433	69.6	126	1 HV3K_HUMAN	P01772 homo sapien
6	417	67.0	116	1 HV3T_HUMAN	P01781 homo sapien
7	415.5	67.0	119	1 HV3L_HUMAN	P01782 homo sapien
8	413	66.4	120	1 HV3U_HUMAN	P01782 homo sapien
9	405	65.1	117	1 HV3C_HUMAN	P01764 homo sapien
10	405	65.1	136	1 HV16_MOUSE	P01783 mus musculu
11	402	64.6	114	1 HV3B_HUMAN	P01763 homo sapien
12	399.5	64.2	115	1 HV3F_HUMAN	P01767 homo sapien
13	398.5	64.1	117	1 HV02_CANFA	P01785 canis famli
14	396	63.7	119	1 HV3M_HUMAN	P01773 homo sapien
15	391	62.9	119	1 HV3N_HUMAN	P01774 homo sapien
16	389.5	62.6	120	1 HV3E_HUMAN	P01766 homo sapien
17	385	61.9	114	1 HV01_CANFA	P01784 canis famli
18	384	61.7	122	1 HV3A_HUMAN	P01762 homo sapien
19	383.5	61.7	116	1 HV05_CARAU	P0181 carassius a
20	379.5	61.0	115	1 HV3D_HUMAN	P01765 homo sapien
21	373.5	60.0	115	1 HV32_MOUSE	P01801 mus musculu
22	368.5	59.2	113	1 HV30_MOUSE	P01799 mus musculu
23	368	59.2	119	1 HV37_MOUSE	P01807 mus musculu
24	367	59.0	119	1 HV3P_HUMAN	P01777 homo sapien
25	365	58.7	122	1 HV20_MOUSE	P01789 mus musculu
26	364.5	58.6	142	1 HV01_RAT	P01805 rattus norv
27	364	58.5	117	1 HV55_MOUSE	P18526 mus musculu
28	363.5	58.4	113	1 HV27_MOUSE	P01796 mus musculu
29	363	58.4	117	1 HV54_MOUSE	P18525 mus musculu
30	363	58.4	119	1 HV40_MOUSE	P01810 mus musculu
31	362.5	58.3	115	1 HV33_MOUSE	P01802 mus musculu
32	362	58.2	98	1 HV57_MOUSE	P18528 mus musculu
33	361.5	58.1	113	1 HV31_MOUSE	P01800 mus musculu

34	359	57.7	117	1 HV3O_HUMAN	P01776 homo sapien
35	358.5	57.6	113	1 HV34_MOUSE	P01803 mus musculu
36	358.5	57.6	123	1 HV18_MOUSE	P01787 mus musculu
37	357.5	57.5	113	1 HV28_MOUSE	P01797 mus musculu
38	357.5	57.5	117	1 HV17_MOUSE	P01786 mus musculu
39	356.5	57.3	123	1 HV19_MOUSE	P01788 mus musculu
40	356	57.2	119	1 HV38_MOUSE	P01808 mus musculu
41	356	57.2	122	1 HV21_MOUSE	P01790 mus musculu
42	355.5	57.2	123	1 HV22_MOUSE	P01791 mus musculu
43	355.5	57.2	123	1 HV25_MOUSE	P01794 mus musculu
44	355	57.1	115	1 HV35_HUMAN	P01780 homo sapien
45	353.5	56.8	113	1 HV29_MOUSE	P01798 mus musculu

ALIGNMENTS

RESULT 1	
ID	HV3G_HUMAN
AC	P01768;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V-II region CAM.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RA	MEDLINE=81013859; PubMed=6774332;
RX	Lehman D.W., Putnam F.W.;
RT	"Amino acid sequence of the variable region of a human mu chain:
RT	location of a possible JH segment."
RL	Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC	-I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC	PATIENT WITH MACROGLOBULINEMIA.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A02051; M3HUM.
DR	HSSP; P01772; 2PB4.
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; IGv_1.
DR	PROSITE; PS50835; IG LIKE; 1.
KW	Immunoglobulin V region; Pyroliidone carboxylic acid.
FT	DOMAIN 1 112 IG-LIKE.
FT	MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT	NON_TER 122 122
SQ	SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
Query Match 76.7%; Score 477; DB 1; Length 122;	
Best Local Similarity 73.0%; Pred. No. 2.1e-43;	
Matches 89; Conservative 14; Mismatches 17; Indels 2; Gaps 1	
QY	1 EVQLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMHWYRQAFGAGLEWVAISYDGNDRY 60
DB	1 QVRLVESGGGVVZPGRSRLISCAASGTFPSNYAMHWYQPGKGLIEWAVISYGBBRY 60
QY	61 ADSYKGRPAISRDNAKNTLYIQNNSLTIEDTAVYYCAKD--LIISNTAALMGQGLTVTV 118
DB	61 ABSYVGRFTISRDSKSTLYLNNSLRABRYAVYYCARDRPLVGYBRYAFNTYMGQGLTVTV 120
QY	119 SS 120
DB	121 SS 122

QY 61 ADSVKGKFAISRDNKNTLYLQNMNSLTIEDTAVYYCAKDLIESNIAEALMGCGTLTVSS 120
 |||||
 DB 80 ADSVKGKFTISRDNKNTLYLQNMNSLRABDTAVYYCARE-----SRGDYVGGCTLVTVSS 134

RESULT 11

S70442
 Ig heavy chain precursor V region (mu) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
 C/Accession: S70442
 R/Cuisinier, A.M.; Fougereau, M.; Tonnelle, C.
 Mol. Immunol. 29, 1363-1373, 1992
 A/Title: IGM kappa/lambda BBV human B cell clone: an early step of differentiation of B
 A/Reference number: S70442; MUID:93024508; PMID:1383655
 A/Accession: S70442
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-140 <CUI>
 A/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 488; DB 2; Length 140;
 Best Local Similarity 78.3%; Pred. No. 8.8e-39;
 Matches 94; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAIVSYDGNKYY 60
 :|||
 DB 20 QVQLVSGGCVVQPGKSLRLSCAASGFTFSYGMHWROAPGKLEWVAIFRDGSKYY 79
 |||||
 QY 61 ADSVKGKFAISRDNKNTLYLQNMNSLTIEDTAVYYCAKDLIESNIAEALMGCGTLTVSS 120
 |||||
 DB 80 ADSVKGKFTISRDNKNTLYLQNMNSLRABDTAVYYCARDHVGATYDYVGGCTLVTVSS 139

RESULT 12

A49028
 Ig heavy chain V-III region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
 C/Accession: A49028
 R/Timmers, B.; Kenter, M.; Thompson, A.; Kraakman, M.B.; Berman, J.E.; Alt, F.W.; Schuur
 Eur. J. Immunol. 21, 2355-2363, 1991
 A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
 A/Reference number: A49028; MUID:92008140; PMID:1915549
 A/Accession: A49028
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-133 <TIM>
 A/Cross-references: GB:S64471; NID:g236904; PIDN:AA20011.1; PID:g236905
 A/Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
 A/Note: sequence extracted from NCBI backbone (NCBI:64471, NCBI:P:64470)
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 485.5; DB 2; Length 133;
 Best Local Similarity 78.2%; Pred. No. 1.4e-38;
 Matches 97; Conservative 6; Mismatches 16; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAIVSYDGNKYY 60
 :|||
 DB 1 QVQLVSGGCVVQPGKSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVSYDGNKYY 60
 |||||
 QY 61 ADSVKGKFAISRDNKNTLYLQNMNSLTIEDTAVYYCAKDLIESNIAEALMGCGTLTV 116
 :|||
 DB 61 ADSVKGKFTISRDNKNTLYLQNMNSLRABDTAVYYCARDHVGATYDYVGGCTLV 119
 :|||
 QY 117 TVSS 120
 :|||
 DB 120 TVSS 123
 :|||

RESULT 13
 S48797
 Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
 C/Accession: S48797; S26893
 R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 Submitted to the EMBL Data Library, October 1994
 A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A/Reference number: S48797
 A/Accession: S48797
 A/Molecule type: mRNA
 A/Residues: 1-128 <MAH>
 A/Cross-references: EMBL:246379; NID:9587147; PIDN:CAA86512.1; PID:g1340168
 R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
 A/Reference number: S26885; MUID:93021117; PMID:1404388
 A/Accession: S26893
 A/Molecule type: DNA
 A/Residues: 1-98 <TOM>
 A/Cross-references: EMBL:212350; NID:g32922; PIDN:CAA78220.1; PID:g32923
 A/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 485; DB 2; Length 128;
 Best Local Similarity 75.0%; Pred. No. 1.5e-38;
 Matches 96; Conservative 9; Mismatches 15; Indels 8; Gaps 2;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAIVSYDGNKYY 60
 :|||
 DB 1 QVQLVSGGCVVQPGKSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVSYDGNKYY 60
 |||||
 QY 61 ADSVKGKFAISRDNKNTLYLQNMNSLTIEDTAVYYCAKD-LIESN-----IAEALMGQ 112
 :|||
 DB 61 ADSVKGKFTISRDNKNTLYLQNMNSLRABDTAVYYCARDNYVSSGGYVYVGGMDVWGQ 120
 :|||

RESULT 14

S31701
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31701
 R/Cuisinier, A.M.; Gaubier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31701
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-137 <CUI>
 A/Cross-references: EMBL:214177; NID:g31020; PIDN:CAA78546.1; PID:g31021
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 484; DB 2; Length 137;
 Best Local Similarity 78.3%; Pred. No. 2e-38;
 Matches 94; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAIVSYDGNKYY 60
 :|||
 DB 20 QVQLVSGGCVVQPGKSLRLSCAASGFTFSYGMHWROAPGKLEWVAIVSYDGNKYY 79
 :|||
 QY 61 ADSVKGKFAISRDNKNTLYLQNMNSLTIEDTAVYYCAKDLIESNIAEALMGCGTLTVSS 120
 :|||

```
D6      | | | | : | | | | | | | | | | : | | | | |  
        61 AD|SVAGRFTTISKDNSKNITLYLOMNSIRAEEDAVYYCARD--RKDMGMALEFDYNGOGLVT   118  
  
Q7      | | | VSS    120  
          |||  
D8      | | | VSS    121
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RESULT 7

IG heavy chain V region (M72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence _revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: E36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable genes
A:Reference number: A6005; MUID:90349571; PMID:2117273
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Ct08a-references: GB:M34030
C:Genetic8:
C:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodetramer; immunoglobulin
C:15-98/Domain: immunoglobulin homology <IMM>

Query Match	79.4%	Score	494	DB	2	Length	122
Similarity	78.7%	Pred.	No.	2	1e-39		
Best Local							
Matches	96	Conservative	8	Mismatches	16	Indels	2
						Gaps	1

Qy 1 EVLVLESGGGLVQPRSLRLSCVDSGLATSSKVMHVVRA PGAGLEPMVAIVSDGNDKYY 60

Db 1 QVQLVSGGGLVQPRSLRLSCAASFTTSSYMMHVVRA PGAGLEPMVAIVSDGSKYY 60

Qy 61 ADVSVGRPAISDNAKNTLYLQMSLTIEDTAVYYCAKDLISN--IAERLQGGTLTVY 118

Db 61 ADVSVGRFTISDNSKNTLYLQMSLTIRADTAVYYCARRHSSSWYGGDWQGGTLYVY 120

qy	119	ss	120
db	121	ss	122

RESULT 8

Ig heavy chain V region (VH3DJH4) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19666
R/Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A/Title: Bypassing immunization. Human antibodies from V-gene libraries displayed on phage
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19666
A/Molecule type: mRNA
A/Residues: 1-121 <MAR>
A/Cross-references: EMBL:X61646; NID:g37688; PIDD:CAA43827.1; PID:q335369
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
C/15-98/Domain: Immunoglobulin homology <IMM>

Query Match	79.3%	Score 493.5;	DB 2;	Length 121;
Best Local Similarity	80.2%	Pred. No. 2.3e-39;		
Matches 97; Conservative		6; Mismatches 17;	Indels 1;	Gaps 1

Oy 1 EVQLVESGGGLVQPGKSLRLSCTYDSGLTSSGYGMHWRAAPGAGLEWNAVISYDGNKKY 60
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 1 QVQLVSGGGLVQPGKSLRLSCAASGFTSSGYGMHWRAAPGKGLEWNAVISYDGSKYY 60

Qy	61	ADSVKGRFAISRDNKNTLYLQNMSLTIEDTAVVYCAKDLIESNIAE-ALNCGQGLTVTS	119
		:	
Db	61	ADSVKGRFITSRDNKNTLYLQNMSLRAEDTAVVYCAKTISSGKGFDYNGQGLTVTS	120

QY	120 S	120
Db	121 S	121

RESULT 9

Ig heavy chain human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raphoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Bur, J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62367
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
#:15-98/Domain: immunoglobulin homology <IMM>

Query Match	78.9%	Score 491;	DB 2;	Length 122;
Best Local Similarity	79.5%	Pred. No. 4e-39;		
Matches 97; Conservative	7;	Mismatches 16;	Indels 2;	Gaps 2;

[illegible]

QY	119	SS	120
Db	121	SS	122

RESULT 10

IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence _revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31679
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31679
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <CUI>
A/Cross-references: EMBL:Z14203; NID:G30965; PIDN:CAA76572.1; PID:G30966
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
C/34-117/Domain: immunoglobulin homology <IMM>

Query Match	78.7%	Score 489.5;	DB 2;	Length 134;
Best Local Similarity	79.2%	Pred. No. 6.4e-39;		
Match 95; Conservative	7;	Mismatches 13;	Indels 5;	Gaps 1;

Oy **1** EVQLVESGGGLVQPGSRLLRLSCVDSGLTFFSSYGMHWVAQAPGAGLEMWAVISYDGNKYY 60
 :
 :
Db **20** QVQLVESGGGVQPGSRLLRLSCASGCTFSSITAMHWVAQAPGKLEMWAVISYDSNKKY 79

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 / Search time 11.5028 Seconds
(without alignment)
1003.251 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622
Sequence: 1 EVQLVESGGGLVQPGSRSLRL.....IESNIAELMGQGLTVTVSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502.5	80.8	132	2 S31603	Ig heavy chain V r
2	502	80.7	118	2 S31116	Ig heavy chain - h
3	501.5	80.6	119	2 P36005	Ig heavy chain V r
4	500	80.4	120	2 S31112	Ig heavy chain - h
5	499	80.2	114	2 S46390	Ig heavy chain V r
6	494.5	79.5	121	2 G36005	Ig heavy chain V r
7	494	79.4	122	2 E36005	Ig heavy chain V r
8	493.5	79.3	121	2 S19666	Ig heavy chain V r
9	491	78.9	122	2 S31117	Ig heavy chain - h
10	489.5	78.7	134	2 S31679	Ig heavy chain V r
11	488	78.5	140	2 S70442	Ig heavy chain pre
12	485.5	78.1	133	2 S49028	Ig heavy chain V r
13	485	78.0	128	2 S48797	Ig heavy chain V r
14	484	77.8	137	2 S31701	Ig heavy chain V r
15	483	77.7	139	2 S31674	Ig heavy chain V r
16	482.5	77.6	130	2 S31601	Ig heavy chain V r
17	482	77.5	114	2 S46392	Ig heavy chain V r
18	481.5	77.4	135	2 S31598	Ig heavy chain V r
19	480.5	77.3	130	2 PLO098	Ig heavy chain pre
20	478.5	76.9	111	2 P16143	Ig heavy chain V r
21	478	76.8	151	2 A60943	Ig heavy chain pre
22	477	76.7	122	1 M3H04M	Ig heavy chain V r
23	475	76.4	122	1 S31119	Ig heavy chain - h
24	473	76.0	114	2 S46391	Ig heavy chain V r
25	472.5	76.0	109	2 P16146	Ig heavy chain V r
26	470	75.6	136	2 S31587	Ig heavy chain V r
27	468	75.2	133	2 S31550	Ig heavy chain - h
28	466.5	75.0	123	2 S38493	Ig heavy chain - h
29	466	74.9	108	2 P16142	Ig heavy chain V r

30	460.5	74.0	109	2 P16144	Ig heavy chain V r
31	460	74.0	147	2 I37780	Ig variable region
32	459	73.8	98	2 PLO116	Ig heavy chain V r
33	458.5	73.7	111	2 P16145	Ig heavy chain V r
34	457.5	73.6	119	2 S31107	Ig heavy chain - h
35	456.5	73.4	119	2 S31111	Ig heavy chain - h
36	456	73.3	128	2 S31595	Ig heavy chain V r
37	455.5	73.2	140	2 S31588	Ig heavy chain V r
38	455	73.2	122	2 S69910	Ig V-D region (K
39	454.5	73.1	117	2 S78486	Ig heavy chain V r
40	454.5	73.1	123	2 S31114	Ig heavy chain - h
41	454	73.0	120	2 S48798	Ig heavy chain V r
42	454	73.0	120	2 S44111	Ig heavy chain V r
43	453.5	72.9	113	2 S38490	Ig heavy chain - h
44	453.5	72.9	119	1 GH001	Ig heavy chain V r
45	453.5	72.9	119	2 S31108	Ig heavy chain - h

ALIGNMENTS

RESULT 1

S31603

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31603

R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31603

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <CUI>

A/Cross-references: EMBL:Z14168; NID:930999; PIDN:CAW78537.1; PID:G31000

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/30-113/Domain: immunoglobulin homology <IMM>

Query Match Score 502.5; DB 2; Length 132;

Best Local Similarity 81.7%; Pred. No. 3.6e-40;

Matches 98; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 1 EVQLVESGGGLVQPGSRSLRLSCVDSGLTFSYSGMMWRQAPAGLEWVAIVSYDNDKY 60

Db 16 QVQLVESGGGLVQPGSRSLRLSCAASGFTFSYSGMMWRQAPAGLEWVAIVSYDGNKY 75

Qy 61 ADSVKGRAISRDNKNTLYLQNSLTEDTAVYVCADLISSNIAELMGQGLTVTVSS 120

Db 76 ADSVKGRTISRDNKNTLYLQNSLTEDTAVYVCADLISSNIAELMGQGLTVTVSS 132

RESULT 2

S31116

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31116

R/Asaphort, F.M.; Timmerg, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A/Reference number: S31104; M0ID:92111633; PMID:1730252

A/Accession: S31116

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-116 <PAA>

A/Cross-references: EMBL:X62966

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

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/ FILE REFERENCE: 2183-4080US
/ CURRENT APPLICATION NUMBER: US/09/315,926A
/ CURRENT FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: EP 99201593.3
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: EP 98201693.3
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 80
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Description of Artificial Sequence: phage
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(248)
/ OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80
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Query Match          70.2%; Score 467; DB 4; Length 248;
Best Local Similarity 69.2%; Pred. No. 3.4e-37;
Matches 90; Conservative 16; Mismatches 10; Indels 14; Gaps 2;
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QY      1 QVQLVDSGGGLVDPGKSLRLSCAASGFTFGDPAIHWYROAPGEGLEWVSGVTWGGTTIGF 60
Db      23 QVQLVDSGGGLVDPGKSLRLSCAASGFTFGDPAIHWYROAPGEGLEWVAVISYDGSNKY 82
QY      61 ADSYKGRFTISRDNKSNLYLWNLSRAEDTALYYCALPYINSSNYRGV---AAPDIW 116
Db      83 ADSYKGRFTISRDNKSNLYLWNLSRAEDTALYYCA-----RGITVTKSRFDYW 132
QY      117 GCGTMTVSS 126
Db      133 GCGTLTVSS 142
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Search completed: December 30, 2003, 11:05:35
Job time : 13.8778 secs

APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakcalan, Zehra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Milton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1975
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-125-098-10

Query Match 70.3%; Score 467.5; DB 3; Length 121;
Best Local Similarity 69.0%; Pred. No. 1.4e-37;
Matches 87; Conservative 17; Mismatches 17; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTGDDYAIHMVRAQPGKLEWYSGYTWGSGTTIGF 60
DB 1 QVQLVSSGGGLVQPGKSLRLSCAASGFTDYAMHWVRAQPGKLDWVSATITWNSGHIDY 60

QY 61 ADSVAGRFTTISRDNKNSLYLYMNSLRADDTALYYCALPYINSSNYRRGVAAPDIWGCGT 120
DB 61 ADSVGRFAVSRDNKALNYLYMNSLRADDTAVYYC-----TKASYLTSSSLDWWGCGT 115

QY 121 MYTVSS 126
DB 116 LVTWSS 121

RESULT 14
US-09-540-018-10
Sequence 10, Application US/09540018
Patent No. 6509015
GENERAL INFORMATION:
APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.

APPLICANT: Kaymakcalan, Zehra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: White, Michael
APPLICANT: Milton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1975
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540,018
FILING DATE: 31-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-540-018-10

Query Match 70.3%; Score 467.5; DB 4; Length 121;
Best Local Similarity 69.0%; Pred. No. 1.4e-37;
Matches 87; Conservative 17; Mismatches 17; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTGDDYAIHMVRAQPGKLEWYSGYTWGSGTTIGF 60
DB 1 QVQLVSSGGGLVQPGKSLRLSCAASGFTFDYAMHWVRAQPGKLDWVSATITWNSGHIDY 60

QY 61 ADSVAGRFTTISRDNKNSLYLYMNSLRADDTALYYCALPYINSSNYRRGVAAPDIWGCGT 120
DB 61 ADSVGRFAVSRDNKALNYLYMNSLRADDTAVYYC-----TKASYLTSSSLDWWGCGT 115

QY 121 MYTVSS 126
DB 116 LVTWSS 121

RESULT 15
US-09-315-926A-80
Sequence 80, Application US/09315926A
Patent No. 6498027
GENERAL INFORMATION:
APPLICANT: Be van, Helmut
APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

```

; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESS: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Kinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fuses fusion phage construct
; CLONE: V13
; FEATURE:
; NAME/KEY: heavy chain
; US-08-983-607-28

Query Match          70.5%; Score 469; DB 3; Length 131;
Best Local Similarity 73.0%; Pred. No. 1,1e-37;
Matches 92; Conservative 11; Mismatches 13; Indels 10; Gaps 1;

QY 1 QVQLVQSGGGLVQPQKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWGTTIGF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVQSGGGLVQPQKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSAISGSGSTYY 60
QY 61 ADSVKGRTTISRDNKNSLYLWNLSRAEDTALYYCALPYINSSNYRGRVAAPFIMGCGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRTTISRDNKNSLYLWNLSRAEDTALYYCALPYINSSNYRGRVAAPFIMGCGT 120
QY 121 MVTSS 126
   :|||:
DB 111 PVTSS 116
   :|||:

RESULT 12
US-08-599-226-10
; Sequence 10, Application us/08599226
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; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenaut, David
; APPLICANT: Vaughan, Trestan J.
; APPLICANT: White, Michael
; APPLICANT: Milton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Decont, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; US-08-599-226-10

Query Match          70.3%; Score 467.5; DB 3; Length 121;
Best Local Similarity 69.0%; Pred. No. 1,1e-37;
Matches 87; Conservative 17; Mismatches 17; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPQKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWGTTIGF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVQSGGGLVQGRSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVAITWNSGHIDY 60
QY 61 ADSVKGRTTISRDNKNSLYLWNLSRAEDTALYYCALPYINSSNYRGRVAAPFIMGCGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRTTISRDNKNSLYLWNLSRAEDTALYYCALPYINSSNYRGRVAAPFIMGCGT 115
QY 121 MVTSS 126
   :|||:
DB 116 LVTSS 121
   :|||:

RESULT 13
US-09-125-098-10
; Sequence 10, Application us/09125098
; Patent No. 6258562
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
```

LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-30

Query Match 71.1%; Score 472.5; DB 4; Length 123;
Best Local Similarity 73.8%; Pred. No. 4.7e-38;
Matches 93; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGVAIHWVROAPGSEGLEWVSQVTMGTTIGF 60
DB 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGVAIHWVROAPGSEGLEWVSQVTMGTTIGF 60
QY 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 120
DB 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 117
QY 121 MWTVSS 126
DB 118 LVTVSS 123

RESULT 9
US-08-652-816A-14
Sequence 14, Application US/08652816A
Patent No. 5872215

GENERAL INFORMATION:
APPLICANT: Oobourn, JK
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652, 816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA: US 08/244, 597
FILING DATE: 01-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-14

Query Match 70.8%; Score 471; DB 2; Length 116;
Best Local Similarity 72.0%; Pred. No. 6.2e-38;
Matches 90; Conservative 12; Mismatches 13; Indels 10; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGVAIHWVROAPGSEGLEWVSQVTMGTTIGF 60
DB 1 EVQLVQSGGGLVQPGKSLRLSCAASGFTPEGVAIHWVROAPGSEGLEWVSQVTMGTTIGF 60
QY 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 120
DB 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 110
QY 121 MWTVSS 125
DB 111 LVTVSS 115

RESULT 10
US-08-918-148-75
Sequence 75, Application US/08918148A
Patent No. 6342220

GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918, 148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
US-08-918-148-75

Query Match 70.7%; Score 470; DB 4; Length 245;
Best Local Similarity 73.8%; Pred. No. 1.7e-37;
Matches 93; Conservative 12; Mismatches 13; Indels 8; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGVAIHWVROAPGSEGLEWVSQVTMGTTIGF 60
DB 3 EVQLVQSGGGLVQPGKSLRLSCAASGFTPEGVAIHWVROAPGSEGLEWVSQVTMGTTIGF 62
QY 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 120
DB 63 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 114
QY 121 MWTVSS 126
DB 115 MWTVSS 120

RESULT 11
US-08-983-607-28
Sequence 28, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:

STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: in house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-24

Query Match 71.3%; Score 474; DB 1; Length 117;
Best Local Similarity 75.6%; Pred. No. 3-2e-38;
Matches 90; Conservative 11; Mismatches 14; Indels 4; Gaps 2;

Qy 1 QVQLVSGGGLVOPGSLRLSCAASGFTFGDYAIHWVROAPGLEGVSGVTWGGTTIGF 60
Db 1 EVQLVESGGGLVOPGSRSLRLSCAASGFTFNDYAMHWVQAPGKGLEWVSGISWSSSSIGY 60

Qy 61 ADSVKGRTISRDNKNSLYLYMNSLRADPTALYYCC-ALPYINSSNRRGVAAFDIMG 117
Db 61 ADSVKGRTISRDNKNSLYLYMNSLRADPTALYYCCVKGGRDYSGY-FTVAFDIMG 117

RESULT 7
US-08-665-202-30
Sequence 30, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-30

Query Match 71.1%; Score 472.5; DB 2; Length 123;
Best Local Similarity 73.8%; Pred. No. 4.7e-38;
Matches 93; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

Qy 1 QVQLVSGGGLVOPGSLRLSCAASGFTFGDYAIHWVROAPGLEGVSGVTWGGTTIGF 60
Db 1 EVQLVESGGGLVOPGSRSLRLSCAASGFTFSYEMHWVQAPGKGLEWVSISSSGTITTY 60

Qy 61 ADSVKGRTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNRRGVAAFDIMGQGT 120
Db 61 ADSVKGRTISRDNKNSLYLYMNSLRADPTALYYCAR--DLGGVSYGVGLDYWGQGT 117

Qy 121 MVTVSS 126
Db 118 LVTVSS 123

RESULT 8
US-09-315-574-30
Sequence 30, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:

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APPLICANT: Vaughan, Tristram J.
APPLICANT: White, Michael
APPLICANT: Walton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-125-098-2

Query Match          73.2%; Score 486.5; DB 3; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.2e-39;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

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QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPGSEGLVWGVTWGTTIGF 60
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Db 1 EVQLVDSGGGLVQPGKSLRLSCAASGFTFDDYAMHWVQAQPGKLEWVAITWNSGHIDY 60
QY 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQT 115
QY 121 MVTWSS 126
   :|||:|||||
Db 116 LVTWSS 121

```

```

APPLICANT: White, Michael
APPLICANT: Walton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540,018
FILING DATE: 31-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-540-018-2

Query Match          73.2%; Score 486.5; DB 4; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.2e-39;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

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QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPGSEGLVWGVTWGTTIGF 60
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Db 1 EVQLVDSGGGLVQPGKSLRLSCAASGFTFDDYAMHWVQAQPGKLEWVAITWNSGHIDY 60
QY 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQT 115
QY 121 MVTWSS 126
   :|||:|||||
Db 116 LVTWSS 121

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RESULT 6
US-07-942-245-24
Sequence 24, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESS: Sughrue, Mion, Zimm, Macpeak & Seas
STREET: 2100 Penneylvanla Avenue, N.W.
CITY: Washington

```


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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 12.7945 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-43

Perfect score: 665
Sequence: 1 OVALVQSGGLVQPKSLURL.....RRGVAFPIWGGIMVTWSS 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/BCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509	76.5	120	2	US-08-958-201-10 Sequence 10, Appl
2	508	76.4	120	2	US-08-958-201-8 Sequence 8, Appl
3	486.5	73.2	121	3	US-08-599-226-2 Sequence 2, Appl
4	486.5	73.2	121	3	US-09-125-098-2 Sequence 2, Appl
5	486.5	73.2	121	4	US-09-540-018-2 Sequence 24, Appl
6	474	71.3	117	1	US-07-842-245-24 Sequence 30, Appl
7	472.5	71.1	123	2	US-08-665-202-30 Sequence 30, Appl
8	472.5	71.1	123	3	US-09-315-574-30 Sequence 30, Appl
9	471	70.8	116	2	US-08-652-816A-14 Sequence 14, Appl
10	470	70.7	245	4	US-08-918-148-75 Sequence 75, Appl
11	469	70.5	131	3	US-08-983-607-28 Sequence 28, Appl
12	467.5	70.3	121	3	US-08-599-226-10 Sequence 10, Appl
13	467.5	70.3	121	3	US-09-125-098-10 Sequence 10, Appl
14	467.5	70.3	121	4	US-09-540-018-10 Sequence 10, Appl
15	467	70.2	120	4	US-09-315-926A-80 Sequence 80, Appl
16	458.5	68.8	128	1	US-07-942-245-35 Sequence 35, Appl
17	457.5	68.8	119	2	US-08-331-398A-46 Sequence 46, Appl
18	457.5	68.8	119	2	US-08-331-397B-46 Sequence 46, Appl
19	457.5	68.8	119	2	US-08-759-804A-46 Sequence 46, Appl
20	457.5	68.8	119	3	US-09-227-693-46 Sequence 46, Appl
21	456	68.6	116	3	US-08-983-607-36 Sequence 36, Appl
22	455.5	68.3	309	4	US-09-079-029-9 Sequence 9, Appl
23	454	68.3	118	3	US-08-545-809A-97 Sequence 48, Appl
24	454	68.3	126	3	US-08-983-607-48 Sequence 11, Appl
25	453	68.1	310	4	US-09-079-029-11 Sequence 24, Appl
26	452.5	68.0	117	4	US-09-025-769B-24 Sequence 99, Appl
27	452.5	68.0	125	1	US-08-478-039-99 Sequence 99, Appl

28	452.5	68.0	125	1	US-08-476-349A-99 Sequence 99, Appl
29	452.5	68.0	125	3	US-09-240-274-151 Sequence 151, App
30	452	68.0	120	2	US-07-934-373C-4 Sequence 4, Appl
31	452	68.0	120	3	US-08-437-642B-4 Sequence 4, Appl
32	452	68.0	120	4	US-08-146-206C-4 Sequence 4, Appl
33	452	68.0	124	3	US-09-240-274-4 Sequence 4, Appl
34	451.5	67.9	127	3	US-09-240-274-27 Sequence 27, Appl
35	451.5	67.9	249	4	US-10-039-785-53 Sequence 53, Appl
36	451	67.8	140	3	US-08-983-607-32 Sequence 32, Appl
37	450.5	67.7	125	2	US-08-428-197-1 Sequence 1, Appl
38	450.5	67.7	125	5	PCT-US93-10555-1 Sequence 1, Appl
39	450	67.7	245	4	US-08-918-148-78 Sequence 78, Appl
40	449.5	67.6	123	4	US-09-560-198A-2 Sequence 2, Appl
41	449	67.5	120	4	US-09-025-769B-38 Sequence 38, Appl
42	449	67.5	120	4	US-09-025-769B-63 Sequence 63, Appl
43	449	67.5	128	3	US-09-240-274-1 Sequence 1, Appl
44	449	67.5	281	4	US-09-025-769B-178 Sequence 178, App
45	448	67.4	117	1	US-07-942-245-36 Sequence 36, Appl

ALIGNMENTS

```
RESULT 1
US-08-958-201-10
; Sequence 10, Application US/08958201
; Patent No. 5977319
;
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: 2Db
;
; US-08-958-201-10
;
; Query Match 76.5%; Score 509; DB 2; Length 120;
; Best Local Similarity 76.2%; Pred. No. 1.5e-41;
; Matches 96; Conservative 14; Mismatches 10; Indels 6; Gaps 2;
;
; QY 1 OVALVQSGGLVQPKSLRLSCAAGFTFGDYAIHMVRQAPGGLBWSGVWSTTIGF 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; DB 1 EVQLVDSGGGLVQPKSLRLSCAASGFTFDYAKMHWQAQPKGLBWSGISMNSGSI 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; QY 61 ADSVGRFTTISDNKNSLYLYMNSLRADPTALYYCALPYTINSNRRGVAFPIWGGOT 120
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
; DB 61 ADSVGRFTTISDNKNSLYLYMNSLRADPTALYYCALPYTINSNRRGVAFPIWGGOT 114
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: December 30, 2003, 11:45:24
Job time : 28.0219 secs

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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1324
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1324
```

```
Query Match          73.1%; Score 486; DB 11; Length 246;
Best Local Similarity 73.8%; Pred. No. 7e-40;
Matches 96; Conservative 11; Mismatches 9; Indels 14; Gaps 2;
```

```
OY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTMSGTTIGF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGGLVQPGKSLRLSCTASGFTFGDYAMSWVRQAPGKGLIEWVSAISGSGSTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 61 ADSYKGRFTISRDNKNSLYLYMNSLRADETALYYCA-----LPYINSSNTRRGVAAFDIW 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSYKGRFTISRDNKNSKTLTYLQNMNSLRADETAVYYCAKQOWLPY-----DAFDIW 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 117 GGGMTVTYSS 126
   |||||:|||||
Db 111 GGGMTVTYSS 120
   |||||:|||||
```

```
RESULT 15
US-09-972-656-76
; Sequence 76, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-76
```

```
Query Match          72.6%; Score 483; DB 11; Length 227;
Best Local Similarity 73.0%; Pred. No. 1.3e-39;
Matches 92; Conservative 17; Mismatches 15; Indels 2; Gaps 1;
```

```
OY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTMSGTTIGF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVETGGGVQPGKSLRLSCAASGFTFSSYAMTWVRQAPGKGLIEWVAVISYDSNKKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 61 ADSYKGRFTISRDNKNSLYLYMNSLRADETALYYCALPYINSSNTRRGVAAFDIWGGGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSYKGRFTISRDNKNSKTLTYLQNMNSLRADETAVYYCASDLVLTWTSRR--AAFDIWGGGT 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 121 MVTYSS 126
   |||||:|||||
Db 119 MVTYSS 124
   |||||:|||||
```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,185A
FILING DATE: 07-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,226
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 60/031,476
FILING DATE: 25-NOV-1996
APPLICATION NUMBER: US 09/125,098
FILING DATE: 07-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Deconti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-801-185A-2

Query Match      73.2%; Score 486.5; DB 11; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.8e-40;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGDAIHWRQAPGEGLEWVSATITWGSGTTIGF 60
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTTDDYAMHWROAPGKGLIEWVSATITWNSGHIDY 60
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGVAAPDIWGQGT 120
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGVAAPDIWGQGT 120
QY 121 MVTWSS 126
DB 116 LVTWSS 121

RESULT 12
US-10-133-715-2
Sequence 2, Application US/10133715
Publication No. US20030206898A1
GENERAL INFORMATION:
APPLICANT: Fischhoff, Steven
APPLICANT: Chartaeh, Elliot
TITLE OF INVENTION: Use of TNF-a Antibodies and Another Drug
FILE REFERENCE: BBI-186
CURRENT APPLICATION NUMBER: US/10/133,715
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D2E7 heavy chain variable region
US-10-133-715-2

Query Match      73.2%; Score 486.5; DB 12; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.8e-40;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGDAIHWRQAPGEGLEWVSATITWGSGTTIGF 60
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTTDDYAMHWROAPGKGLIEWVSATITWNSGHIDY 60
```

```

QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGVAAPDIWGQGT 120
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGVAAPDIWGQGT 115
QY 121 MVTWSS 126
DB 116 LVTWSS 121

RESULT 13
US-10-302-356A-2
Sequence 2, Application US/10302356A
Publication No. US20030219438A1
GENERAL INFORMATION:
APPLICANT: SALFELD, Jochen G.
APPLICANT: ALLEN, Deborah J.
APPLICANT: HOOGENDOORN, Hendricus R.J.M.
APPLICANT: KATMAKCALAN, Zehra
APPLICANT: LABROVSKY, Boris
APPLICANT: MANKOVICH, John A.
APPLICANT: MCGUINNNESS, Brian T.
APPLICANT: ROBERTS, Andrew J.
APPLICANT: SAKORAPAS, Paul
APPLICANT: SCHOENHAUT, David
APPLICANT: VAUGHAN, Treflan J.
APPLICANT: WHITE, Michael
APPLICANT: WILTON, Alison, J.
TITLE OF INVENTION: Human Antibodies That Bind Human
FILE OF INVENTION: TNFalpha
FILE REFERENCE: BBI-043CPACN2
CURRENT APPLICATION NUMBER: US/10/302,356A
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 09/540018
PRIOR FILING DATE: 2000-03-18
PRIOR APPLICATION NUMBER: 08/599226
PRIOR FILING DATE: 1996-02-09
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mutated human antibody
US-10-302-356A-2

Query Match      73.2%; Score 486.5; DB 12; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.8e-40;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPEGDAIHWRQAPGEGLEWVSATITWGSGTTIGF 60
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTTDDYAMHWROAPGKGLIEWVSATITWNSGHIDY 60
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGVAAPDIWGQGT 120
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRGVAAPDIWGQGT 115
QY 121 MVTWSS 126
DB 116 LVTWSS 121

RESULT 14
US-09-880-748-1324
Sequence 1324, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
```

```

RESULT 8
US-09-791-153A-66
; Sequence 66, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 66
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-66

Query Match      73.5%; Score 488.5; DB 11; Length 123;
Best Local Similarity 73.8%; Pred. No. 1.8e-40;
Matches 93; Conservative 13; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVQVVGSGGLVQPGKSLRLSCAASGFTTGDYAIHWVROAPGEGLEWVSGVTWSGTTIGF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTTDDYAMHWVROAPGEGLEWVSGISNMGRIY 60

QY 61 ADSVKGRTISRDNKNSLYLQNSLRPDTALYYCAKRGVGYDILTRGTYGMD---D 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRTISRDNKNSLYLQNSLRPDTALYYCAKRGVGYDILTRGTYGMD---D 117

QY 121 MVTWSS 126
:|||||
DB 118 LVTWSS 123

RESULT 9
US-09-791-153A-59
; Sequence 59, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 59
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-59

Query Match      73.5%; Score 488.5; DB 11; Length 227;
Best Local Similarity 73.8%; Pred. No. 3.6e-40;
Matches 93; Conservative 13; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVQVVGSGGLVQPGKSLRLSCAASGFTTGDYAIHWVROAPGEGLEWVSGVTWSGTTIGF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 EVQLVESGGGLVQPGKSLRLSCAASGFTTDDYAMHWVROAPGEGLEWVSGISNMGRIY 61

QY 61 ADSVKGRTISRDNKNSLYLQNSLRPDTALYYCAKRGVGYDILTRGTYGMD---D 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

DB 62 ADSVKGRTISRDNKNSLYLQNSLRPDTALYYCAKRGVGYDILTRGTYGMD---D 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 MVTWSS 126
:|||||
DB 119 LVTWSS 124

RESULT 10
US-09-880-748-1416
; Sequence 1416, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1416
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1416

Query Match      73.3%; Score 487.5; DB 11; Length 252;
Best Local Similarity 71.2%; Pred. No. 5.1e-40;
Matches 94; Conservative 14; Mismatches 15; Indels 9; Gaps 2;

QY 1 QVQVVGSGGLVQPGKSLRLSCAASGFTTGDYAIHWVROAPGEGLEWVSGVTWSGTTIGF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTTDDYAMHWVROAPGEGLEWVSGISNMGSIAY 60

QY 61 ADSVKGRTISRDNKNSLYLQNSLRPDTALYYCAKRGVGYDILTRGTYGMD---D 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ADSVKGRTISRDNKNSLYLQNSLRPDTALYYCAKRGVGYDILTRGTYGMD---D 117

QY 115 IMGGTMTWSS 126
:|||||
DB 118 VMGQRTMTWSS 129

RESULT 11
US-09-801-185A-2
; Sequence 2, Application US/09801185A
; Publication No. US20030092059A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

```

Best Local Similarity 75.2%; Pred. No. 1.3e-41;
Matches 97; Conservative 12; Mismatches 7; Indels 13; Gaps 2;

QY 1 QVQLVDSGGGLVDPGKSLRLSCAASGFTPDYAIHWYRQAPGKLEWVSGVTSGTTIGF 60
Db 1 QVQLVDSGGGLVDPGKSLRLSCAASGFTPDYAHMWYRQAPGKLEWVSGISNMSSIGY 60

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNRYRGV---AAPTIG 117
Db 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTATYYCA-----RIGWGGAFDIWG 110

QY 118 QGTMTVSS 126
Db 111 KGLVTVSS 119

RESULT 5
US-09-880-748-1427

Sequence 1427, Application US/09880748
Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: P5523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1427

LENGTH: 254

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1427

Query Match 73.8%; Score 491; DB 11; Length 254;

Best Local Similarity 71.9%; Pred. No. 2.3e-40;

Matches 92; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVDSGGGLVDPGKSLRLSCAASGFTPDYAIHWYRQAPGKLEWVSGVTSGTTIGF 60
Db 1 EAQLVDSGGGLVDPGKSLRLSCAASGFTPDYAHMWYRQAPGKLEWVSGISNMSSIGY 60

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYC--ALPYINSSNRYRGVAAPDIWG 118
Db 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTAVYYCTRGVEYDILTGYNELGAFDIWG 120

QY 119 QGTMTVSS 126
Db 121 KGLVTVSS 128

RESULT 6

US-10-447-331-6

Sequence 6, Application US/10447331

Publication No. US2003021943A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Ridgway, John B.

TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND

FILE REFERENCE: GENENT.122A

CURRENT APPLICATION NUMBER: US/10/447,331

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: US/09/515,825

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 60/122262

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 122

TYPE: PRT

ORGANISM: Homo sapiens

US-10-447-331-6

Query Match 73.5%; Score 489; DB 12; Length 122;

Best Local Similarity 74.8%; Pred. No. 1.6e-40;

Matches 95; Conservative 12; Mismatches 14; Indels 6; Gaps 2;

QY 1 QVQLVDSGGGLVDPGKSLRLSCAASGFTPDYAIHWYRQAPGKLEWVSGVTSGTTIGF 60
Db 1 EVQLVETGGGLVDPGKSLRLSCAASGFTPDYGMHWYRQAPGKLEWVSGISNMSSIGY 60

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSS-NYRGVAAPDIWG 119
Db 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCARDAFGSGSYG----WFDPMGQG 115

QY 120 TMTVSS 126
Db 116 TLVTVSS 122

RESULT 7

US-09-880-748-922

Sequence 922, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: P5523

CURRENT APPLICATION NUMBER: US/09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 922

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-922

Query Match 73.5%; Score 489; DB 11; Length 251;

Best Local Similarity 67.6%; Pred. No. 3.6e-40;

Matches 94; Conservative 14; Mismatches 7; Indels 24; Gaps 2;

QY 1 QVQLVDSGGGLVDPGKSLRLSCAASGFTPDYAIHWYRQAPGKLEWVSGVTSGTTIGF 60
Db 1 QVQLVDSGGGLVDPGKSLRLSCAASGFTPDYGMHWYRQAPGKLEWVSGISNMSSIGY 60

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCA-----LPYINSSNRY 107
Db 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTAVYYCARVPSYDILTGYYLPH----- 113

QY 108 RGVAAFDIWGQMTVSS 126
Db 114 ---APDVWGKGLTVSS 128

RESULT 2
US-09-840-459-88
Sequence 88, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: Horvath, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855,1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 88
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-88

Query Match 76.0%; Score 505.5; DB 10; Length 119;
Best Local Similarity 77.0%; Pred. No. 3.8e-42;
Matches 97; Conservative 12; Mismatches 10; Indels 7; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGKLEWVSQVTWGTTIGF 60
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFDDYAMHWVRQAPGKLEWVSQISWNSGSIQY 60
QY 61 ADSVKGRTISRDNKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCGVAAPDIWGCT 120
DB 61 ADSVKGRTISRDNKNSLYLYNNSLRADDTALYYCATYHY---YYGCM---DWWGCT 113
QY 121 MVTVSS 126
DB 114 TVTVSS 119

RESULT 3
US-08-779-457-50
Sequence 50, Application US/08779457
Publication No. US20020193571A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodriguez, Maria L.
TITLE OF INVENTION: MSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpacin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-50

Query Match 76.0%; Score 505.5; DB 8; Length 241;
Best Local Similarity 77.0%; Pred. No. 8.4e-42;
Matches 97; Conservative 12; Mismatches 10; Indels 7; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGKLEWVSQVTWGTTIGF 60
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFDDYAMHWVRQAPGKLEWVSQISWNSGSIQY 60
QY 61 ADSVKGRTISRDNKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCGVAAPDIWGCT 120
DB 61 ADSVKGRTISRDNKNSLYLYNNSLRADDTALYYCAEPHNTD-----APDIWGCT 113
QY 121 MVTVSS 126
DB 114 LTVVSS 119

RESULT 4
US-09-880-748-1926
Sequence 1926, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patencin Ver. 2.0
SEQ ID NO 1926
LENGTH: 245
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1926

Query Match 75.7%; Score 503.5; DB 11; Length 245;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 27.0219 Seconds

(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-43

Perfect score: 665
Sequence: 1 QVQLVSGGGLVQPGKSLRL.....RRGVAAFDIWGQGMVTYSS 126Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCRUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	77.0	132	11	US-09-791-153A-65
2	505.5	76.0	119	10	US-09-840-459-88
3	505.5	76.0	241	8	US-08-779-457-50
4	503.5	75.7	245	11	US-09-880-748-1926
5	491	73.8	254	11	US-09-880-748-1427
6	489	73.5	122	12	US-10-447-331-6
7	489	73.5	251	11	US-09-880-748-922
8	488.5	73.5	123	11	US-09-791-153A-66
9	488.5	73.5	227	11	US-09-791-153A-59
10	487.5	73.3	252	11	US-09-880-748-1416
11	486.5	73.2	121	11	US-09-801-185A-2
12	486.5	73.2	121	12	US-10-133-715-2
13	486.5	73.1	121	12	US-10-302-356A-2
14	486	73.1	246	11	US-09-880-748-1324
15	483	72.6	227	11	US-09-972-656-6

16	483	72.6	251	11	US-09-880-748-1320	Sequence 1320, Ap
17	481	72.3	251	11	US-09-880-748-1542	Sequence 1542, Ap
18	476	71.6	248	11	US-09-880-748-1890	Sequence 1890, Ap
19	475	71.4	128	15	US-10-269-805-29	Sequence 29, App1
20	475	71.4	239	11	US-09-880-748-2038	Sequence 2038, Ap
21	474	71.3	239	11	US-09-880-748-2015	Sequence 2015, Ap
22	473	71.1	239	11	US-09-880-748-2022	Sequence 2022, Ap
23	472.5	71.1	230	12	US-09-969-748C-2	Sequence 2, App1
24	472.5	71.1	296	12	US-09-969-039-2	Sequence 2, App1
25	472.5	71.1	296	12	US-09-969-039-12	Sequence 12, App1
26	472.5	71.1	239	11	US-09-949-039-75	Sequence 75, App1
27	472	71.0	239	11	US-09-880-748-2023	Sequence 2023, Ap
28	471	70.8	239	11	US-09-880-748-937	Sequence 937, App
29	469.5	70.6	121	12	US-10-010-942B-9	Sequence 9, App1
30	469.5	70.6	259	11	US-09-880-748-1664	Sequence 1664, Ap
31	469	70.5	116	15	US-10-091-300-24	Sequence 24, App1
32	469	70.5	122	15	US-10-269-805-7	Sequence 7, App1
33	469	70.5	122	15	US-10-269-805-11	Sequence 11, App1
34	469	70.5	249	11	US-09-880-748-1109	Sequence 1109, Ap
35	468	70.4	136	12	US-10-045-674-487	Sequence 487, App
36	468	70.4	248	11	US-09-880-748-1974	Sequence 1974, Ap
37	468	70.4	367	12	US-10-045-674-453	Sequence 453, App
38	467.5	70.3	119	15	US-10-073-644C-6	Sequence 6, App1
39	467.5	70.3	121	11	US-09-801-185A-10	Sequence 10, App1
40	467.5	70.3	121	12	US-10-133-715-10	Sequence 10, App1
41	467.5	70.3	121	12	US-10-302-356A-10	Sequence 10, App1
42	467.5	70.3	225	11	US-09-453-234-68	Sequence 82, App1
43	467.5	70.3	244	11	US-09-880-748-82	Sequence 82, App1
44	467.5	70.3	244	11	US-09-880-748-164	Sequence 164, App
45	467.5	70.3	244	11	US-09-880-748-280	Sequence 280, App

ALIGNMENTS

```
RESULT 1
US-09-791-153A-65
; Sequence 65, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hiltz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent version 3.0
; SEQ ID NO 65
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-65

Query Match 77.0%; Score 512; DB 11; Length 132;
Best Local Similarity 75.0%; Pred. No. 9.9e-43;
Matches 99; Conservative 12; Mismatches 15; Indels 6; Gaps 1;
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1 QVQLVSGGGLVQPGKSLRLAEDTALYYCAAPYINSNYRGVA-----FD 114
1 EVQLVSGGGLVQPGKSLRLAEDTALYYCAAPYINSNYRGVA-----FD 60
ADVVKRPTISRNANKSLTYLNNSLRADDTALYYCAAPYINSNYRGVA-----FD 114
ADVVKRPTISRNANKSLTYLNNSLRADDTALYYCAAPYINSNYRGVA-----FD 120
115 YWGQGMVTYSS 126
121 YWGQGMVTYSS 132

CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and actively such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 245 AA:

Query Match 75.7%; Score 503.5; DB 23; Length 245;
 Best Local Similarity 75.2%; Pred. No. 2e-40; 7; Indels 13; Gaps 2;
 Matches 97; Conservative 12; Mismatches 7;

QY 1 QVQLVQSGGGLVQPGRSLRLSCAASGFTFGDVAIHMRQAPEGLEWVSGVTWSTGTTGF 60
 DB 1 QVQLVQSGGGLVQPGRSLRLSCAASGFTFGDVAIHMRQAPEGLEWVSGVTWSTGTTGF 60
 QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALTYCA-----LPYINSSNYRQVA 117
 DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALTYCA-----LPYINSSNYRQVA 110
 QY 118 OCTWTVTVSS 126
 DB 111 RCTLVTVSS 119

RESULT 13

AAV64737
 ID AAV64737 standard; Protein; 149 AA.

XX AAV64737;
 DT 01-FEB-2000 (first entry)

XX Human 5' EST related polypeptide SEQ ID NO:898.

XX Human, 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence;
 KW forensic; location; development; protein synthesis; stability;
 KW regulation; identification.

OS Homo sapiens.

XX WO953051-A2.

XX 21-OCT-1999.

XX 09-APR-1999; 99WO-IB00712.

XX 09-APR-1998; 98US-0057719.

XX 28-APR-1998; 98US-0069047.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclet A, Giordano J;

XX WPI; 2000-038446/03.

XX N-PSDB; AA42351.

XX Novel secreted protein 5' expressed sequence tag sequences used in
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures

XX Claim 3; Page 627; 837pp; English.

CC AA42265 to AA43075 represent novel 5' expressed sequence tag (EST)
 CC sequences, corresponding to human secreted proteins. AAV64651 to
 CC AAV65438 represent the EST-related proteins corresponding to AA42265 to
 CC AA43052. The 5' ESTs can be used for producing secreted human gene

CC products. They can be used to identify and isolate 5' untranslated
 CC regions (UTRs) and upstream regulatory regions which control the
 CC location, development stage, rate, and quantity of protein synthesis, as
 CC well as stability of mRNA. The ESTs are also useful as probes for
 CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
 CC also be used in forensic procedures to identify individuals, or in
 CC diagnostic procedures to identify individuals having genetic diseases
 CC resulting from abnormal gene expression. The products may also be used in
 CC gene therapy protocols. The nucleic acids encoding signal peptides can be
 CC used for directing extracellular secretion of a polypeptide or the
 CC insertion of a polypeptide into a membrane, or importing a polypeptide
 CC into a cell. The proteins encoded by the EST sequences may be useful in
 CC treating a variety of human conditions. Secreted proteins have
 CC therapeutic value, and the identification of new secreted proteins is
 CC valuable. AA42249 to AA42264 and AAV64644 to AAV64650 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 149 AA:

Query Match 74.1%; Score 492.5; DB 21; Length 149;
 Best Local Similarity 70.4%; Pred. No. 1.3e-39;
 Matches 95; Conservative 11; Mismatches 12; Indels 17; Gaps 2;

QY 1 QVQLVQSGGGLVQPGRSLRLSCAASGFTFGDVAIHMRQAPEGLEWVSGVTWSTGTTGF 60
 DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTFGDVAIHMRQAPEGLEWVSGVTWSTGTTGF 79
 QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADTALTYCA-----LPYINSSNYRQVA 111
 DB 80 ADSVKGRTTISRDNKNSLYLYMNSLRADTALTYCA-----LPYINSSNYRQVA 131

QY 112 AFDIWGQGTWTVSS 126

DB 132 AMDYWGQGTWTVSS 146

RESULT 14

ABP45416
 ID ABP45416 standard; Protein; 254 AA.

XX ABP45416;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1427.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineutritic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

XX 17-OCT-2000; 2000US-240816P.

XX 16-MAR-2001; 2001US-276248P.

XX 21-MAR-2001; 2001US-277379P.

XX 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

[illegible]

DT	16-OCT-2001	(first entry)
DE	Human heavy chain variable (VH) region, UBI-24.	
XX		
XX	Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;	
XX	neuroprotective; immunosuppressive; human immunodeficiency virus;	
KW	HIV infection; cytotoxic; vasotropic; leukocyte trafficking; allergy;	
KW	inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock	
KW	multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;	
KW	anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;	
KW	fibrotic disease; angiotensin; acquired immune deficiency syndrome;	
KW	AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody;	
XX	neointimal hyperplasia; VH; heavy chain variable region.	
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Region	31..35
FT		/label= CDR1
FT		/note= "Complementarity determining region 1"
FT	Region	50..68
FT		/label= CCR2
FT		/note= "Complementarity determining region 2"
FT	Region	99..108
FT		/label= CDR3
FT		/note= "Complementarity determining region 3"
XX		
PN	WO200157226-A1.	
XX		
PD	09-AUG-2001.	
XX		
PD	02-FEB-2001; 2001WO-US03537.	
PR	03-FEB-2000; 2000US-0497625.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
PI	Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;	
XX	WPI; 2001-488888/53.	
XX		
PT	Humanised immunoglobulin for treating a CC-chemokine receptor	
PT	2-mediated disorder in a patient, comprises a binding specificity for	
PT	CCR2, and a non-human antigen binding region and human immunoglobulin	
XX	-	
PS	Disclosure; Page 173; 183pp; English.	
XX		
CC	The patent discloses a humanised antibody or its antigen-binding	
CC	fragment, having binding specificity for CC-chemokine receptor 2	
CC	(CCR2), comprising an antigen binding region of non-human origin	
CC	and at least a portion of an immunoglobulin of human origin. The	
CC	humanised antibodies are useful for inhibiting the interaction of	
CC	a cell expressing CCR2. They are useful for inhibiting or treating	
CC	HIV infection. The proteins of the invention are useful for inhibiting	
CC	leukocyte trafficking, for treating CCR2-mediated disorders such as	
CC	inflammatory disorder, autoimmune disorders such as rheumatoid	
CC	arthritis and multiple sclerosis, atherogenesis and atherosclerosis,	
CC	and for inhibiting restenosis. They are useful in therapy or diagnosis,	
CC	and in the manufacture of a medicament for treating CCR-2 mediated	
CC	disease. They are also useful for treating allergy, anaphylaxis,	
CC	malignancy, chronic and acute inflammation, histamine and IgE-	
CC	mediated allergic reaction, shock, stenosis, allograft rejection,	
CC	fibrotic disease, asthma, inflammatory glomerulopathies, acquired	
CC	immune deficiency syndrome (AIDS), restenosis associated with vascular	
CC	intervention, including angioplasty and/or stent placement in a mammal.	
CC	Humanised antibodies are also useful for inhibiting narrowing of the	
CC	lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of	
CC	a vessel in a mammal, preferably associated with vascular intervention.	
CC	The present sequence is human heavy chain variable (VH) region, UBI-24.	
XX		
Sequence	119 AA;	

[illegible]

Db	115	LTVSS	120
<hr/>			
RESULT 8			
ID	AAG65553	standard; protein.	120 AA.
AC	AAG65553;		
XX			
DT	30-NOV-2001	(first entry)	
XX			
DE	Amino acid sequence of VH3-4.		
XX			
KX	Gene library; immunoglobulin; antibody library; VH3-4.		
XX			
OS	Homo sapiens.		
PX	WO200162907-A1.		
PD	30-AUG-2001.		
PF	22-FEB-2001; 2001WO-JP01298.		
PR	22-FEB-2000; 2000JP-0050543.		
PA	(MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.		
PI	Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;		
PI	Okuno Y, Shiraki K;		
DR	WPI; 2001-565420/63.		
XX			
PT	Producing gene libraries and antibody libraries, involves selecting a		
PT	light chain that binds to a heavy chain product to produce a functional		
PT	formation, and producing a gene library of the light chain variable		
PT	regions -		
PS			
XX			
XX	Disclosure; Page 20; 181pp; Japanese.		
CC	The invention relates to producing gene libraries, comprising		
CC	immunoglobulin light and heavy variable region. The method involves		
CC	selecting light chain that binds with the heavy chain product to produce		
CC	a functional conformation, producing a gene library comprising a		
CC	collection of these light chain variable genes, and combining with gene		
CC	library of heavy chain variable genes. The method is used for production		
CC	of gene and antibody libraries. The present sequence represents the amino		
CC	acid sequence of VH3-4.		
SQ	Sequence	120 AA;	
<hr/>			
Query Match	76.4%; Score 508; DB 22; Length 120;		
Best Local Similarity	77.8%; Pred. No. 3.4e-41;		
Matches	98; Conservative 11; Mismatches 11; Indels 6; Gaps 1;		
DB	1 QVOIVSGGGLVOPKSLRLSCAASGFTFGDYAIHWRAQAPBGLMWVGVTWGTTIGF 60		
	EVQLVESGGGLVPGPGRSLRLSCAASGFTFDYAMHWYQADPKGLEWVSGISMSNGSIGY 60		
QY	61 ADSVKGRRTTIRDNAAKSLLYYNMSLRAPEDLTALYYCALPYINSNYRGVAAPFIWGCT 120		
DB	61 ADSVKGRRTTIRDNAAKSLLYYNMSLRAPEDLTALYYCALPYINSNYRGVAAPFIWGCT 114		
QY	121 MYTVSS 126		
DB	115 TTVTSS 120		
<hr/>			
RESULT 9			
ID	ABB06276	standard; Protein.	120 AA.
XX	ABB06276;		
AC	ABB06276;		

Key	Location/Qualifiers
FT Region	1..30 /label= FR1 /note= "framework region 1"
FT Region	31..35 /label= CDR1 /note= "complementarity determining region 1"
FT Region	36..49 /label= FR2 /note= "framework region 2"
FT Region	50..66 /label= CDR2 /note= "complementarity determining region 2"
FT Region	67..99 /label= FR3 /note= "framework region 3"
FT Region	100..113 /label= CDR3 /note= "complementarity determining region 3"
FT Region	114..124 /label= FR4 /note= "framework region 4"
PD WO9855619-A1.	
PD 10-DEC-1998.	
PF 05-JUN-1998;	98WO-EP03397.
PR 08-MAY-1998;	98DE-1020663.
PR 06-JUN-1997;	97DE-1023904.
PR 12-DEC-1997;	97DE-1055227.
PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.	
PI Berchtold P, Escher RFA:	
XX WPI; 1999-105496/09.	
XX N-PSDB; AAV72231.	
XX Nucleic acid encoding human autoantibodies against platelet glycoprotein IIb/IIIa - used for diagnosis, treatment and prevention of autoimmune thrombocytopenic purpura and for modulation of fibrinogen binding	
XX Disclosure; Page 58-59; 93pp; German.	
XX This invention describes novel nucleic acid fragments that encode human auto-antibodies and anti-idiotypic antibodies against blood platelet membrane protein, GPIIb/IIIa. The products of the invention are used for diagnosis (including monitoring and determining predisposition), prevention and treatment of autoimmune thrombocytopenic purpura (ATP) and also for modulating binding of fibrinogen to thrombocytes (particularly to dissolve thrombi and/or prevent their formation, e.g. in cases of cardiac infarction or pulmonary embolism). Unlike murine antibodies, human antibodies (hAb) do not induce adverse side effects and persist for longer in vivo than small peptides.	
XX Sequence 124 AA:	
QY Query Match 76.8%; Score 511; DB 20; Length 124;	
QY Best Local Similarity 77.3%; Pred. No. 1.8e-41;	
QY Matches 99; Conservative 11; Mismatches 12; Indels 6; Gaps 2	
DB 1 QVQLVSGGGLVPGKSLRLSCAASGFTEDVAIHWRQAPGGELRWVGVTSGTIGF 60	
DB 1 QVQLTSSGGGLVPGKSLRLSCAASGTFEDVAIHWRQAPGGELRWVGISINDSTIGY 60	
QY 61 ASVVKRFTISRDNAKNSLYLNNSLRADETALYYCALPYNS--SNYRGAAPDIWQ 118	
DB 61 ASVVKRFTISRDNAKNSLYLNNSLRADETALYYCYKMGSSVATYN----APDIWQ 116	
QY 119 GTMVTVSS 126	

Db 117 GTWTVSS 124

RESULT 6
ID AAY43255 standard; Protein; 120 AA.
XX AAY43255;
AC
DT 13-JAN-2000 (first entry)
XX
DE VH domain CDR of anti-estradiol antibody.

KM Estradiol; complementarity determining region; CDR; estriol-3-sulphate;
KM antibody antigen binding domain; steroid hormone; estriol; testosterone;
KW dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;
KV menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;
diagnosis; VH domain.
KM
XX Homo sapiens.
OS
PN US5977319-A.
EN
PD 02-NOV-1999.
XX
PF 21-OCT-1997; 97US-0958201.
XX
PR 21-OCT-1996; 96US-0028897.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Johnson KS, Pope AR, Pritchard K, Williams AJ;
DR WPI; 1999-619713/53.
XX N-PSDB; AAZ31653.
PT New specific binding partners for estradiol, used for monitoring
PT estradiol levels during the menstrual cycle, in hormone replacement
PT therapy and for diagnosing oestrogen secreting tumours -
XX
PS Claim 1; Column 25-26; 26pp; English.

This sequence represents a VH domain complementarily determining region (CDR) from an antibody specific for estradiol. The invention relates to specific binding members (sbp) comprising a polypeptide that comprises an antibody antigen binding domain (AABD) which has a dissociation constant of less than 1.0×10^{-8} M for estradiol, and a dissociation constant of at least 500-fold higher for the steroid hormones selected from estriol, testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate and estriol 3-beta-di-glucuronide, where the polypeptide comprises an antibody VH domain. The sbps can be used in an immunoassay for determining the presence or absence of estradiol in a sample. They can be used for monitoring estradiol levels, e.g. during the menstrual cycle, in hormone replacement therapy and for diagnosing oestrogen secreting tumours. The sbps can provide for discrimination between estradiol and other related steroids.

SQ Sequence 120 AA;

Query Match 76.5%; Score 509; DB 20; Length 120;
Best Local Similarity 76.2%; Pred.No. 2.7e-41;
Matches 96; Conservative 14; Mismatches 10; Indels 6; Gaps 2

1 QVALVGSGGLVQPCKSLRLSCAAAGFTFGDYAIHMVRCAPEGELEWVSQTITGF 60
:|||||:|||||:|||||:|||||:|||||:
1 EQVLVBSGGGLVQPKSRLLSCLASGFTTDDYAMHVVRCAPKGLEWVSIGMSISGY 60
ADSVNGRFTIISDNANKSLIYLTMNSLRPBDTLILTYCALPYTISSNTRRGVAAFDIWGOT 120
61 ADGVNGRPFTISRDNANKSLIYLQMNSIRPBDTIVYYCCARPL-----YPKG-TQYDFWGOT 114
121 MTTVSS 126

```

PN WO9118983-A.
XX
XX 12-DEC-1991.
XX
XX 28-MAY-1991; 91WO-1000067.
XX PF
XX 29-MAY-1990; 90AT-0001178.
XX PR
XX (JUNG/) JUNGBAUER A.
XX PA
XX Felgenhauer M, Himmler G, Kohl J, Steindl F;
XX
XX WPI; 1992-007468/01.
XX DR N-PSDB; AAQ20068.
XX
XX Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
XX
XX Claim 4; Page 31; 52pp; German.
XX
XX The cell line 3D6 (87110301; Porton Down) produces a Mab of the
CC IgG1/Kappa type that reacts specifically with HIV-1 gp120 and also
CC weakly cross-reacts with HIV-1 gp120. Gene construct 3D6 was
CC engineered using the variable region coding region of the heavy
CC and light chains of antibody 3D6, joined by a linker. The
CC recombinant protein binds to HIV gp160.
CC See also AAQ20066 and AAQ20067.
XX
XX Sequence 248 AA;
SQ
Query Match 77.6%; Score 516; DB 13; Length 248;
Best Local Similarity 77.3%; Pred. No. 1.3e-41;
Matches 99; Conservative 11; Mismatches 14 Indels 4; Gaps 2;
QY 1 QVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAIHWVR PEGGLEWVGVTWSTTIGF 60
DB 2 EVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAMHWVR PGKGLWVSGISWDSSTIGY 61
QY 61 ADSVKGRFTISRDNKNSLYLNNSLRADDTALYYC-- PYNSNSYRRGVAAPDIWQ 118
DB 62 ADSVKGRFTISRDNKNSLYLNNSLRADDTALYYC-- DYVDSGY--FTVAFDIWQ 119
QY 119 GTMTVTSS 126
DB 120 GTMTVTSS 127
RESULT 4
AAR20057
ID AAR20057 standard; Protein; 475 AA.
XX
XX AAR20057;
XX
XX 25-MAR-1992 (first entry)
XX
XX Heavy chain of 3D6 anti-HIV antibody.
XX
XX Plasmid pUC3D6HC; human immunodeficiency virus; IDS;
XX KW complementarity determining region.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19 /label= signal
XX Region 20..49 /label= Framework_1
XX Region 50..54 /label= CDR-1
XX Region 55..68 /label= Framework_2
XX Region 69..85

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FT /label= CDR_2
FT Region 86..117 /label= Framework_3
FT Region 118..134 /label= CDR_3
FT Region 135..145 /label= Framework_4
FT Region 146..475 /label= Constant_region
XX
XX WO9118983-A.
XX
XX 12-DEC-1991.
XX
XX 28-MAY-1991; 91WO-1000067.
XX PF
XX 29-MAY-1990; 90AT-0001178.
XX PR
XX (JUNG/) JUNGBAUER A.
XX PA
XX Felgenhauer M, Himmler G, Kohl J, Steindl F;
XX
XX WPI; 1992-007468/01.
XX DR N-PSDB; AAQ20068.
XX
XX Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
XX
XX Claim 2; Page 24; 52pp; German.
XX
XX The variable region of the heavy chain is used in a recombinant
CC protein with the variable region from the kappa light chain of 3D6,
CC the two V regions being joined by a linker. The recombinant protein
CC binds to HIV gp160.
CC See also AAQ20067 and AAQ20068.
XX
XX Sequence 475 AA;
SQ
Query Match 77.6%; Score 516; DB 13; Length 475;
Best Local Similarity 77.3%; Pred. No. 2.6e-41;
Matches 99; Conservative 11; Mismatches 14; Indels 4; Gaps 2;
QY 1 QVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAIHWVRQAPGKGLWVSGVTWSTTIGF 60
DB 20 EVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAMHWVRQAPGKGLWVSGISWDSSTIGY 79
QY 61 ADSVKGRFTISRDNKNSLYLNNSLRADDTALYYC--ALPYNSNSYRRGVAAPDIWQ 118
DB 80 ADSVKGRFTISRDNKNSLYLNNSLRADDTALYYC--FTVAFDIWQ 137
QY 119 GTMTVTSS 126
DB 138 GTMTVTSS 145
RESULT 5
AAW90286
ID AAW90286 standard; Protein; 124 AA.
XX
XX AAW90286;
XX
XX 07-SEP-1999 (first entry)
XX
XX Human anti-GPIIb/IIIa antibody heavy chain protein from phagemid AI-X40.
XX
XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
XX KW blood platelet membrane protein; predilection; prevention; treatment;
XX KW autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
XX KW thrombocyte; cardiac infarction; pulmonary embolism; heavy chain.
XX
XX Homo sapiens.
XX

```

XX
PS Example 8; Fig 9A; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful as a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC factor VIII antibody A3-C1 specific scfv protein B18 which is used
CC in the method of the invention.
XX
SQ Sequence 126 AA;
Query Match 100.0%; Score 665; DB 21; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.1e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OVQLVQSGGGLVQPKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMSGTTIGF 60
DB 1 OVQLVQSGGGLVQPKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMSGTTIGF 60
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRABDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRABDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
QY 121 MVTVSS 126
DB 121 MVTVSS 126
DT 23-MAR-2000 (first entry)
XX
DE Human FVIII antibody heavy chain variable region B18 protein fragment.
XX
KM Human; heavy chain; antibody; factor VIII; hemostatic; variable region;
KM hemophilia A.
OS Homo sapiens.
XX
PN WO9958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98BP-0201543.
XX
PA (SANG-) STICHTING SANGUIN BLOEDVOORZIENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX
DR MPI; 2000-053102/04.
DR N-PSDB; AA243864.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
PS Example 8; Fig 9C; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful as a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents a fragment
CC of the human factor VIII antibody heavy chain variable region protein B18
CC which is used in the method of the invention.
XX
SQ Sequence 126 AA;
Query Match 100.0%; Score 665; DB 21; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.1e-56;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 OVQLVQSGGGLVQPKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMSGTTIGF 60
DB 1 OVQLVQSGGGLVQPKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMSGTTIGF 60
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRABDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRABDTALYYCALPYINSSNYRRGVAAFDIWGQGT 120
QY 121 MVTVSS 126
DB 121 MVTVSS 126
DT 25-MAR-1992 (first entry)
XX
AC AAR20059;
XX
DT 25-MAR-1992 (first entry)
XX
DE Recombinant sc3d6 anti-HIV gp160 antibody.
XX
KM Plasmid pUC3d6LC; pUC3d6HC; human immunodeficiency virus; AIDS;
KM complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT /label= Framework_1_heavy_chain
FT /label= Framework_1_heavy_chain
FT /label= CDR_1_heavy_chain
FT /label= Framework_2_heavy_chain
FT /label= Framework_2_heavy_chain
FT /label= CDR_2_heavy_chain
FT /label= Framework_3_heavy_chain
FT /label= Framework_3_heavy_chain
FT /label= CDR_3_heavy_chain
FT /label= Framework_4_heavy_chain
FT /label= Framework_4_heavy_chain
FT /label= linker
FT /label= Framework_1_light_chain
FT /label= Framework_1_light_chain
FT /label= CDR_1_light_chain
FT /label= Framework_2_light_chain
FT /label= Framework_2_light_chain
FT /label= CDR_2_light_chain
FT /label= Framework_3_light_chain
FT /label= Framework_3_light_chain
FT /label= CDR_3_light_chain
FT /label= Framework_4_light_chain
FT /label= Framework_4_light_chain

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 40.5329 Seconds
(without alignments)
493,415 Million cell updates/sec

Title: US-09-674-752-43

Perfect score: 665
Sequence: 1 QVQLVQSGGGLVQPGRSLRL.....RRGVAAPDIWGQGTWVTS 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	665	100.0	126	21	AA150961 Human FVIII antio
2	665	100.0	126	21	AA150967 Human FVIII antio
3	516	77.6	248	13	AA120059 Recombinant sc3D6
4	516	77.6	475	13	AA120057 Heavy chain of 3D6
5	511	76.8	124	20	AA150286 Human anti-GPIIb/I
6	509	76.5	120	20	AA143255 VH domain CDR of a
7	508	76.4	120	20	AA143254 VH domain CDR of a
8	508	76.4	120	22	AA165553 Amino acid sequenc
9	508	76.4	120	23	AB106276 VH3-4 amino acid s

10	505.5	76.0	119	22	AA107025 Human heavy chain
11	505.5	76.0	241	18	AA124063 Human MSX receptor
12	503.5	75.7	245	23	AB145915 Human Blys binding
13	492.5	74.1	149	21	AA164737 Human 5' EST relat
14	491	73.8	254	23	AB145416 Human Blys binding
15	489	73.5	122	21	AA196065 Human anti-DAF ant
16	489	73.5	251	23	AB144911 Human Blys binding
17	488.5	73.3	127	22	AA1008385 Anti-ORGP antiod
18	487.5	73.3	126	22	AA1002623 Anti-CD40 monoclon
19	487.5	73.3	146	24	AB136923 Anti-hEDRF antiod
20	487.5	73.3	252	23	AB145405 Human Blys binding
21	487.5	73.3	118	22	AA1002560 Anti-adipocyte mon
22	486.5	73.2	121	18	AA1027569 Anti-TNF-alpha ant
23	486.5	73.2	121	24	AA1016460 Human anti-TNF-aip
24	486.5	73.1	246	23	AB145313 Human Blys binding
25	486	72.6	251	23	AB145309 Human Blys binding
26	483	72.6	127	23	AB176513 HCV E1 antigen mon
27	481	72.3	131	23	AB176547 HCV E1 antigen mon
28	481	72.3	121	23	AB145531 Human Blys binding
29	481	72.3	251	23	AB145531 Human antibody IM9
30	480.5	72.3	118	22	AA1002605 Anti-adipocyte mon
31	480	72.2	118	22	AA1002593 Anti-adipocyte mon
32	479	72.0	120	22	AA1002501 Human Blys binding
33	476	71.6	248	23	AB145879 Human Blys binding
34	476	71.6	239	23	AB146027 Human Blys binding
35	475	71.4	239	23	AB146004 Heavy chain variab
36	474	71.3	239	23	AB146004 Human Blys binding
37	474	71.3	239	23	AB146011 Human Blys binding
38	473	71.1	117	23	AA1015187 Human antibody heav
39	472.5	71.1	123	18	AA1008582 Human antibody C4
40	472.5	71.1	290	24	AB155318 Pelb/SAF/myc/6His
41	472.5	71.1	291	23	AB155318 Immunoglobulin rel
42	472.5	71.1	296	23	AB155318 Human secreted pro
43	472.5	71.1	519	23	AB155318 Human Blys binding
44	472.5	71.1	239	23	AB146012
45	472	71.0	239	23	AB146012

ALIGNMENTS

RESULT 1	AA150961	AA150961 standard; Protein; 126 AA.
ID	AA150961	AA150961 standard; Protein; 126 AA.
AC	AA150961	(first entry)
DT	23-MAR-2000	
XX	Human FVIII antibody A3-C1 scFv heavy chain protein B18.	
XX	Human: heavy chain; antibody; factor VIII; hemostatic;	
KW	hemophilia A; scFv; A3-C1.	
OS	Homo sapiens.	
XX	MO9958680-A2.	
PN	18-NOV-1999.	
XX	07-MAY-1999;	99MO-NL00285.
XX	08-MAY-1998;	98EP-0201543.
PR	(SAND-) STITCHING SANDUIN BLOEDVOORZIEENING.	
PA	Voorberg JJ, Van Den Brink EN, Turenhout EM;	
PI	WPI; 2000-053102/04.	
XX	New polynucleotide, polypeptide and antibody useful for diagnosing the	
PT	presence of neutralizing antibodies against factor VIII and for	
PT	treatment of hemophilia A patients with these antibodies -	


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Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh3 protein (Fragment).
GN Vh3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vesicic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:11948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match
Best Local Similarity 64.2%; Score 427; DB 4; Length 147;
Matches 84; Conservative 16; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDIAIHWVRQAPGQLEWVGSGVTSGTTIGF 60
DB 1 QVHLVSGGGVQVQPGKSLRLSCAASGFTFGDIAIHWVRQAPGQLEWVGSGVTSGTTIGF 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALTYCALP--YINSSN--RGVAAPDIMGQ 118
DB 61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYCAKQGNYPDSV--YAGIDYWGQ 118
QY 119 GTMTVTSS 126
DB 119 GTLVTVSS 126

RESULT 12
Q9UTL84
ID Q9UTL84 PRELIMINARY; PRT; 122 AA.
AC Q9UTL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE "Myosin-reactive immunoglobulin heavy chain variable regi
DE (Fragment)".
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Hom
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis an normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.

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DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 122 AA; 13579 MW; 36054DA1366545B8 CRC64;

Query Match
Best Local Similarity 63.2%; Score 420; DB 4; Length 122;
Matches 82; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDIAIHWVRQAPGQLEWVGSGVTSGTTIGF 60
DB 1 EVQLVSGGGVQVQPGKSLRLSCAASGFTFGDIAIHWVRQAPGQLEWVAISDGSNKFY 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALTYCALTYINSSNVRGVAAPDIMGQGT 120
DB 61 ADSVKGRTISRDNSKNTLYLQMTSLRVEDTAVYCA---KDERGLVGTTFDYGQGT 116
QY 121 MYTVSS 126
DB 117 LVTVSS 122

RESULT 13
Q8NCL6
ID Q8NCL6 PRELIMINARY; PRT; 493 AA.
AC Q8NCL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Mammary gland;
RA Iwagui T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuhara Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RT "NEO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/Genbank/DBD databases.
DR EMBL; AK074651; BAC11114.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGCL; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00280; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 53224 MW; 12BCD7E094777101 CRC64;

Query Match
Best Local Similarity 63.1%; Score 419.5; DB 4; Length 493;
Matches 83; Conservative 13; Mismatches 25; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDIAIHWVRQAPGQLEWVGSGVTSGTTIGF 60
DB 20 QVQLVSGGGVQVQPGKSLRLSCAASGFTFGDIAIHWVRQAPGQLEWVAISDGSNKFY 79
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALTYCALTYINSSNVRGVAAPDIMGQGT 120
DB 80 SDVKGRLTVSRDNYKNTLYLEMKSLGABDTAVYCA----RDGY-AGYGVFDHMGQGT 134

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 116 AA; 12434 MW; 0DA0348154D6061 CRC64;
SQ
Query Match
Best Local Similarity 66.7%; Score 443.5; DB 4; Length 116;
Matches 85; Conservative 15; Mismatches 16; Indels 9; Gaps 1;
QY 2 VOLVSGGGVLPQKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 61
DB 1 VOLVESGGGVVQPGKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 60
QY 62 DSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCALYINSSNRRGVAAFDIWGGGT 121
DB 61 DSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCALYINSSNRRGVAAFDIWGGGT 111
QY 122 VTVSS 126
DB 112 VTVSS 116
RESULT 9
Q9N5K4 PRELIMINARY; PRT; 499 AA.
AC Q9N5K4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DDBJ databases.
DR EMBL; BC032249; AAH32249.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IG1; 2.
DR SMART; SM00406; IG; 1.

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DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
RW Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;
Query Match
Best Local Similarity 66.1%; Score 439.5; DB 4; Length 499;
Matches 86; Conservative 14; Mismatches 23; Indels 7; Gaps 2;
QY 1 QVLVSGGGVLPQKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 60
DB 20 EVLVESGGGVVQPGKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 79
QY 61 ADSVKGRTISRDNKNSLYLNNSLRAPDYLALYGCALPYINSSNRRGVAAFDIWGGGT 116
DB 80 ADSVKGRTISRDNKNSLYLNNSLRAPDYLALYGCALPYINSSNRRGVAAFDIWGGGT 136
QY 117 GQGTMTVSS 126
DB 137 GQGTMTVSS 146
RESULT 10
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
SQ
Query Match
Best Local Similarity 67.5%; Score 437.5; DB 4; Length 113;
Matches 85; Conservative 14; Mismatches 14; Indels 13; Gaps 2;
QY 1 QVLVSGGGVLPQKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 60
DB 1 EVLVESGGGVVQPGKSLRLSCAASGFTFGDYAIHWYRQAPGEGLEWVAFIRYGSNRY 60
QY 61 ADSVKGRTISRDNKNSLYLNNSLRAPDYLALYGCALPYINSSNRRGVAAFDIWGGGT 120
DB 61 ADSVKGRTISRDNKNSLYLNNSLRAPDYLALYGCALPYINSSNRRGVAAFDIWGGGT 107
QY 121 MVTSS 126
DB 108 LTVSS 113
RESULT 11

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QY 121 MVTSS 126
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 Db 116 MVTSS 121

RESULT 5

09HCC1

ID 09HCC1 PRELIMINARY; PRT; 112 AA.

AC 09HCC1;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Single chain Fv (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kikuchi M., Takeda C., Teujimoto Y., Asada S., Nagata K.,

RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB049915; BAB16829.1; -

DR HSSP; P01772; 2PB4.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 112

FT SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 68.6%; Score 456; DB 4; Length 112;

Best Local Similarity 70.5%; Pred. No. 6.6e-39;

Matches 86; Conservative 13; Mismatches 13; Indels 10; Gaps 1;

QY 1 QVQLVSGGGLVQPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTSGTTIGF 60

Db 1 EVQLVESGGGVVRRPGSLRLSCAASGFTFPDYGMWVROAPGKGLWVSGVINGSTY 60

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWGQ 120

Db 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCA-----RRRYALDYWGQGT 110

QY 121 MV 122

Db 111 LV 112

RESULT 6

08TC77 PRELIMINARY; PRT; 471 AA.

AC 08TC77;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE=Spleen;

RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC024289; AAH24289.1; -

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; IGV; 4.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 2.

KW Hypothetical protein.

SEQUENCE 471 AA; 51791 MW; 388F7FACF588660E CRC64;

Query Match 67.7%; Score 450; DB 4; Length 471;

Best Local Similarity 70.3%; Pred. No. 1.6e-37;

Matches 90; Conservative 16; Mismatches 14; Indels 8; Gaps 2;

QY 1 QVQLVSGGGLVQPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTSGTTIGF 60

Db 20 EVQLVESGGGLVQPGKSLRLSCAASGFTSYISMMWVROAPGKGLWVSGVSSSYIYY 79

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCA--LPYINSSNYRGVAAPDIWGQ 118

Db 80 ADSVKGRTISRDNAKNSLYLNMSLRADDTAVYCAKRLRLQTSYMY-----FDLMGR 133

QY 119 GTMVTSS 126

Db 134 GTLVTVSS 141

RESULT 7

096BB9 PRELIMINARY; PRT; 597 AA.

AC 096BB9;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE=B-cell;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC015760; AAH15760.1; -

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 5.

DR PROSITE; PS00290; IG_MHC; 3.

KW Hypothetical protein.

SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 67.1%; Score 446.5; DB 4; Length 597;

Best Local Similarity 68.2%; Pred. No. 4.9e-37;

Matches 88; Conservative 17; Mismatches 17; Indels 7; Gaps 2;

QY 1 QVQLVSGGGLVQPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTSGTTIGF 60

Db 20 EVQLVESGGGLVQPGKSLRLSCAASGFTSYISMMWVROAPGKGLWVSGVSSSYIYY 79

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALP--YINSSNYRGVAAPDIWG 117

Db 80 ADSVKGRTISRDNSRDLYLNMSLRADDTAVYCAKDPGVSASGNTRE---DYWG 135

QY 118 OGTMVTSS 126

Db 136 OGTLTVSS 144

RESULT 8

09UL93 PRELIMINARY; PRT; 116 AA.

ID 09UL93

```

APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESSES:
ADDRESSER: Sughtue, Mion, Zlun, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 510
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-35

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Query Match 78.9%; Score 490.5; DB 1; Length 120;
Best Local Similarity 79.5%; Pred. No. 1,1e-41;
Matches 97; Conservative 7; Mismatches 13; Indels 5; Gaps 2;

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QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMHWROAPGAGLEWVAIVSYDGNKYY 60
DB 1 QVQLVSGGSGVQPGKSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKRFAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIAEL---WGQTLVLT 117
DB 61 ADSVKRFTISRDNSKNTLYLQNSLTAEADTAVYYCARD--RKDWGVALFDYWGQTLVLT 118
QY 118 VS 119
DB 119 VS 120

```

```

RESULT 3
US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 415
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin"
OTHER INFORMATION: 56PI "CL Variable Heavy chain (V-H)"
US-08-331-398A-46

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Query Match 78.2%; Score 486.5; DB 1; Length 119;
Best Local Similarity 78.3%; Pred. No. 2.7e-41;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

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QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMHWROAPGAGLEWVAIVSYDGNKYY 60
DB 1 QVQLVSGGSGVQPGKSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVSYDGSNKYY 60
QY 61 ADSVKRFAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIAELWGQTLVLT 120
DB 61 ADSVKRFTISRDNSKNTLYLQNSLTAEADTAVYYCARSAARTYFD-YWGQTLVLT 119

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RESULT 4
US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331.397B
FILING DATE: 28-OCT-1994

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 12.1852 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 1 EVOLVESGGGLVPGKSLRL.....IESNIAELWGQGLTVTVSS 120

Sequence: 1 EVOLVESGGGLVPGKSLRL.....IESNIAELWGQGLTVTVSS 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patente AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	79.6	248	4	US-09-315-926A-80
2	490.5	78.9	120	1	US-07-942-245-35
3	486.5	78.2	119	1	US-08-331-398A-46
4	486.5	78.2	119	2	US-08-331-397B-46
5	486.5	78.2	119	2	US-08-759-804A-46
6	486.5	78.2	119	3	US-09-227-693-46
7	485.5	78.1	123	4	US-09-560-198A-2
8	484.5	77.9	117	4	US-09-025-769B-24
9	478.5	76.9	123	4	US-09-560-198A-4
10	477.5	76.8	123	4	US-09-560-198A-10
11	477.5	76.8	125	3	US-09-240-274-8
12	477.5	76.8	125	3	US-09-240-274-20
13	477.5	76.8	125	3	US-09-240-274-21
14	477.5	76.8	125	3	US-09-240-274-22
15	473.5	76.1	125	3	US-09-240-274-24
16	472.5	76.0	125	3	US-09-240-274-9
17	469.5	75.5	125	3	US-09-240-274-23
18	469	75.4	310	4	US-09-079-039-11
19	468	75.2	124	3	US-09-240-274-4
20	468	75.2	141	1	US-08-259-372A-2
21	468	75.2	141	1	US-08-468-671-2
22	467.5	75.2	125	3	US-09-240-274-140
23	467	75.1	124	3	US-09-240-274-6
24	467	75.1	126	3	US-09-240-274-26
25	466	74.9	126	3	US-09-240-274-149
26	466	74.9	126	3	US-09-240-274-149
27	464.5	74.7	125	3	US-09-240-274-151

28	464	74.6	124	3	US-09-240-274-7	Sequence 7, Appli
29	462	74.3	120	2	US-07-934-373C-4	Sequence 4, Appli
30	462	74.3	120	3	US-08-437-642B-4	Sequence 4, Appli
31	462	74.3	120	4	US-08-146-206C-4	Sequence 4, Appli
32	462	74.3	122	2	US-07-934-373C-21	Sequence 21, Appli
33	462	74.3	122	3	US-08-437-642B-21	Sequence 21, Appli
34	462	74.3	122	4	US-08-146-206C-21	Sequence 21, Appli
35	462	74.3	124	5	PCT-US93-07832-21	Sequence 21, Appli
36	462	74.3	124	3	US-09-240-274-2	Sequence 2, Appli
37	461.5	74.2	121	3	US-09-202-181-4	Sequence 4, Appli
38	461	74.1	123	3	US-08-983-607-38	Sequence 38, Appli
39	461	74.1	126	3	US-09-240-274-153	Sequence 153, App
40	459.5	73.9	113	3	US-08-974-899-6	Sequence 6, Appli
41	459.5	73.9	127	3	US-09-240-274-18	Sequence 18, Appli
42	459.5	73.9	127	3	US-09-240-274-19	Sequence 19, Appli
43	459	73.8	126	3	US-09-240-274-25	Sequence 25, Appli
44	458.5	73.7	125	2	US-08-428-197-5	Sequence 5, Appli
45	458.5	73.7	125	2	US-08-428-197-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315, 926A
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

Query Match      79.6% Score 495; DB 4; Length 248;
Best Local Similarity 78.3% Pred. No. 9.1e+42;
Matches 94; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGKSLRLSCVDSGLTFSSYGHWYRQPGAGLEWVAIVSYGNDKYY 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 23 QVQLVQSGGGLVPGKSLRLSCAASGFTSSYAMHWYRQPGKLEWVAIVSYGSKITY 82
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 ADVYKGRPAISRDAKNTLYLQNNSLTIEDTAVYYCAKDLIESNIAELWGQGLTVTVSS 120
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 83 ADVYKGRFTISRDSKNTLYLQNNSLAEDTAVYYCARGITVTKSRPRDYWGQGLTVTVSS 142
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 2
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
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RESULT 14
099LC4      PRELIMINARY;      PRT;      463 AA.
AC 099LC4:
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS IGH-4.
SN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AA03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW;  EAA674C6BBC30783 CRC64;

Query Match
Best Local Similarity 59.0%; Score 376; DB 11; Length 463;
Matches 72; Conservative 24; Mismatches 16; Indels 10; Gaps 3;

QY 1 QVQVQSGAEVKKPGSSVKVSCKASGCTFSSHAISWTRQAPGQGLEWMGDIPIILGTGN- 59
DB 20 QVQLQSGAEVKKPGASVVSCKASGCTFTGVSWMVKQRTGQGLEWVGEIYP--GSGNT 77
QY 60 -YAKFGQGVTTITADESTSTAYMELSTLSEPTAVYYC-----ELDFYIWGQGTMTV 112
DB 78 YSEKFGKATLTIDKSSSTAYMHLSTLSEDSAVYFCARSSYSYIDLFAVWGQGLTVV 137
QY 113 SS 114
DB 138 SA 139

RESULT 15
08WY24      PRELIMINARY;      PRT;      497 AA.
AC 08WY24:
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DS SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SMC66, a Ig-like gene which is
RT down-regulated in colorectal cancer.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR283666; AAL36987.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.

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SQ SEQUENCE 497 AA; 53665 MW;  F24D08DFA5A63E5 CRC64;

Query Match
Best Local Similarity 62.6%; Score 373.5; DB 4; Length 497;
Matches 74; Conservative 17; Mismatches 23; Indels 11; Gaps 1;

QY 1 QVQVQSGAEVKKPGSSVKVSCKASGCTFSSHAISWTRQAPGQGLEWMGDIPIILGTGN 60
DB 20 QVQLQSGAEVTKPGASVKVSCKASGCTFTGVDINWTRQAPGQGLEWMGMNPTGTNER 79
QY 61 AOKFGQGVTTITADESTSTAYMELSTLSEPTAVYYC-----LDFYIWGQGTMT 109
DB 80 AOKFGRLTFSRDTSINTAYVLSLSTEDSAITFCARGNLRGGRFGYIMFDPWGHTL 139
QY 110 VTSS 114
DB 140 VTSS 144

Search completed: December 30, 2003, 11:01:09
Job time : 27.7823 secs

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QY 1 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 60
 DB 20 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 79
 QY 61 AAKFGQGVITITADESTSTAYMELSTLTSBDTAVYYC-----DWFIYWGQGMVTYSS 114
 DB 80 AAEFGQGVITITADESTSTAYMELSTLTSBDTAVYYCAVPPDAFDMGQGMVTYSS 136

RESULT 11
 ID Q92400 PRELIMINARY; PRT; 143 AA.
 AC Q92400;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-MAR-2003 (TrEMBLrel. 19, Last sequence update)
 DE V165-D-J-C mu protein (Fragment).
 GN V165-D-J-C MU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB069915; BAB63931.1; -
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 143
 SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match 64.5%; Score 385; DB 11; Length 143;
 Best Local Similarity 62.7%; Pred. No. 1.6e-32;
 Matches 74; Conservative 20; Mismatches 20; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 60
 DB 1 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 60
 QY 61 AAKFGQGVITITADESTSTAYMELSTLTSBDTAVYYC-----WFIYWGQGMVTYSS 114
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSTSEDSAVYYCAPDSNHLDFYWGQGMVTYSS 118

RESULT 12
 ID Q8VDC9 PRELIMINARY; PRT; 168 AA.
 AC Q8VDC9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Anti-MOG 212 variable gamma 2a (Fragment).
 GN Anti-MOG 212 variable gamma 2a (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cherkasovskiy Y.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Sembli P.;
 RT "Targeting T cells to the CNS."
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ416332; CAC94867.1; -
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR NON_TER 168
 SQ SEQUENCE 168 AA; 18293 MW; 1E3719FC0E72723 CRC64;

Query Match 63.7%; Score 380.5; DB 11; Length 168;
 Best Local Similarity 60.5%; Pred. No. 5.8e-32;
 Matches 72; Conservative 21; Mismatches 21; Indels 5; Gaps 2;

QY 1 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 60
 DB 20 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 79
 QY 61 AAKFGQGVITITADESTSTAYMELSTLTSBDTAVYYC-----ELDMFY-IMGQGMVTYSS 114
 DB 80 NEKFKSKATLTVDKPSSTAYMQLSTSEDSAVYYCAPDSNHLDFYWGQGMVTYSS 138

RESULT 13
 ID Q9BRV0 PRELIMINARY; PRT; 500 AA.
 AC Q9BRV0;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005951; AAH05951.1; -
 DR HSSP: P01789; IMCP.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 4.
 DR PROSITE: PS00280; IG_MHC; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 63.3%; Score 378; DB 4; Length 500;
 Best Local Similarity 59.4%; Pred. No. 4.2e-31;
 Matches 76; Conservative 15; Mismatches 23; Indels 14; Gaps 2;

QY 1 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 60
 DB 20 QVQLVQSGAEVKKPKGSSVSKVSCAKSGTFSHAISWVROAPGGGLEWMDIIPILGTGNY 79
 QY 61 AAKFGQGVITITADESTSTAYMELSTLTSBDTAVYYC-----CELDMFY-----IMGQ 106
 DB 80 AAKFGQGVITITADESTSTAYMELSTLTSBDTAVYYCARRYSYSCQNDYIYMDVWGK 139

QY 107 GFMVTYSS 114
 DB 140 GTTIVYSS 147


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Db      1 VOSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPGQGLEMMGRIIPILCIANYAKF 60
Qy      65 OGRVITITADESTAYMELSTLTSEDTAVYYCELD-----WFIYMGQTMVTVS 114
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL      fetus.";
DR      Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
HSSP; P01772; 2PB4.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; IG_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER 1
FT      NON_TER 124
SQ      SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACDZA2 CRC64;

Query Match      70.7%; Score 422; DB 4; Length 124;
Best Local Similarity 68.5%; Pred. No. 1.8e-36;
Matches 85; Conservative 12; Mismatches 17; Indels 10; Gaps 1;

Qy      1 OVQLVOSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPGQGLEMMGDIIPILGTGNY 60
Db      1 EVQLVDSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPGQGLEMMGIIINPSGGSISY 60
Qy      61 AOKFGQRTVITADESTAYMELSTLTSEDTAVYYCELDWFIY-----WGQGTNV 110
Db      61 AOKFGQRTVITADESTAYMELSTLTSEDTAVYYCARGLYVVPAFSPFDYWGQGTIV 120
Qy      111 TVSS 114
Db      121 TVSS 124

RESULT 3
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
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RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL      fetus.";
DR      Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; P01910; 2PB4.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; IG_1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER 1
FT      NON_TER 119
SQ      SEQUENCE 119 AA; 13205 MW; 13B64F5345FAA16E CRC64;

Query Match      69.8%; Score 416.5; DB 4; Length 119;
Best Local Similarity 70.6%; Pred. No. 6.5e-36;
Matches 84; Conservative 10; Mismatches 20; Indels 5; Gaps 1;

Qy      1 OVQLVOSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPGQGLEMMGDIIPILGTGNY 60
Db      1 EVQLVDSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPGQGLEMMGIIINPSWTNY 60
Qy      61 AOKFGQRTVITADESTAYMELSTLTSEDTAVYYCELD-----WFIYMGQTMVTVS 114
Db      61 AOKFGQRTVITADESTAYMELSTLTSEDTAVYYCARGLYVVPAFSPFDYWGQGTIV 119

RESULT 4
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AB-cell;
RA Struhsberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR      InterPro; IPR000005; HTHARAC.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; IG_5.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR      PROSITE; PS50835; IG_LIKE; 5.
DR      PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ      SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match      69.3%; Score 413.5; DB 4; Length 614;
Best Local Similarity 71.1%; Pred. No. 1e-34;
Matches 86; Conservative 6; Mismatches 22; Indels 7; Gaps 1;

Qy      1 OVQLVOSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPGQGLEMMGDIIPILGTGNY 60
Db      20 OMQLVOSGAEVKKPSSVYKSCASGCTFSSVAISMVROAPQALBMMGWIIPENGNTY 79
Qy      61 AOKFGQRTVITADESTAYMELSTLTSEDTAVYYCELD-----WFIYMGQTMVTVS 113
Db      80 AOKFGQRTVITADESTAYMELSTLTSEDTAVYYCARGLYVVPAFSPFDYWGQGTIV 139
Qy      114 S 114
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RX MEDLINE=81234548; PubMed=6788376;
RA Bozhwell A.L.M., Paekind M., Reih M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
-1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
(MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: J00529; AAA8170.1; -.
DR PIR: A08089; MEMS18.
DR PDB: 1A6U; 27-MAY-98.
DR PDB: 1A6W; 15-JUL-98.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 1 139
FT DOMAIN 20 49 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 50 54 FRAMEWORK-1.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 69 85 FRAMEWORK-2.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 124 FRAMEWORK-3.
FT DOMAIN 125 139 D SEGMENT.
FT DISULFID 41 115 JH2 SEGMENT.
FT NON_TER 139 139 BY SIMILARITY.
SQ SEQUENCE 139 AA; 15419 MW; 1B57DDAFDCC9F465 CRC64;

Query Match 59.0%; Score 352; DB 1; Length 139;
Best Local Similarity 57.5%; Pred. No. 4.9e-29;
Matches 69; Conservative 20; Mismatches 25; Indels 6; Gaps 1;

QY 1 OVQLVQSGAEVKKPGSSVKCSKASGTFSSHAISWVROAPQGLEWMGDIIPILGTYN 60
DB 20 QVQLQPGAEVKKPGASVKSASGTFSTYMMHWVKORPGLEWIGRIDPNSGTRY 79
QY 61 AOKFOGRVTITADSTAYMELSTLSEDTAVYCE-----LDMFYIWGGTMTYVSS 114
DB 80 NEKFSKATLTIVDKSSATYMWELSTLSEDSAVYVCARYDYGSYFDYWGQGITLTVSS 139

RESULT 13
HY51 MOUSE
ID HY51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
OX NCBI_SEQUENCE.
RN 1;
RP MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovera J., Silevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";

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RL EMB0 J. 3:517-523(1984).
DR PIR: A02040; MEMS38.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEEAC762A018 CRC64;

Query Match 58.8%; Score 351; DB 1; Length 118;
Best Local Similarity 57.6%; Pred. No. 5.2e-29;
Matches 68; Conservative 21; Mismatches 25; Indels 4; Gaps 1;

QY 1 OVQLVQSGAEVKKPGSSVKCSKASGTFSSHAISWVROAPQGLEWMGDIIPILGTYN 60
DB 1 EVQLQSGPELVKPGASVKISCKASGYFTDYMMHWVKORPGLEWIGRIDPNSGTRY 60
QY 61 AOKFOGRVTITADSTAYMELSTLSEDTAVYCE-----LDMFYIWGGTMTYVSS 114
DB 61 NOKFKGKATLTIVDKSSATYMWELSTLSEDSAVYVCARYDYGSYFDYWGQGITLTVSS 118

RESULT 14
HY51 HUMAN
ID HY51_HUMAN STANDARD; PRT; 124 AA.
AC P01761;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
OX NCBI_SEQUENCE.
RN 1;
RP MEDLINE=82046599; PubMed=7028111;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of heavy chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5822-5830(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02044; MHUS1.
DR HSSP: P01825; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Pyrolysine carboxylic acid.
FT DOMAIN 1 112 IG-LIKE
FT MOD_RES 1 1 PYROLYSINE CARBOXYLIC ACID.
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13732 MW; 62CED4573BDE59F CRC64;

Query Match 58.0%; Score 346; DB 1; Length 124;
Best Local Similarity 56.2%; Pred. No. 1.8e-28;
Matches 72; Conservative 12; Mismatches 24; Indels 20; Gaps 3;

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DR EMBL: J00493; AAA38128.1; -
DR PIR: A94264; HVM5G7.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT CHAIN 1 19
FT DOMAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON TER 20 139 IG-LIKE.
FT SEQUENCE 140 AA; 15514 MW; 25A4CB831DA5CE8 CRC64;

Query Match 60.7%; Score 362.5; DB 1; Length 140;
Best Local Similarity 58.7%; Pred. No. 4.2e-30;
Matches 71; Conservative 21; Mismatches 22; Indels 7; Gaps 1;

QY 1 QVQVSGAEVKKRQSSVKKVSCKASGTFSSHAISWVRQAPGGGLEWMDIIPILGTGNY 60
DB 20 EVQLQSGAEGLVRAAGSSVKKVSCKASGTFSSHAISWVRQAPGGGLEWMDIIPILGTGNY 79
QY 61 AQKQGRVITTDSESTAYMELSTLTSEDTAVYYCELDWY-----IMGGTMTVSS 113
DB 80 NEKFKGKTLTVDKSSATYMQLRSLTSEDSAVYFCARSHYGGSYDPDWGCGTTLTVSS 139
QY 114 S 114
DB 140 S 140

RESULT 10
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8313846; Pubmed=6186498;
RA Stekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiootype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT. JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF0454A167B654AF CRC64;

Query Match 59.7%; Score 356.5; DB 1; Length 120;
Best Local Similarity 58.3%; Pred. No. 1.4e-29;
Matches 70; Conservative 20; Mismatches 23; Indels 7; Gaps 1;

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QY 2 VOLVSGAEVKKRQSSVKKVSCKASGTFSSHAISWVRQAPGGGLEWMDIIPILGTGNYA 61
DB 1 VOLQSGAEGLVRAAGSSVKKVSCKASGTFSSHAISWVRQAPGGGLEWMDIIPILGTGNYK 60
QY 62 QKQGRVITTDSESTAYMELSTLTSEDTAVYYCELDWY-----IMGGTMTVSS 114
DB 61 EKFKGKTLTVDKSSATYMQLRSLTSEDSAVYFCARSHYGGSYDPDWGCGTTLTVSS 120

RESULT 11
HV50_MOUSE STANDARD; PRT; 120 AA.
ID HV50_MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; Pubmed=6201362;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMO J. 3:517-523(1984).
DR PIR: A02037; MEMS15.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 120 120
FT SEQUENCE 120 AA; 13311 MW; 914453F426F09634 CRC64;

Query Match 59.1%; Score 353; DB 1; Length 120;
Best Local Similarity 58.3%; Pred. No. 3.3e-29;
Matches 70; Conservative 19; Mismatches 25; Indels 6; Gaps 2;

QY 1 QVQVSGAEVKKRQSSVKKVSCKASGTFSSHAISWVRQAPGGGLEWMDIIPILGTGNY 60
DB 1 QVQLPGELVRAAGSSVKKVSCKASGTFSSHAISWVRQAPGGGLEWMDIIPILGTGNY 60
QY 61 AQKQGRVITTDSESTAYMELSTLTSEDTAVYYC-----ELD-WFYWGQTMVSS 114
DB 61 NEKFKGKTLTVDKSSATYMQLRSLTSEDSAVYFCARSHYGGSYDPDWGCGTTLTVSS 120

RESULT 12
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;

```

Best Local Similarity 67.5%; Pred. No. 7.2e-31;
Matches 77; Conservative 13; Mismatches 20; Indels 4; Gaps 1;

QY 1 OVOLVSGAEVKKRGSSVVKSCKASGGTFSSHAISWROAPGQGLMMGDIIPILGTGNY 60
DB 1 EVOLQSGAEVLVKRGSSVVKSCKASGGTFSSHAISWROAPGQGLMMGDIIPILGTGNY 60

QY 61 AOKFGRTITADSTAYMELSTLTSEDAVYVCYEL---DWFYVGQGTWY 110
DB 61 AOKFGRTITADSTAYMELSTLTSEDAVYFCVAVRVSRYFDGNGGCTIV 114

RESULT 7
HVI2 MOUSE STANDARD; PRT; 117 AA.

AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 95 N-LINKED (GLCNAC. . .) (COMPLEX).
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACB4BE447E41 CRC64;

Query Match 61.6%; Score 367.5; DB 1; Length 117;
Best Local Similarity 59.0%; Pred. No. 1.1e-30;
Matches 69; Conservative 25; Mismatches 20; Indels 3; Gaps 2;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RX MEDLINE=60078170; PubMed=6765993;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 60.9%; Score 363.5; DB 1; Length 117;
Best Local Similarity 59.0%; Pred. No. 2.7e-30;
Matches 69; Conservative 24; Mismatches 21; Indels 3; Gaps 2;

QY 1 OVOLVSGAEVKKRGSSVVKSCKASGGTFSSHAISWROAPGQGLMMGDIIPILGTGNY 60
DB 1 EVOLQSGAEVLVKRGSSVVKSCKASGGTFSSHAISWROAPGQGLMMGDIIPILGTGNY 60

QY 61 AOKFGRTITADSTAYMELSTLTSEDAVYVCYEL---WFFYVGQGTWY 114
DB 61 AOKFGRTITADSTAYMELSTLTSEDAVYFCVAVRVSRYFDGNGGCTIV 117

RESULT 9
HVI2 MOUSE STANDARD; PRT; 140 AA.

AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RX MEDLINE=82152818; PubMed=6801765;
RA Sline J., Rabbitts T.H., Esteve P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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EMBL, X07448, -; NOT_ANNOTATED_CDS.

DR PIR, S00476; HYH035.

DR HSSP, P01772; 2FB4.

DR GO, GO:0005576; C:extracellular; NAS.

DR GO, GO:0003823; P:antigen binding activity; NAS.

DR GO, GO:0006955; P:immune response; NAS.

DR InterPro, IPR007110; IG-like.

DR InterPro, IPR003006; IG_MHC.

DR Pfam, PF00047; Ig_V.

DR SMART, SM00406; IGV, 1.

DR PROSITE, PS50835; IG LIKE; 1.

DR Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.

FT DOMAIN 20 >117 IG-LIKE.

FT NON TER 117 117

SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 62.1%; Score 371; DB 1; Length 117;
Best Local Similarity 77.1%; Pred. No. 4, 7e-31;
Matches 74; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

1 QVQLVQSGAEVKKPGSSVKASGCTFSSHAISMVRQAPGQGLFWMGDIPIILGTNY 60
20 QVQLVQSGAEVKKPGASVSVSCASGCTFTGYMHVRQAPGQGLFWMGRINPNSGTTY 79

61 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC 96
80 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC 115

Db 80 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC 115

RESULT 5
HYVC HUMAN STANDARD; PRT; 147 AA.

AC P01741; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR Ig heavy chain V-I region NP precursor (Fragments).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Nølgard H.V., Houghton M., Derbyshire R.B., Viney J.,

Bell L.O., Gould H.J.;

"Cloning and sequence determination of the gene for the human

immunoglobulin epsilon chain expressed in a myeloma cell line.";

Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).

[2]

SEQUENCE OF 20-147.

RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

(in) Bach M.K. (eds.);

Immediate hypersensitivity: modern concepts and developments, pp.1-36,

Marcel Dekker, New York (1978).

-1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

PROTEIN.

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.

HSSP, P01789; IMCP.

DR GO, GO:0005576; C:extracellular; NAS.

DR GO, GO:0003823; P:antigen binding activity; NAS.

DR GO, GO:0006955; P:immune response; NAS.

DR InterPro, IPR007110; IG-like.

DR InterPro, IPR003006; IG_MHC.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR InterPro, IPR003596; Ig_V.

DR Pfam, PF00047; IGV, 1.
DR SMART, SM00406; IGV, 1.
DR PROSITE, PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL 1 19

FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.

FT DOMAIN 20 131 IG-LIKE.

FT MOD RES 20 20 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 41 115

FT CONFLICT 21 21 T -> V (IN REF. 2).

FT CONFLICT 53 54 IH -> HI (IN REF. 2).

FT CONFLICT 67 68 VG -> GV (IN REF. 2).

FT CONFLICT 125 125 MISSING (IN REF. 2).

FT NON TER 147 147

SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 62.1%; Score 371; DB 1; Length 147;
Best Local Similarity 59.4%; Pred. No. 6e-31; 24; Indels 14; Gaps 2;
Matches 76; Conservative 14; Mismatches 24;

1 QVQLVQSGAEVKKPGSSVKASGCTFSSHAISMVRQAPGQGLFWMGDIPIILGTNY 60
20 QVQLVQSGAEVKKPGASVSVSCASGCTFTGYMHVRQAPGQGLFWMGRINPNSGTTY 79

61 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC-----ELDMFY---IMQ 106
80 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC-----ELDMFY---IMQ 139

Db 107 GTMTVSS 114
140 GTTVSS 147

RESULT 6
HV00 MOUSE STANDARD; PRT; 114 AA.

AC P01741; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR Ig heavy chain V region (Anti-arsenate antibody).

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE.

STRAIN=A/J;

MEDLINE=79195438; PubMed=109536;

RA Capra J.D., Nisoneff A.;

"Structural studies on induced antibodies with defined idiotypic

specificities. VII. The complete amino acid sequence of the heavy

chain variable region of anti-p-azophenylarsenate antibodies from A/J

mice bearing a cross-reactive idiotype.";

J. Immunol. 123:279-284 (1979).

-1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF

THE IGH1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V

REGION SEQUENCE.

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A02022; GIMSA.

DR HSSP, P01772; 2FB4.

DR InterPro, IPR007110; IG-like.

DR InterPro, IPR003006; IG_MHC.

DR InterPro, IPR003596; Ig_V.

DR Pfam, PF00047; IGV, 1.

DR SMART, SM00406; IGV, 1.

DR PROSITE, PS50835; IG LIKE; 1.

DR Immunoglobulin V region.

FT DOMAIN 1 106 IG-LIKE.

FT NON TER 114 114

SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

Query Match 61.8%; Score 369; DB 1; Length 114;

OY 61 AOKFGQRYTTADSESTAYMELSTLTSEDTAVVYCELDMPFYNG-----OGTMTVSS 114
 DB 61 AOKFGQRYTTADSESTAYMELSLRSDTAIFYC-AGCYGIVSPEPEXNGSLVTVSS 117

RESULT 2

HV1B_HUMAN STANDARD; PRT; 117 AA.
 ID HV1B_HUMAN
 AC P01743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region H03 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83144028; PubMed=6298778;
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
 RT "Evolutionary aspects of immunoglobulin heavy chain variable region
 (VH) gene subgroups.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 CC EMBL; J00240; AAMS2988.1; -.
 DR PIR; A02024; HVH0HG.
 DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 KM SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H03.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1EF7 CRC64;
 Query Match 64.5%; Score 385; DB 1; Length 117;
 Best Local Similarity 79.2%; Pred. No. 1,7e-32;
 Matches 76; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 OY 1 OVQLVSGAEVKKPGSSVYKSCASGCTSSHAISWVRQAPQGLGEMMGDIPIILGTGNY 60
 DB 20 OVQLVSGAEVKKPGSSVYKSCASGCTSSHAISWVRQAPQGLGEMMGDIPIILGTGNY 79
 OY 61 AOKFGQRYTTADSESTAYMELSTLTSEDTAVVYCC 96
 DB 80 AOKFGQRYTTADSESTAYMELSLRSDTAIFYC 115

RESULT 3

HV4B_MOUSE STANDARD; PRT; 138 AA.
 AC P03960;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region TEPC 1017 precursor.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84248078; PubMed=6429663;
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
 RA Tucker P.W.;
 RT "Illegitimate recombination generates a class switch from C mu to C
 RT delta in an Igd-secreting plasmacytoma.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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HV1G_HUMAN STANDARD; PRT; 117 AA.
 ID HV1G_HUMAN
 AC P23083;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296408; PubMed=2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
 RA Ohno H., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 RT heavy-chain locus.";
 RL EMBO J. 7:1047-1051(1988).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

Query Match 62.6%; Score 373.5; DB 1; Length 138;
 Best Local Similarity 58.8%; Pred. No. 3.1e-31;
 Matches 70; Conservative 21; Mismatches 23; Indels 5; Gaps 1;

OY 1 OVQLVSGAEVKKPGSSVYKSCASGCTSSHAISWVRQAPQGLGEMMGDIPIILGTGNY 60
 DB 20 OVQLVSGAEVKKPGSSVYKSCASGCTSSHAISWVRQAPQGLGEMMGDIPIILGTGNY 79
 OY 61 AOKFGQRYTTADSESTAYMELSTLTSEDTAVVYCC-----LDVFIWGGTMTVSS 114
 DB 80 NEKFGKATLVTDKSSSTAYMQLSLTPEBFAVYCCASDGYDVFYWGCTLVTFSA 138

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using bw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.1121 Seconds
(without alignment)

877.119 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597
Sequence: 1 QVQLVDSGAEVKKPGSSSVK.....YCELMFRTMGCTMTYSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.5	72.1	117	1	HV1A_HUMAN
2	385	64.5	117	1	HV1B_HUMAN
3	373.5	62.6	138	1	HV48_MOUSE
4	371	62.1	117	1	HV1G_HUMAN
5	371	62.1	147	1	HV1C_HUMAN
6	369	61.8	114	1	HV00_MOUSE
7	367.5	61.6	117	1	HV12_MOUSE
8	363.5	60.9	117	1	HV13_MOUSE
9	362.5	60.7	110	1	HV02_MOUSE
10	356.5	59.7	120	1	HV03_MOUSE
11	353	59.1	120	1	HV50_MOUSE
12	352	59.0	139	1	HV07_MOUSE
13	351	58.8	118	1	HV51_MOUSE
14	346	58.0	124	1	HV1E_HUMAN
15	345.5	57.9	121	1	HV01_MOUSE
16	342	57.3	137	1	HV11_MOUSE
17	334.5	56.0	125	1	HV1F_HUMAN
18	333	55.8	124	1	HV1D_HUMAN
19	331	55.4	117	1	HV06_MOUSE
20	326	54.6	117	1	HV05_MOUSE
21	326	54.6	117	1	HV52_MOUSE
22	316.5	53.0	136	1	HV15_MOUSE
23	316.5	53.0	136	1	HV15_MOUSE
24	315	52.8	114	1	HV3B_HUMAN
25	312	52.3	117	1	HV09_MOUSE
26	312	52.3	117	1	HV49_MOUSE
27	309	51.8	117	1	HV14_MOUSE
28	304	50.9	112	1	HV10_MOUSE
29	299	50.1	127	1	HV3G_HUMAN
30	298	49.9	119	1	HV40_MOUSE
31	295.5	49.5	119	1	HV31_HUMAN
32	295	49.4	119	1	HV37_MOUSE
33	294	49.2	119	1	HV38_MOUSE

34	293.5	49.2	115	1	HV3D_HUMAN	P01765 homo sapien
35	292	48.9	114	1	HV01_CANFA	P01784 canis fam1
36	291.5	48.8	121	1	HV3J_HUMAN	P01771 homo sapien
37	291.5	48.8	142	1	HV01_RAT	P01805 rattus norv
38	289	48.4	120	1	HV1H_HUMAN	P80421 homo sapien
39	286	47.9	119	1	HV3P_HUMAN	P01777 homo sapien
40	285.5	47.8	117	1	HV42_MOUSE	P01812 mus musculu
41	284.5	47.7	117	1	HV41_MOUSE	P01811 mus musculu
42	284	47.6	122	1	HV3H_HUMAN	P01769 homo sapien
43	283.5	47.5	115	1	HV3J_MOUSE	P01801 mus musculu
44	283.5	47.5	115	1	HV3F_HUMAN	P01767 homo sapien
45	283.5	47.5	117	1	HV02_CANFA	P01785 canis fam1

ALIGNMENTS

RESULT 1

ID HV1A_HUMAN STANDARD; PRT; 117 AA.

AC P01742;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region EU.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

RA Maxdel M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino

acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";

RL Biochemistry 9:3161-3170(1970).

RN [2]

RP DISULFIDE BOND.

RX MEDLINE=71064027; PubMed=4923144;

RA "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";

RL Biochemistry 9:3188-3196(1970).

CC -I- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS

MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR, A90563; GIBRU.

DR HSSP, P01772; 2F84.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig-1ike.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_V.

DR SMART, SM00406; IGV_1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Pyroglutamate carboxylic acid.

FT DOMAIN 1 112 IG-LIKE.

FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT NON_TER 117 117

SO SEQUENCE 117 AA; 12472 MW; 99D60ADAE8D52818 CRC64;

Query Match 72.1%; Score 430.5; DB 1; Length 117;

Best Local Similarity 75.4%; Pred. No. 4e-37;

Matches 89; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

QY 1 QVQLVDSGAEVKKPGSSSVKCAKSGTFSNHSVWROAPGQLEPMGDIPIIGTGY 60
DB 1 QVQLVDSGAEVKKPGSSSVKCAKSGTFSNHSVWROAPGQLEPMGDIPIIGTGY 60

Db 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANH 60
 QY AOKFGRTVITADSTSTAYMELSTLTSEDTAVYYC-----LDMF---FY-- 102
 Db 61 AOKFGRTVITADSTSTAYMELSLRSEDTAVYCARPQADTGILEWLPSTYYTMD 120
 QY 103 IWGGCTMTVSS 114
 :|||||
 Db 121 VMGKCTMTVSS 132

RESULT 10

PH0962
 Ig heavy chain V region (G6+ T-142) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0962
 R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0962
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-120 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3

Query Match 83.9%; Score 501; DB 2; Length 120;
 Best Local Similarity 84.2%; Pred. No. 2,6e-38;
 Matches 101; Conservative 3; Mismatches 10; Indels 6; Gaps 1;

QY 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
 Db 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
 QY 61 AOKFGRTVITADSTSTAYMELSTLTSEDTAVYYC-----LDMFYIWGGCTMTVSS 114
 Db 61 AOKFGRTVITADSTSTAYMELSLRSEDTAVYCARPQADTGILEWLPSTYYTMD 120

RESULT 11

PH0954
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0954
 R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0954
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-132 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-120/Region: complementarity-determining 3

Query Match 83.9%; Score 501; DB 2; Length 132;

Best Local Similarity 77.3%; Pred. No. 2,9e-38;
 Matches 102; Conservative 5; Mismatches 7; Indels 18; Gaps 2;

QY 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
 Db 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
 QY 61 AOKFGRTVITADSTSTAYMELSTLTSEDTAVYYC-----ELDMFY----- 102
 Db 61 AOKFGRTVITADSTSTAYMELSLRSEDTAVYCARPHASIDDFWGGYPPNYYYGMD 120
 QY 103 IWGGCTMTVSS 114
 :|||||
 Db 121 VMGKCTMTVSS 132

RESULT 12

PH0958
 Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0958
 R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0958
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-122 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-110/Region: complementarity-determining 3

Query Match 83.4%; Score 498; DB 2; Length 122;
 Best Local Similarity 80.8%; Pred. No. 5e-38;
 Matches 101; Conservative 4; Mismatches 6; Indels 14; Gaps 2;

QY 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
 Db 1 QVOLVSGAEVKKPGSSVVKVSCASGCTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
 QY 61 AOKFGRTVITADSTSTAYMELSTLTSEDTAVYYC-----LDMFYIWGGCTM 109
 Db 61 AOKFGRTVITADSTSTAYMELSLRSEDTAVYCARPQADTGILEWLPSTYYTMD 117
 QY 110 VTVSS 114
 :|||||
 Db 118 VTVSS 122

RESULT 13

PH0955
 Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C/Accession: PH0955
 R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A/Title: Evidence for somatic selection of natural autoantibodies.
 A/Reference number: PH0952; MUID:92202880; PMID:1552291
 A/Accession: PH0955
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-127 <MAR>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Db 61 AOKPQGRVITITADKSTSTAYMELSLRSEDTAVYTCARGNDYIWGSTRSDAPDIWQ 120

QY 107 GTMVTYSS 114
:|||||
Db 121 GTMVTYSS 128

RESULT 6

C33548
Ig heavy chain V-1 region (783) - human

C/Species: Homo sapiens (man)

C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996

C/Accession: C33548

R/Klpps, T.J.; Tomhave, E.; Pratz, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr

A/Reference number: A33548; MUID:89345575; PMID:2503826

A/Accession: C33548

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: DNA

A/Residues: 1-133 <RIP>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 504.5; DB 2; Length 133;

Best local similarity 76.7%; Pred. No. 1.4e-38;

Matches 102; Conservative 5; Mismatches 7; Indels 19; Gaps 2;

QY 1 QVQLVDSGAEVKKPKSSVKVSCASGCTFSSHAISWRQAPQGLEWMDIPIIGTGY 60
:|||||
Db 1 QVQLVDSGAEVKKPKSSVKVSCASGCTFSSVAISWRQAPQGLEWMDIPIIGTANY 60

QY 61 AOKPQGRVITITADESTSTAYMELSLTSEDTAVYTC-----ELDMFY--- 102
:|||||
Db 61 AOKPQGRVITITADESTSTAYMELSLRSEDTAVYTCAGTGILGIPYSGWYPSNDYYVGM 120

QY 103 -IWGGTMTYSS 114
:|||||
Db 121 DVMGGCTTYTSS 133

RESULT 7
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999

C/Accession: S14683; S08047

R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A/Title: Complete nucleotide sequence of the membrane form of the human Igm heavy chain.

A/Reference number: S14683; MUID:90332450; PMID:2115996

A/Accession: S14683

A/Molecule type: mRNA

A/Residues: 1-627 <FRI>

C/Cross-references: EMBL:X17115; NID:933450; PIDN:CAA4971.1; PID:933451

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin, membrane protein

F/15/Domain: signal sequence #status predicted <SIG>

F/16-627/Product: Ig mu chain #status predicted <NAT>

F/14-117/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 504.5; DB 2; Length 627;
Best local similarity 76.7%; Pred. No. 6.6e-38;
Matches 102; Conservative 5; Mismatches 7; Indels 19; Gaps 2;

Db 80 AOKPQGRVITITADESTSTAYMELSLRSEDTAVYTCAGTGILGIPYSGWYPSNDYYVGM 139

QY 103 -IWGGTMTYSS 114
:|||||
Db 140 DVMGGCTTYTSS 152

RESULT 8

PH0953
Ig heavy chain V region (G6+ CLJ-SIC) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C/Accession: PH0953

R/Martin, T.; Duffly, S.F.; Carson, D.A.; Klpps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0953; MUID:92202880; PMID:1552291

A/Accession: PH0953

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-135 <MAR>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/36-50/Region: complementarity-determining 2

F/51-67/Region: complementarity-determining 3

F/68-98/Region: framework 3

F/99-123/Region: complementarity-determining 3

Query Match 84.3%; Score 503.5; DB 2; Length 135;

Best local similarity 77.8%; Pred. No. 1.8e-38;

Matches 105; Conservative 2; Mismatches 7; Indels 21; Gaps 2;

QY 1 QVQLVDSGAEVKKPKSSVKVSCASGCTFSSHAISWRQAPQGLEWMDIPIIGTGY 60
:|||||
Db 1 QVQLVDSGAEVKKPKSSVKVSCASGCTFSSVAISWRQAPQGLEWMDIPIIGTANY 60

QY 61 AOKPQGRVITITADESTSTAYMELSLTSEDTAVYTC-----ELDMFY--- 99
:|||||
Db 61 AOKPQGRVITITADESTSTAYMELSLRSEDTAVYTCARGYCGDCYRWEILRPFSSD 120

QY 100 WFIWGGTMTYSS 114
:|||||
Db 121 AFDWGGTMTYSS 135

RESULT 9
S46394
Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C/Accession: S46394

R/Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A/Title: In vitro assembly of repertoire of antibody chains on the surface of phage by

A/Reference number: S46394; MUID:94254092; PMID:8196048

A/Accession: S46394

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-132 <FIG>

C/Cross-references: EMBL:Z31681; NID:9509788; PIDN:CAA83486.1; PID:91335147

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 502; DB 2; Length 132;
Best local similarity 77.3%; Pred. No. 2.4e-38;
Matches 102; Conservative 7; Mismatches 5; Indels 18; Gaps 3;

QY 1 QVQLVDSGAEVKKPKSSVKVSCASGCTFSSHAISWRQAPQGLEWMDIPIIGTGY 60
:|||||
Db 1 QVQLVDSGAEVKKPKSSVKVSCASGCTFSSVAISWRQAPQGLEWMDIPIIGTANY 60

C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-107/Region: complementarity-determining 3

Query Match 86.0%; Score 513.5; DB 2; Length 119;
 Best Local Similarity 84.9%; Pred. No. 1.9e-39;
 Matches 101; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

Oy 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTGNY 60
 |||||
 Db 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTANY 60
 |||||
 Oy 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVVYCC-----IMGQITWTVSS 114
 |||||
 Db 61 AOKFGRTITADESTSTAYMELSLRSEDTAVVYCCARGPRLADVLLMFGESEFDYWG 119

RESULT 3

PH0957
 Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0957
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0957

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-125 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-113/Region: complementarity-determining 3

Query Match 85.5%; Score 510.5; DB 2; Length 125;
 Best Local Similarity 80.8%; Pred. No. 3.8e-39;
 Matches 101; Conservative 5; Mismatches 8; Indels 11; Gaps 1;

Oy 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTGNY 60
 |||||
 Db 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTANY 60
 |||||
 Oy 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVVYCC-----IMFYIGQGTIM 109
 |||||
 Db 61 AOKFGRTITADESTSTAYMELSLRSEDTAVVYCCARDGCGSGCYRWGMPDPMGQTL 120
 |||||
 Oy 110 VTWSS 114
 |||||
 Db 121 VTWSS 125

RESULT 4

A33548

Ig heavy chain V-1 region (NEI) - human

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996

C:Accession: A33548; PH0956

R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr

A:Reference number: A33548; MUID:89345575; PMID:2503826

A:Accession: A33548

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-129 <KIP>

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0956

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-129 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-117/Region: complementarity-determining 3

Query Match 85.2%; Score 508.5; DB 2; Length 129;
 Best Local Similarity 79.8%; Pred. No. 6e-39;
 Matches 103; Conservative 3; Mismatches 8; Indels 15; Gaps 1;

Oy 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTGNY 60
 |||||
 Db 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTANY 60
 |||||
 Oy 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVVYCC-----ELDWFIYWG 105
 |||||
 Db 61 AOKFGRTITADESTSTAYMELSLRSEDTAVVYCCARGPRLADVLLMFGESEFDYWG 120
 |||||
 Oy 106 QGTWTVSS 114
 |||||
 Db 121 QGTWTVSS 129

RESULT 5

PH0952
 Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0952

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0952

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-128 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-116/Region: complementarity-determining 3

Query Match 84.9%; Score 507; DB 2; Length 128;
 Best Local Similarity 80.5%; Pred. No. 8.1e-39;
 Matches 103; Conservative 3; Mismatches 8; Indels 14; Gaps 1;

Oy 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTGNY 60
 |||||
 Db 1 QVOLVQSAEYKPKGSSVVKVSCKASGGTFSSHAISWVROAPGQGLEWMDIIPILGTANY 60
 |||||
 Oy 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVVYCC-----BLDFYIWGO 106
 |||||

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 10.9277 Seconds

(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597
Sequence: 1 QVQLVQSGAEVKKPGSSVKRV.....YCELDMPFIYGGTMTVSS 114Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summariesDatabase : PIR 76:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	86.4	116	2 PH0959	Ig heavy chain V r
2	513.5	86.0	119	2 PH0961	Ig heavy chain V r
3	510.5	85.5	125	2 PH0957	Ig heavy chain V r
4	508.5	85.2	129	2 A33548	Ig heavy chain V-1
5	507	84.9	128	2 PH0952	Ig heavy chain V r
6	504.5	84.5	133	2 C33548	Ig heavy chain V-1
7	504.5	84.5	627	2 S14683	Ig mu chain precut
8	503.5	84.3	135	2 PH0953	Ig heavy chain V r
9	502	84.1	132	2 S46394	Ig heavy chain V r
10	501	83.9	120	2 PH0962	Ig heavy chain V r
11	501	83.9	132	2 PH0954	Ig heavy chain V r
12	498	83.4	122	2 PH0958	Ig heavy chain V r
13	495.5	83.0	127	2 PH0955	Ig heavy chain V r
14	493	82.6	126	2 B33548	Ig heavy chain V-1
15	493	82.6	136	2 PH0960	Ig heavy chain V r
16	472	79.1	135	2 B32774	Ig heavy chain V r
17	465	77.9	116	2 S36261	Ig heavy chain V r
18	462	77.4	98	2 S26915	Ig heavy chain V r
19	462	77.4	116	2 S31698	Ig heavy chain pre
20	462	77.4	123	2 S44108	Ig heavy chain V-D
21	458	76.7	98	2 S24680	Ig heavy chain V1
22	457.5	76.6	113	2 PH1653	Ig heavy chain V r
23	456.5	76.5	109	2 PH1671	Ig heavy chain V r
24	454	76.0	108	2 PH1664	Ig heavy chain V r
25	453	75.9	119	2 S44106	Ig heavy chain V-D
26	451	75.5	98	2 S46463	Ig heavy chain V1
27	443	74.2	97	2 PH0870	Ig heavy chain V r
28	438.5	73.5	121	2 A49590	Ig heavy chain V r
29	436	73.0	171	2 S23623	Ig heavy chain V r

30	432.5	72.4	122	2 C49590	Ig heavy chain V r
31	432	72.4	118	2 S36265	Ig heavy chain V r
32	430.5	72.1	117	1 G1H9EU	Ig heavy chain V-1
33	428.5	71.8	122	2 B49590	Ig heavy chain V r
34	424	71.0	116	2 S31667	Ig heavy chain V r
35	422	70.7	136	2 S31600	Ig heavy chain V r
36	419.5	70.3	122	2 S36271	Ig heavy chain V r
37	418.5	70.1	123	2 D33548	Ig heavy chain V-1
38	417.5	69.9	129	2 S36260	Ig heavy chain V r
39	416.5	69.8	142	2 A32483	Ig heavy chain V r
40	415	69.5	98	2 A30523	Ig heavy chain V-1
41	415	69.5	135	2 S49510	anti-Sm antibody V
42	414	69.3	124	2 S19665	Ig heavy chain V r
43	407.5	68.3	129	2 S46393	Ig heavy chain V r
44	406	68.0	119	2 P49590	Ig heavy chain V r
45	399.5	66.9	160	2 PL0105	anti-PR2 erythrocy

ALIGNMENTS

RESULT 1

Ig heavy chain V region (G6+ T-L26) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0959
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J: Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0959

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-116 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterocyclamer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-104/Region: complementarity-determining 3

Query Match 86.4%; Score 516; DB 2; Length 116;
Best Local Similarity 87.9%; Pred. No. 1,1e-39;
Matches 102; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVSCAKSGCTFSSHAISGVRQAPOGLEWNGDIIPILGTNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSCAKSGCTFSSVAISVRQAPOGLEWNGDIIPILGTNY 60
QY 61 AOKFGKRVITTDSESTAYMELSLTSTEDTAIVYCELDMPFIYGGTMTVSS 114
DB 61 AOKFGKRVITTDSESTAYMELSLTSTEDTAIVYCARGDWDFWGGTMTVSS 116

RESULT 2

PH0961 Ig heavy chain V region (G6+ T-L33) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0961

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J: Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0961

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-119 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-4

Query Match 67.4%; Score 443.5; DB 2; Length 120;
Best Local Similarity 70.4%; Pred. No. 2.9e-37;
Matches 88; Conservative 14; Mismatches 18; Indels 5; Gaps 2;

QY 1 EVOLVKSGBGLVYKPGSGRLSCAASGFTFRYDIHWVQTPKGLIEWSSISGQNYIDY 60
DB 1 EVOLVSSGGGLVQPGSGRLSCAASGFTFSDIYAMSWVROAPEGLEWAVISENSDITY 60

QY 61 ADSVKGRTISRDNANNNVYLYQNNSLRAEDMAVYFCARDGTFGSAATWRAFDIWRGTM 120
DB 61 ADSVKGRTISRDDSXTLYLYQNNSLRAEDTAVYVCARD---GGAVSY--FDVWGQGTLL 115

QY 121 VTWSS 125
DB 116 VTWSS 120

RESULT 14
US-08-437-642B-4
Sequence 4, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Prestea
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-4

Query Match 67.4%; Score 443.5; DB 3; Length 120;
Best Local Similarity 70.4%; Pred. No. 2.9e-37;
Matches 88; Conservative 14; Mismatches 18; Indels 5; Gaps 2;

QY 1 EVOLVKSGBGLVYKPGSGRLSCAASGFTFRYDIHWVQTPKGLIEWSSISGQNYIDY 60
DB 1 EVOLVSSGGGLVQPGSGRLSCAASGFTFSDIYAMSWVROAPEGLEWAVISENSDITY 60

QY 61 ADSVKGRTISRDNANNNVYLYQNNSLRAEDMAVYFCARDGTFGSAATWRAFDIWRGTM 120
DB 61 ADSVKGRTISRDDSXTLYLYQNNSLRAEDTAVYVCARD---GGAVSY--FDVWGQGTLL 115

QY 121 VTWSS 125
DB 116 VTWSS 120

RESULT 15
US-08-146-206C-4
Sequence 4, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Prestea, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:

RESULT 11
PCT-US93-10555-1
Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTE
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGE
TITLE OF INVENTION: THEROP
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
PCT-US93-10555-1

Query Match 67.6%; Score 445; DB 5; Length 125
Best Local Similarity 67.2%; Pred. No. 2.2e-37;
Matches 84; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVOLVKSGBGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVS:SGGNVYIDY 60
DB 1 EVQLLESGGGLVPGGSLRLSCAASGFTFSYAMSVRQAPKGLIEWVS:SGSGSTYY 60
QY 61 ADSVKGFTISRDNANVVYLVQNSLRADMAVYFCARDITIGSAATW:DIWGRGTM 120
DB 61 ADSVKGFTISRDNANVVYLVQNSLRADMAVYFCARDITIGSAATW:DIWGRGTM 120
QY 121 VTVSS 125
DB 121 VTVSS 125

RESULT 12
US-08-379-057-32
Sequence 32, Application US/08379057
Patent No. 5876950
GENERAL INFORMATION:
APPLICANT: Siodak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gilliland, Lisa K.

APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Aruffo, Alejandro A.
TITLE OF INVENTION: Monoclonal Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human gp93 and Methods For Their Use
TITLE OF INVENTION: In Diagnosis and Therapy
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 28-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 727-3670
TELEFAX: (206) 727-3601
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-379-057-32

Query Match 67.6%; Score 444.5; DB 2; Length 109;
Best Local Similarity 72.6%; Pred. No. 2.1e-37;
Matches 90; Conservative 8; Mismatches 11; Indels 15; Gaps 2;

QY 1 EVOLVKSGBGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVS:SGGNVYIDY 60
DB 1 EVQLLESGGGLVPGGSLRLSCAASGFTFSYAMSVRQAPKGLIEWVS:SSYIYY 59
QY 61 ADSVKGFTISRDNANVVYLVQNSLRADMAVYFCARDITIGSAATWRAFDINGRGTM 120
DB 60 ADSVKGFTISRDNANVVYLVQNSLRADMAVYFCARDITIGSAATWRAFDINGRGTM 120
QY 121 VTVSS 124
DB 106 VTVSS 109

RESULT 13
US-07-934-373C-4
Sequence 4, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 144
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH24
US-09-240-274-144

Query Match 68.0%; Score 447.5; DB 3; Length 1;
Best Local Similarity 68.3%; Pred. No. 1.2e-37;
Matches 86; Conservative 15; Mismatches 24; Indels 1; Gaps 1;

QY 1 EVOLVSGEGLVPGSGSLRLSCAASGFTFRYYDIHWVROTPGKLEWV:SSGGNYIDY 60
DB 1 EVOLLESQGGVAPGSRSLRLSCVASFSLRSYGMHWVRAQAPGKLEWV:WFDGSDNDY 60
QY 61 ADSVKGRTISRDNANNNVYLQNNSLRAEDMAVYFCARDGTFGSAAT:AFDIWGGGT 119
DB 61 ADSVKGRTISRDNNSKNTLYLQNNSLRAEDTAVYVCARDMVRAPFSSG:AFDIWGGGT 120
QY 120 MVTWSS 125
DB 121 MVTWSS 126

RESULT 9

US-09-240-274-150
Sequence 150, Application US/09240274
Patent No. 6253455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 150
LENGTH: 126
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH44
US-09-240-274-150

Query Match 68.0%; Score 447.5; DB 3; Length 1;
Best Local Similarity 68.3%; Pred. No. 1.2e-37;
Matches 86; Conservative 15; Mismatches 24; Indels 1; Gaps 1;
QY 1 EVOLVSGEGLVPGSGSLRLSCAASGFTFRYYDIHWVROTPGKLEWV:SSGGNYIDY 60
DB 1 EVOLLESQGGVAPGSRSLRLSCVASFSLRSYGMHWVRAQAPGKLEWV:WFDGSDNDY 60
QY 61 ADSVKGRTISRDNANNNVYLQNNSLRAEDMAVYFCARDGTFGSAAT:AFDIWGGGT 119
DB 61 ADSVKGRTISRDNNSKNTLYLQNNSLRAEDTAVYVCARDMVRAPFSSG:AFDIWGGGT 120

QY 120 MVTWSS 125
DB 121 MVTWSS 126

RESULT 10
US-08-428-197-1
Sequence 1, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubae & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howell, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURES:
NAME/KEY: Peptide
LOCATION: 1..125
US-08-428-197-1

Query Match 67.6%; Score 445; DB 2; Length 125;
Best Local Similarity 67.2%; Pred. No. 2.2e-37;
Matches 84; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVOLVSGEGLVPGSGSLRLSCAASGFTFRYYDIHWVROTPGKLEWV:SSGGNYIDY 60
DB 1 EVOLLESQGGVAPGSRSLRLSCVASFSLRSYGMHWVRAQAPGKLEWV:WFDGSDNDY 60
QY 61 ADSVKGRTISRDNANNNVYLQNNSLRAEDMAVYFCARDGTFGSAAT:AFDIWGGGT 120
DB 61 ADSVKGRTISRDNNSKNTLYLQNNSLRAEDTAVYCTGQVLYYGGSGSYHWFDPWGGGT 120
QY 121 MVTWSS 125
DB 121 MVTWSS 125

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 12.692 Seconds

(without alignments)
416,677 Million cell

Title: US-09-674-752-49

Perfect score: 658

Sequence: 1 EVOLVSGEGLVKGSGSLRL.....ATWRAFDWGRGTMV VSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/ECTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to give a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.5	71.0	245	4	US-08-918-148-78 Sequ. 78, Appl.
2	460.5	70.0	245	4	US-08-918-148-75 Sequ. 75, Appl.
3	460	69.9	127	3	US-09-240-274-27 Sequ. 27, Appl.
4	456	69.3	123	2	US-08-655-202-30 Sequ. 30, Appl.
5	456	69.3	123	4	US-09-315-574-30 Sequ. 30, Appl.
6	448	68.1	121	3	US-09-202-181-4 Sequ. 4, Appl.
7	447.5	68.0	126	3	US-09-240-274-10 Sequ. 10, Appl.
8	447.5	68.0	126	3	US-09-240-274-144 Sequ. 144, Appl.
9	447.5	68.0	126	3	US-09-240-274-150 Sequ. 150, Appl.
10	445	67.6	125	2	US-08-428-197-1 Sequ. 1, Appl.
11	445	67.6	125	2	PCT-US93-10555-1 Sequ. 1, Appl.
12	444.5	67.6	109	5	US-08-379-057-32 Sequ. 32, Appl.
13	443.5	67.4	120	2	US-07-934-373C-4 Sequ. 4, Appl.
14	443.5	67.4	120	2	US-08-437-6428-4 Sequ. 4, Appl.
15	443.5	67.4	120	4	US-08-146-206C-4 Sequ. 4, Appl.
16	442.5	67.2	135	3	US-08-579-378A-20 Sequ. 20, Appl.
17	442.5	67.2	443	5	PCT-US86-13152-4 Sequ. 4, Appl.
18	442	67.2	117	4	US-09-025-769B-24 Sequ. 24, Appl.
19	442	67.2	120	1	US-07-942-245-35 Sequ. 35, Appl.
20	442	67.2	125	3	US-09-240-274-24 Sequ. 24, Appl.
21	442	67.2	131	3	US-09-240-274-28 Sequ. 28, Appl.
22	441	67.0	125	3	US-09-240-274-9 Sequ. 9, Appl.
23	441	67.0	249	4	US-10-039-785-53 Sequ. 53, Appl.
24	440.5	66.9	120	4	US-09-025-769B-38 Sequ. 38, Appl.
25	440.5	66.9	120	4	US-09-025-769B-63 Sequ. 63, Appl.
26	440.5	66.9	140	3	US-08-983-607-32 Sequ. 32, Appl.
27	440.5	66.9	281	4	US-09-025-769B-178 Sequ. 178, Appl.

28	439.5	66.8	124	4	US-09-425-638A-49	Sequence 49, Appl.
29	439.5	66.8	124	4	US-09-543-004-49	Sequence 49, Appl.
30	439.5	66.8	139	1	US-08-129-930B-96	Sequence 96, Appl.
31	439.5	66.8	139	3	US-08-134-346A-51	Sequence 51, Appl.
32	439.5	66.8	139	4	US-08-976-288A-96	Sequence 96, Appl.
33	439.5	66.8	245	4	US-08-918-148-76	Sequence 76, Appl.
34	439	66.7	125	3	US-09-240-274-151	Sequence 151, Appl.
35	438	66.6	121	3	US-08-599-226-2	Sequence 2, Appl.
36	438	66.6	121	3	US-09-125-098-2	Sequence 2, Appl.
37	438	66.6	121	4	US-09-540-018-2	Sequence 2, Appl.
38	438	66.6	127	3	US-09-240-274-19	Sequence 19, Appl.
39	437.5	66.5	312	4	US-09-079-029-10	Sequence 10, Appl.
40	437	66.4	113	3	US-08-974-899-6	Sequence 6, Appl.
41	435.5	66.2	124	3	US-08-983-607-47	Sequence 47, Appl.
42	435	66.1	125	1	US-08-478-039-99	Sequence 99, Appl.
43	435	66.1	125	1	US-08-476-349A-99	Sequence 99, Appl.
44	434.5	66.0	120	2	US-08-958-201-10	Sequence 10, Appl.
45	434.5	66.0	124	4	US-09-425-638A-54	Sequence 54, Appl.

ALIGNMENTS

```
RESULT 1
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT PILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match
Best Local Similarity 71.0%; Score 467.5; DB 4; Length 245;
Matches 93; Conservative 11; Mismatches 14; Indels 7; Gaps 2;

QY 1 EVOLVSGEGLVKGSGSLRLSCAASGFTFRYYDHWVQTGKGLIEWSSISGNTYDY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 QVQLVSSGSGVLRPGGSLRLSCAASGFTFSNNMHWQAQKGLIEWSSISSTYY 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVGRFTISRDNNMNYVLTQNSLRRAEDMAYFCARDGTIFGSAATWRAFDWGRGTM 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 ADSVGRFTISRDNNKNSLVLTQNSLRRAEDTAIVYICARDR---GST---GMDVGRGTL 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 VTVSS 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 116 VTVSS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
```



```

; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1179
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1179
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Query Match          70.7%; Score 465; DB 11; Length 250;
Best Local Similarity 71.7%; Pred. No. 3.5e-36;
Matches 91; Conservative 12; Mismatches 22; Indels 2; Gaps 1;
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QY 1 EVOLVSGEGLVKPGSLRLSCAASGTFRRYDIHWRTQTPGKLEWVSISSGNTYDY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLVETGGGLVYKPGSLRLSCAASGTFSSYEMWVRQAPGKLEWVSISSGSTIYY 60
```

```
QY 61 ADSVKGRFTISRDNANVYVLTQNNSLRAEDMAVYFCARDG--TIFGSAATWRAFDIMGRG 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
DB 61 ADSVKGRFTISRDNANVYVLTQNNSLRAEDTAVYCTTGDYDILGYSVYGGDWGRG 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 119 TWVTSS 125
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DB 121 TLVTSS 127
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RESULT 13
US-09-880-748-1937
; Sequence 1937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1937
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1937
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Query Match          70.4%; Score 463; DB 11; Length 241;
Best Local Similarity 75.0%; Pred. No. 5.1e-36;
Matches 93; Conservative 8; Mismatches 15; Indels 8; Gaps 2;
```

```
QY 2 VOLVSGEGLVKPGSLRLSCAASGTFRRYDIHWRTQTPGKLEWVSISSGNTYDYA 61
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 VOLVSGGGLVYKPGSLRLSCAASGTFSSYEMWVRQAPGKLEWVSISSGSTIYYA 61
```

```
QY 62 DSVKGRFTISRDNANVYVLTQNNSLRAEDMAVYFCARDGTIFGSAATWRAFDIMGRGTW 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 DSVKGRFTISRDNANVYVLTQNNSLRAEDTAVYCCAR-GHPTG-----MDVWGRGTW 113
|||:|||||
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```
QY 122 TWSS 125
|||:|||||
DB 114 TWSS 117
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RESULT 14
US-09-880-748-2019
; Sequence 2019, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2019
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2019
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Query Match          70.3%; Score 462.5; DB 11; Length 237;
Best Local Similarity 73.6%; Pred. No. 5.6e-36;
Matches 92; Conservative 9; Mismatches 13; Indels 11; Gaps 1;
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QY 1 EVOLVSGEGLVKPGSLRLSCAASGTFRRYDIHWRTQTPGKLEWVSISSGNTYDY 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVOLVSGGGLVQPGSLRLSCAASGTFSSYEMWVRQAPGKLEWVSISSGSTIYY 60
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QY 61 ADSVKGRFTISRDNANVYVLTQNNSLRAEDMAVYFCARDGTIFGSAATWRAFDIMGRGTW 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
DB 61 ADSVKGRFTISRDNANVYVLTQNNSLRAEDTAVYICARDTT-----DYGGRGTW 109
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 121 TWSS 125
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DB 110 TWSS 114
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RESULT 15
US-09-880-748-2040
; Sequence 2040, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
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; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-13

Query Match
Best Local Similarity 71.7%; Score 471.5; DB 12; Length 126;
Matches 95; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVSGGLVPRGSLRLSCAASGFTFRRIYDIHWRTPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGLVPRGSLRLSCAASGFTFRYNNMWRQAPGKLEWVSSISSSSNIYY 60
QY 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDMAVYFCARDGTI-FGSAATWRAPDIWGRGT 119
Db 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDTAVYCCARDIMITFGIILASFYFDYWGQGT 120
QY 120 MVTWSS 125
Db 121 LVTWSS 126

RESULT 6
US-10-041-860-208
; Sequence 208, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Pong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binayam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-208

Query Match
Best Local Similarity 71.7%; Score 471.5; DB 12; Length 126;
Matches 95; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVSGGLVPRGSLRLSCAASGFTFRRIYDIHWRTPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGLVPRGSLRLSCAASGFTFRYNNMWRQAPGKLEWVSSISSSSNIYY 60
QY 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDMAVYFCARDGTI-FGSAATWRAPDIWGRGT 119
Db 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDTAVYCCARDIMITFGIILASFYFDYWGQGT 120
QY 120 MVTWSS 125
Db 121 LVTWSS 126

RESULT 7
US-10-091-300-31
; Sequence 31, Application US/10091300
; Publication No. US20030108545A1
```

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; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 31
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Human
US-10-091-300-31

Query Match
Best Local Similarity 71.5%; Score 470.5; DB 15; Length 116;
Matches 94; Conservative 8; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVOLVSGGLVPRGSLRLSCAASGFTFRRIYDIHWRTPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGLVPRGSLRLSCAASGFTFSYMMWRQAPGKLEWVSSISSSSYIYY 60
QY 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGT 120
Db 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDTAVYCCAR-----VTDAFDIWGQGT 111
QY 121 VTWSS 125
Db 112 VTWSS 116

RESULT 8
US-09-880-748-1318
; Sequence 1318, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1318
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1318

Query Match
Best Local Similarity 71.4%; Score 469.5; DB 11; Length 256;
Matches 93; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

QY 1 EVOLVSGGLVPRGSLRLSCAASGFTFRRIYDIHWRTPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGLVPRGSLRLSCAASGFTFSYSMMWRQAPGKLEWVSSISSSSYIYY 60
QY 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDMAVYFCARD-GTIFGSAATWR----AFDIW 115
Db 61 ADSVKGRFTISRDNANNVYLQNNSLRAEDTAVYCCARDLGSFYDILTALRLENYGMQDW 120
```

Db 61 ADVKGRFTISRDNKNSLYLQWNSLRADTAIVYVCARGHYDILGYFG-----FDY 113
Qy 115 WGRGTMVTSS 125
Db 114 WGRGTLVTSS 124

RESULT 2
US-10-091-300-24

; Sequence 24, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 24
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Human
US-10-091-300-24

Query Match 72.3%; Score 475.5; DB 15; Length 116;
Best Local Similarity 76.0%; Pred. No. 1,6e-37;
Matches 95; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

Qy 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTPOKGLIEWVSSISGGNYIDY 60
Db 1 EVOLVSGGGLVYKPGSLRLSCAASGFTSSISMVWQAQPKGLEWVSSISSSYIYY 60
Qy 61 ADVKGRFTISRDNANNVYLYQWNSLRADMAVYFCARDGTFGSAATWRAPDIWGRGTM 120
Db 61 ADVKGRFTISRDNKNSLYLQWNSLRADTAIVYCAR-----VTDAPDIWGGTM 111

Qy 121 VTVSS 125
Db 112 VTVSS 116

RESULT 3
US-10-150-475A-6

; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody Biwa 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

Query Match 71.8%; Score 472.5; DB 15; Length 444;
Best Local Similarity 73.6%; Pred. No. 1,3e-36;
Matches 92; Conservative 8; Mismatches 14; Indels 11; Gaps 1;
Qy 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTPOKGLIEWVSSISGGNYIDY 60
Db 1 EVOLVSGGGLVYKPGSLRLSCAASGFTSSISMVWQAQPKGLEWVSSISSSYIYY 60

Db 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTSSISMVWQAQPKGLEWVSSISGGSYIYY 60
Qy 61 ADVKGRFTISRDNANNVYLYQWNSLRADMAVYFCARDGTFGSAATWRAPDIWGRGTM 120
Db 61 LDISKGRFTISRDNKNSLYLQWNSLRADTAIVYVCARG-----LDYGRGTL 109
Qy 121 VTVSS 125
Db 110 VTVSS 114

RESULT 4
US-09-880-748-913

; Sequence 913, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 913
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-913

Query Match 71.7%; Score 472; DB 11; Length 248;
Best Local Similarity 72.0%; Pred. No. 7,5e-37;
Matches 90; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTPOKGLIEWVSSISGGNYIDY 60
Db 1 EVOLVSGGGLVYKPGSLRLSCAASGFTSSISMVWQAQPKGLEWVSSISSNRSYIYY 60
Qy 61 ADVKGRFTISRDNANNVYLYQWNSLRADMAVYFCARDGTFGSAATWRAPDIWGRGTM 120
Db 61 ADVKGRFTISRDNKNSLYLQWNSLRADTAIVYVCARGRDILTGYYVYGLDVWGQTL 120

Qy 121 VTVSS 125
Db 121 VTVSS 125

RESULT 5
US-10-041-860-13

; Sequence 13, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezebel, Binayam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USBS
; FILE REFERENCE: ABGENIX-051A
; CURRENT APPLICATION NUMBER: US/10/041,860

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 26.8075 Seconds
(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-49

Perfect score: 1 EVOLVSGGGLVPGGSLRL.....AATRAFDIWRGTMVTS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing filter 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477.5	72.6	252	US-09-880-748-1362	Sequence 1362, Ap
2	475.5	72.3	116	US-10-091-300-24	Sequence 24, Ap
3	472.5	71.8	444	US-10-150-475A-6	Sequence 6, Appl
4	472	71.7	248	US-09-880-748-913	Sequence 913, Ap
5	471.5	71.7	126	US-10-041-860-13	Sequence 13, Appl
6	471.5	71.7	126	US-10-041-860-208	Sequence 208, Appl
7	470.5	71.5	116	US-10-091-300-31	Sequence 31, Appl
8	469.5	71.4	256	US-09-880-748-1318	Sequence 1318, Ap
9	468.5	71.2	256	US-09-880-748-883	Sequence 883, Ap
10	467.5	71.0	126	US-10-041-860-270	Sequence 270, Ap
11	467.5	71.0	247	US-09-880-748-1764	Sequence 1764, Ap
12	465	70.7	250	US-09-880-748-1179	Sequence 1179, Ap
13	463	70.4	241	US-09-880-748-1937	Sequence 1937, Ap
14	462.5	70.3	237	US-09-880-748-2019	Sequence 2019, Ap
15	462.5	70.3	237	US-09-880-748-2040	Sequence 2040, Ap

16	462.5	70.3	240	US-09-880-748-2007	Sequence 2007, Ap
17	462.5	70.3	248	US-09-880-748-1974	Sequence 1974, Ap
18	461.5	70.1	124	US-10-040-244-16	Sequence 16, Appl
19	461.5	70.1	249	US-09-880-748-1856	Sequence 1856, Ap
20	461	70.1	255	US-09-880-748-1608	Sequence 1608, Ap
21	460.5	70.0	247	US-09-880-748-1703	Sequence 1703, Ap
22	460	69.9	127	US-09-848-798-27	Sequence 27, Appl
23	459.5	69.8	240	US-09-880-748-2025	Sequence 2025, Ap
24	458.5	69.7	236	US-09-880-748-2010	Sequence 2010, Ap
25	458.5	69.7	237	US-09-880-748-2006	Sequence 2006, Ap
26	458.5	69.7	237	US-09-880-748-2020	Sequence 2020, Ap
27	458.5	69.7	237	US-09-880-748-2036	Sequence 2036, Ap
28	458.5	69.7	237	US-09-880-748-2014	Sequence 2014, Ap
29	458.5	69.7	239	US-09-880-748-2034	Sequence 2034, Ap
30	458.5	69.7	240	US-09-880-748-2030	Sequence 2030, Ap
31	458.5	69.7	240	US-09-880-748-2044	Sequence 2044, Ap
32	457.5	69.5	237	US-09-880-748-2039	Sequence 2039, Ap
33	457.5	69.5	248	US-09-880-748-1965	Sequence 1965, Ap
34	456.5	69.4	237	US-09-880-748-2003	Sequence 2003, Ap
35	456.5	69.4	240	US-09-880-748-2029	Sequence 2029, Ap
36	456.5	69.4	240	US-09-880-748-2045	Sequence 2045, Ap
37	456.5	69.4	254	US-09-880-748-1428	Sequence 1428, Ap
38	456	69.3	250	US-10-120-414-72	Sequence 72, Appl
39	456	69.3	255	US-09-880-748-1819	Sequence 1819, Ap
40	455.5	69.2	237	US-09-880-748-2005	Sequence 2005, Ap
41	455.5	69.2	237	US-09-880-748-2110	Sequence 2110, Ap
42	455.5	69.2	237	US-09-880-748-2111	Sequence 2111, Ap
43	455.5	69.2	237	US-09-880-748-2115	Sequence 2115, Ap
44	455.5	69.2	237	US-09-880-748-2118	Sequence 2118, Ap
45	455.5	69.2	238	US-09-880-748-2024	Sequence 2024, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1362
; Sequence 1362, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1362
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1362

Query Match 72.6%; Score 477.5; DB 11; Length 252;
Best Local Similarity 74.0%; Pred. No. 2,3e-37;
Matches 97; Conservative 6; Mismatches 15; Indels 13; Gaps 2;

QY 1 EVOLVSGGGLVPGGSLRLSCAASGFTFRRIYIHVWQTPGKGLRWVSISGCVIYD 60
DB 1 EVOLVSGGGLVPGGSLRLSCAASGFTFRRIYIHVWQTPGKGLRWVSISGCVIY 60
QY 61 ADSVKGRTISRDNANNVYLTQNSLRADMAVYFCAR-----DGTIFGSAATRAFDI 114
|||||

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XX 22-FEB-2001; 2001MO-JP01298.
PF
XX
XX 22-FEB-2000; 2000JP--0050543.
PR
XX
XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA
XX Kurosawa Y, Akahori Y, Ida Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
XX WPI; 2001-565420/63.
DR N-PSDB; AAH47732.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions -
XX
XX Examples; p 168-169; 181pp; Japanese.
PS
XX
XX The invention relates to producing gene libraries, comprising
XX immunoglobulin light and heavy variable region. The method involves
XX selecting light chain that binds with the heavy chain product to produce
XX a functional conformation, producing a gene library comprising a
XX collection of these light chain variable genes, and combining with gene
XX library of heavy chain variable genes. The method is used for production
XX of gene and antibody libraries.
XX
SQ Sequence 119 AA;

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CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 256 AA;

Query Match 71.4%; Score 469.5; DB 23; Length 256;
 Best Local Similarity 72.1%; Pred. No. 1.5e-35;
 Matches 93; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTPRRIYDIHWYRQPGKLEWVSISGGRNYIDY 60
 DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTPRSYSNWYRQAPGKLEWVSISSSSTIYY 60

QY 61 ADSVKGRTISRDNANNVYLYQNSLRAEDMAVYFCARD-GTIFGSAATWR---AFDIW 115
 DB 61 ADSVKGRTISRDNANKSVLYLQNSLRAEDTAVYYCARDLGSFYDILTLRLNMGMDW 120

QY 116 GRTMTVTS 124
 DB 121 GKGTLVTS 129

RESULT 12

ID ABP44872 standard; Protein; 250 AA.

XX AC ABP44872;

XX DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 883.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antitumoral;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX MO200202641-A1.

XX PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX MPI, 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX Claim 1; Page 1455-1456, 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytotatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antitumoral and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX Sequence 250 AA;

Query Match 71.2%; Score 468.5; DB 23; Length 250;
 Best Local Similarity 75.8%; Pred. No. 1.5e-35;
 Matches 94; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 2 VOLVSGEGLVPGGSLRLSCAASGFTPRRIYDIHWYRQPGKLEWVSISGGRNYIDY 61
 DB 2 VOLVSGGGLVPGGSLRLSCAASGFTPRSYSNWYRQAPGKLEWVSISSSSTIYY 60

QY 62 DSVKGRFTISRDNANNVYLYQNSLRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGTW 121
 DB 61 DSVKGRFTISRDNANKSVLYLQNSLRAEDTAVYYCARDSDYDILTLGRGYTFWKGTLV 120

QY 122 TVSS 125
 DB 121 TVSS 124

RESULT 13

ID AAY06717 standard; Protein; 245 AA.

XX AAY06717;

XX DT 17-JUN-1999 (first entry)

DE Antibody 12B5 single chain Fv (scFv) fragment.

XX Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
 XX megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
 XX bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
 XX myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MDS; CDR;
 XX neuromuscular; muscular dystrophy; complementarity determining region.

OS Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 208 /note= "unspecified"

XX MO9910494-A2.

XX PD 04-MAR-1999.

PP 21-AUG-1998; 98WO-US17364.

PR 25-AUG-1997; 97US-0918148.

XX (GETH) GENENTECH INC.

XX Adams CW, Carter PJ, Fendly BM, Gurney AL;

XX MPI, 1999-204666/17.

CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
 CC It is preferably useful for treating subjects with both solid tumours,
 CC preferably high vascular tumours and non-solid tumour. The inhibition
 CC or reduction of tumour growth includes prevention or inhibition of the
 CC progression of tumour, including cancers and non-cancerous tumours,
 CC where the progression of tumours includes the invasiveness, metastasis,
 CC recurrence and increase in size of the tumour. The present sequence is
 CC human KDR (VEGFR-2) Fab antibody heavy chain protein.

XX Sequence 116 AA:

Query Match 71.5%; Score 470.5; DB 23; Length 116;
 Best Local Similarity 75.2%; Pred. No. 4.3e-36;
 Matches 94; Conservative 8; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVKGSGEGLVKGSGSLRLSCAASGFTFRRIYDHMRQTPKGLIEWSSISGQNYDY 60
 DB 1 EVQLVQSGGGLVKGSGSLRLSCAASGFTFSYSNMWVRQAPGKGLIEWSSISSSYIYY 60
 QY 61 ADSVKGRTISRDNANNNVYVYLOMNSLRADMAVYFCARDGTIFGSAATWRADFIMGRGTM 120
 DB 61 ADSVKGRTISRDNKDSLYLOMNSLRADTAIVYTCAR-----VTDADFIMGQGTM 111
 QY 121 VTVSS 125
 DB 112 VTVSS 116

RESULT 10
 ABJ26766

ID ABJ26766 standard; Protein; 116 AA.

XX ABJ26766;

DT 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID No 83.

KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;

KM leukaemia cell; vascular endothelial growth factor; tumour;

KW bispecific antigen-binding protein; human.

XX Homo sapiens.

PN WO2003002144-A1.

PD 09-JAN-2003.

PF 26-JUN-2002; 2002WO-US20332.

PR 26-JUN-2001; 2001US-301299P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2003-201468/19.

PT N-PSDB; ABT3330.

PT New bispecific antibodies having antigen-binding sites specific for a

PT first vascular endothelial growth factor (VEGF) receptor and for a

PT second VEGF receptor, useful for inhibiting migration of leukemia

PT cell, or for treating tumors -

XX Claim 15; Page 74; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding

XX site specific for a first vascular endothelial growth factor (VEGF)

XX receptor and a second antigen-binding site specific for a second VEGF

XX receptor. The bispecific antigen-binding proteins block activation of the

XX VEGF receptor and are useful for reducing or inhibiting VEGF-induced

XX cellular functions such as mitogenesis of vascular endothelial cells

CC and migration of leukaemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This sequence represents a human protein relating to the
 CC bispecific antibodies that bind to the VEGF receptors of the invention.

XX Sequence 116 AA:

Query Match 71.5%; Score 470.5; DB 24; Length 116;
 Best Local Similarity 75.2%; Pred. No. 4.3e-36;
 Matches 94; Conservative 8; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVKGSGEGLVKGSGSLRLSCAASGFTFRRIYDHMRQTPKGLIEWSSISGQNYDY 60
 DB 1 EVQLVQSGGGLVKGSGSLRLSCAASGFTFSYSNMWVRQAPGKGLIEWSSISSSYIYY 60
 QY 61 ADSVKGRTISRDNANNNVYVYLOMNSLRADMAVYFCARDGTIFGSAATWRADFIMGRGTM 120
 DB 61 ADSVKGRTISRDNKDSLYLOMNSLRADTAIVYTCAR-----VTDADFIMGQGTM 111
 QY 121 VTVSS 125
 DB 112 VTVSS 116

RESULT 11
 ABP45307

ID ABP45307 standard; Protein; 256 AA.

XX ABP45307;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1318.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

XX Claim 1; Page 1975-1976; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to

XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

XX tumour necrosis factor (TNF) super family and induces B cell

XX proliferation and differentiation. The antibodies of the invention have

XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

XX antirheumatic and antiAIDS activity and can be used in vaccines to

XX Sequence 444 AA;
 Query Match 71.8%; Score 472.5; DB 24; Length 444;
 Best Local Similarity 73.6%; Pred. No. 1.2e-35; Indels 11; Gaps 1;
 Matches 92; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

QY 1 EVQLVSGGGLVPRGSLRLSCAASGFTFRRYDIHWVROTPGKLEWVSISSGGVYDY 60
 DB 1 EVQLVSGGGLVPRGSLRLSCAASGFTFSSYMSWVRQAPGKLEWVSISSGGVYDY 60
 QY 61 ADSVKGRFTISRDNANNNVYLQNSLRPAEDMAVYFCARDGTIFGSAATRAPDIWGRGT 120
 DB 61 LDSIKGRFTISRDNANNNVYLQNSLRPAEDTAVYVCARQG-----LDYWGRT 109
 QY 121 VTVSS 125
 DB 110 VTVSS 114

RESULT 8
 ID ABP44902 standard; Protein: 248 AA.
 AC ABP44902;
 DT 19-AUG-2002 (first entry)
 XX Human Blys binding scFv SEQ ID 913.
 DE Human Blys binding scFv SEQ ID 913.
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunomodulant; immunomodulatory; antithumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 OS
 PN WO200202641-A1.
 PD 10-JAN-2002.
 PF 15-JUN-2001; 2001WO-US919110.
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI; 2002-114799/15.
 XX
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
 the diagnosis and treatment of cancers and immune disorders -
 XX
 XX Claim 1; Page 1491-1492; 3148bp; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4399-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

QY Sequence 248 AA;
 Query Match 71.7%; Score 472; DB 23; Length 248;
 Best Local Similarity 72.0%; Pred. No. 7.1e-36; Indels 0; Gaps 0;
 Matches 90; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVPRGSLRLSCAASGFTFRRYDIHWVROTPGKLEWVSISSGGVYDY 60
 DB 1 EVQLVSGGGLVPRGSLRLSCAASGFTFSSYMSWVRQAPGKLEWVSISSGGVYDY 60
 QY 61 ADSVKGRFTISRDNANNNVYLQNSLRPAEDMAVYFCARDGTIFGSAATRAPDIWGRGT 120
 DB 61 ADSVKGRFTISRDNANNNVYLQNSLRPAEDTAVYVCARGRDILTVYYGLDVMGRT 120
 QY 121 VTVSS 125
 DB 121 VTVSS 125

RESULT 9
 ID AAE28873 standard; Protein: 116 AA.
 AC AAE28873;
 DT 27-DEC-2002 (first entry)
 XX Human KDR (VEGFR-2) Fab heavy chain (VH) protein from D2H2 clone.
 DE Human KDR (VEGFR-2) Fab heavy chain (VH) protein from D2H2 clone.
 KW Human; tumour; vascular endothelial growth factor receptor; metastasis;
 KM epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
 KM breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.
 XX Homo sapiens.
 OS
 PN WO200270008-A1.
 PD 12-SEP-2002.
 PF 04-MAR-2002; 2002WO-US06762.
 PR 02-MAR-2001; 2001US-0798689.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (ROCK/) ROCKWELL P.
 PA (GOLD/) GOLDSTEIN N I.
 DR WPI; 2002-691738/74.
 DR N-PSDB; AAD46294.
 XX
 PT Inhibiting tumor growth in humans involves administering vascular
 PT endothelial growth factor receptor antagonists in combination with
 PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
 PT antagonists -
 XX
 XX Example 12; Page 127; 151bp; English.
 CC The invention relates to a method of inhibiting tumour growth which
 CC involves administering, vascular endothelial growth factor receptor
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over

CC The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells
 CC and migration of leukemia cells. The antibodies are useful for treating
 CC tumors and for in vivo or in vitro for investigative and diagnostic
 CC methods. This sequence represents a human protein relating to the
 CC bispecific antibodies that bind to the VEGF receptors of the invention.

XX Sequence 116 AA;

Query Match 72.3%; Score 475.5; DB 24; Length 116;
 Best Local Similarity 76.0%; Pred. No. 1.5e-36;
 Matches 95; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVOLVSGEGLVKPGGSLRLSCAAGFTRRYDHWRTQPKGLEWVSSISGSGNYDY 60
 DB 1 EVOLVSGGGLVKGPGSLRLSCAAGFTFSSYDMWVQAPGKLEWVSSISGSGYTY 60
 QY ADSVKGRTISRDNANNVYVYLOMNSLRADMAVYFCARPGTIFGSAATWRAFDINGRTM 120
 DB ADSVKGRTISRDNANNVYVYLOMNSLRADTAVYTCAR-----VTDARFDINGGRTM 111
 QY 121 VTWSS 125
 DB 112 VTWSS 116

RESULT 6
 AAE34873
 ID AAE34873 standard; Protein; 114 AA.

XX AAE34873;

DT 28-MAY-2003 (first entry)

XX B1WA8 antibody heavy chain variable region.

XX B1WA8 antibody; heavy chain variable region; light chain variable region;

XX VH; VL; CD4v6; medicament; cancer; antibody therapy.

XX Unidentified.

XX MO200294879-A1.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-BP05467.

XX 18-MAY-2001; 2001EP-0112237.

XX 26-SEP-2001; 2001US-325147P.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX Adolf G. Ostermann E, Patzelt E, Sproll M, Heider K, Miglietta JJ;

XX Van Dongen AAMS;

XX N-PSDB; AAD53209.

XX MPI; 2003-129413/12.

XX Claim 1; Column 43; 78pp; English.

CC The present invention relates to novel antibody molecules comprising a
 CC variable region of the heavy (VH) and/or light chain (VL) of CD4v6
 CC specific humanised antibody called B1WA8 and B1WA4. Sequences of the
 CC invention are useful for manufacturing a medicament and for treating

CC cancer including colorectum, non-small cell lung, breast, head and neck,
 CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
 CC brain. They are also useful in antibody therapy. The present sequence
 CC is B1WA8 antibody heavy chain variable region. This sequence is used
 CC in the exemplification of the invention.

XX Sequence 114 AA;

Query Match 71.8%; Score 472.5; DB 24; Length 114;
 Best Local Similarity 73.6%; Pred. No. 2.7e-36;
 Matches 92; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

QY 1 EVOLVSGEGLVKPGGSLRLSCAAGFTRRYDHWRTQPKGLEWVSSISGSGNYDY 60
 DB 1 EVOLVSGGGLVKGPGSLRLSCAAGFTFSSYDMWVQAPGKLEWVSSISGSGYTY 60
 QY ADSVKGRTISRDNANNVYVYLOMNSLRADMAVYFCARPGTIFGSAATWRAFDINGRTM 120
 DB ADSVKGRTISRDNANNVYVYLOMNSLRADTAVYTCARQ-----LDVWGRGTL 109
 QY 121 VTWSS 125
 DB 110 VTWSS 114

RESULT 7
 AAE34876
 ID AAE34876 standard; Protein; 444 AA.

XX AAE34876;

DT 28-MAY-2003 (first entry)

XX B1WA4/8 antibody heavy chain mature protein.

XX B1WA8 antibody; heavy chain variable region; light chain variable region;

XX VH; VL; CD4v6; medicament; cancer; antibody therapy.

XX Unidentified.

XX MO200294879-A1.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-BP05467.

XX 18-MAY-2001; 2001EP-0112237.

XX 26-SEP-2001; 2001US-325147P.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX Adolf G. Ostermann E, Patzelt E, Sproll M, Heider K, Miglietta JJ;

XX Van Dongen AAMS;

XX N-PSDB; AAD53212, AAD53215.

XX MPI; 2003-129413/12.

XX Claim 24; Column 44; 78pp; English.

CC The present invention relates to novel antibody molecules comprising a
 CC variable region of the heavy (VH) and/or light chain (VL) of CD4v6
 CC specific humanised antibody called B1WA8 and B1WA4. Sequences of the
 CC invention are useful for manufacturing a medicament and for treating
 CC cancer including colorectum, non-small cell lung, breast, head and neck,
 CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the
 CC brain. They are also useful in antibody therapy. The present sequence
 CC is B1WA4/8 antibody heavy chain mature protein. This sequence is used
 CC in the exemplification of the invention.

CC cytotatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antitumour, immunostimulant, immunomodulatory, immunostimulant,
CC antitumour, immunostimulant, immunomodulatory, immunostimulant,
CC inhibit the expression and activity of Bly5. The antibodies bind to Bly5
CC and so may be used to detect and quantitate the presence of Bly5 in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Bly5. They may also be
CC administered to treat diseases associated with aberrant Bly5 expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABB4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

SQ Sequence 252 AA;

Query Match 72.6%; Score 477.5; DB 23; Length 252;
Best Local Similarity 74.0%; Pred. No. 2.2e-36;
Matches 97; Conservative 6; Mismatches 15; Indels 13; Gaps 2;

QY 1 EVQLVKGEGLVKPGSRLSCAASGFTFRYDIHWYRQPGKLEWVSISGGNYIDY 60
DB 1 EVQLVKGEGLVKPGSRLSCAASGFTFRYDIHWYRQPGKLEWVSISGGNYIDY 60
QY 61 ADSYKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCAR-----DGTIFGSAATWRAFDI 114
DB 61 ADSYKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCAR-----DGTIFGSAATWRAFDI 114
QY 115 WGRGTMTVSS 125
DB 115 WGRGTMTVSS 125
QY 114 WGRGTMTVSS 124
DB 114 WGRGTMTVSS 124

RESULT 4

ID AAE28870 standard; Protein; 116 AA.

AC AAE28870;

DT 27-DEC-2002 (first entry)

DE Human KDR (VEGFR-2) Fab heavy chain protein from D2C6 and D1H4 clone.

KM Human, tumour; vascular endothelial growth factor receptor; metastasis;
KM epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
KM breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; VH.

OS Homo sapiens.

PN WO200270008-A1.

PD 12-SEP-2002.

PP 04-MAR-2002; 2002WO-US06762.

PR 02-MAR-2001; 2001US-0798689.

PA (IMCL-) IMCLONE SYSTEMS INC.

PA (ROCK/) ROCKWELL P.

PA (GOLD/) GOLDSTEIN N I.

DR WPI; 2002-691738/74.

DR N-PSDB; AAD46290, AAD46292.

PT Inhibiting tumor growth in humans involves administering vascular
PT endothelial growth factor receptor antagonists in combination with
PT radiation, chemotherapeutic agents, or epidermal growth factor receptor
PT antagonists -
PS Example 9; Page 123; 151pp; English.

CC The invention relates to a method of inhibiting tumour growth which
CC involves administering, vascular endothelial growth factor receptor

CC (VEGFR) antagonists in combination with radiation, chemotherapeutic
CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method
CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.
CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,
CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,
CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over
CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour
CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.
CC It is preferably useful for treating subjects with both solid tumours,
CC preferably high vascular tumours and non-solid tumours. The inhibition
CC or reduction of tumour growth includes prevention or inhibition of the
CC progression of tumour, including cancerous and non-cancerous tumours,
CC where the progression of tumour includes the invasiveness, metastasis,
CC recurrence and increase in size of the tumour. The present sequence is
CC human KDR (VEGFR-2) Fab antibody heavy chain protein.

SQ Sequence 116 AA;

Query Match 72.3%; Score 475.5; DB 23; Length 116;
Best Local Similarity 76.0%; Pred. No. 1.5e-36;
Matches 95; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVKGEGLVKPGSRLSCAASGFTFRYDIHWYRQPGKLEWVSISGGNYIDY 60
DB 1 EVQLVKGEGLVKPGSRLSCAASGFTFRYDIHWYRQPGKLEWVSISGGNYIDY 60
QY 61 ADSYKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCAR-----DGTIFGSAATWRAFDI 120
DB 61 ADSYKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCAR-----DGTIFGSAATWRAFDI 120
QY 121 VTVSS 125
DB 121 VTVSS 116
QY 112 VTVSS 116
DB 112 VTVSS 116

RESULT 5

ID ABJ26763 standard; Protein; 116 AA.

AC ABJ26763;

DT 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID No 76.

KM Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KM leukemia cell; vascular endothelial growth factor; tumour;
KM bispecific antigen-binding protein; human.

OS Homo sapiens.

PN WO2003002144-A1.

PD 09-JAN-2003.

PP 26-JUN-2002; 2002WO-US20332.

PR 26-JUN-2001; 2001US-301299P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PA (Zhu Z;

DR WPI; 2003-201468/19.

DR N-PSDB; ABT23325.

PT New bispecific antibodies having antigen-binding sites specific for a
PT first vascular endothelial growth factor (VEGF) receptor and for a
PT second VEGF receptor, useful for inhibiting migration of leukemia
PT cells, or for treating tumors -
PS Claim 15; Page 70-71; 98pp; English.

CC

PT treatment of hemophilia A patients with these antibodies -
XX
PS Example 8; Fig 9E; 61pp; English.
CC This invention describes a novel polynucleotide (1) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (1) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents a fragment
CC of the human factor VIII antibody heavy chain variable region protein B04
CC which is used in the method of the invention.
XX
SQ Sequence 125 AA;
Query Match 100.0%; Score 658; DB 21; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.1e-53;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRYDIHWVROTPGKLEWVSSISGNYIDY 60
DB 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRYDIHWVROTPGKLEWVSSISGNYIDY 60
QY 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWGRGTW 120
DB 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWGRGTW 120
QY 121 VTVSS 125
DB 121 VTVSS 125
RESULT 2
AAV50965
ID AAV50965 standard; Protein; 126 AA.
XX
AC AAV50965;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human FvIII antibody A3-C1 scFv heavy chain protein B04.
XX
KM Human, heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; scFv; A3-C1.
XX
OS Homo sapiens.
XX
PN WO9558680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 59WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
PS Example 8; Fig 9A; 61pp; English.
CC This invention describes a novel polynucleotide (1) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (1) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC factor VIII antibody A3-C1 specific scFv protein B04 which is used
CC in the method of the invention.
XX
SQ Sequence 126 AA;
Query Match 100.0%; Score 658; DB 21; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.1e-53;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRYDIHWVROTPGKLEWVSSISGNYIDY 60
DB 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRYDIHWVROTPGKLEWVSSISGNYIDY 60
QY 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWGRGTW 120
DB 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWGRGTW 120
QY 121 VTVSS 125
DB 121 VTVSS 125
RESULT 3
ABP45351
ID ABP45351 standard; Protein; 252 AA.
XX
AC ABP45351;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Bly5 binding scFv SEQ ID 1362.
XX
KM Bly5; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
XX
PR 17-OCT-2000; 2000US-240816P.
XX
PR 16-MAR-2001; 2001US-276248P.
XX
PR 21-MAR-2001; 2001US-277379P.
XX
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2028-2029; 3148pp; English.
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Bly5) polypeptides. Bly5 is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have

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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:42:39 ; Search time 40.2112 Seconds
(without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-49

Sequence: 1 EVQLVKGSGELVKPGGSLRL.....AATRAFDIGRGTMTVSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	125	21	AAVS0969 Human FVIII antibo
2	658	100.0	126	21	AAVS0965 Human FVIII antibo
3	477.5	72.6	252	23	ABP45351 Human BlyS binding
4	475.5	72.3	116	23	AAE28870 Human KDR (VEGFR-2
5	475.5	72.3	116	24	ABJ26763 VEGF binding relat
6	472.5	71.8	114	24	AAE34873 B2M6 antibody hea
7	472.5	71.8	444	24	AAE34876 B2M4/8 antibody h
8	472	71.7	248	23	ABP44902 Human BlyS binding
9	470.5	71.5	116	23	AAE28873 Human KDR (VEGFR-2

10	470.5	71.5	116	24	ABJ26766	VEGF binding relat
11	469.5	71.4	256	23	ABP45307	Human BlyS binding
12	468.5	71.2	250	23	ABP44872	Human BlyS binding
13	467.5	71.0	245	20	AAV06717	Antibody 1285 sing
14	467.5	71.0	247	23	ABP45753	Human BlyS binding
15	466.5	70.9	119	22	AAE55568	Amino acid sequenc
16	466.5	70.9	240	22	AAE46007	Human MUC-1 bcrv c
17	465	70.7	250	23	ABP45166	Human BlyS binding
18	463	70.4	241	23	ABP45926	Human BlyS binding
19	462.5	70.3	237	23	ABP46008	Human BlyS binding
20	462.5	70.3	237	23	ABP46029	Human BlyS binding
21	462.5	70.3	240	23	ABP45996	Human BlyS binding
22	462.5	70.3	248	23	ABP45963	Human BlyS binding
23	461.5	70.1	177	24	ABJ36939	Anti-CD40 monoclona
24	461.5	70.1	249	23	ABP45845	Human BlyS binding
25	461	70.1	255	23	ABP45597	Human BlyS binding
26	460.5	70.0	245	20	AAV06714	Antibody 585 singl
27	460.5	70.0	247	23	ABP45692	Human BlyS binding
28	460	69.9	127	22	AAE33584	Human anti-Rh(D) c
29	459.5	69.8	240	23	ABP46014	Human BlyS binding
30	458.5	69.7	118	22	AAE52191	Human anti-HBs ant
31	458.5	69.7	126	22	AAE52934	Anti-adipocyte mon
32	458.5	69.7	152	22	AAE91111	Amino acid sequenc
33	458.5	69.7	236	23	ABP45999	Human protein SRO
34	458.5	69.7	236	23	ABP45999	Human BlyS binding
35	458.5	69.7	237	23	ABP45995	Human BlyS binding
36	458.5	69.7	237	23	ABP46009	Human BlyS binding
37	458.5	69.7	237	23	ABP46025	Human BlyS binding
38	458.5	69.7	237	23	ABP46103	Human BlyS binding
39	458.5	69.7	239	23	ABP46023	Human BlyS binding
40	458.5	69.7	240	23	ABP46019	Human BlyS binding
41	458.5	69.7	240	23	ABP46033	Human BlyS binding
42	458	69.6	138	21	AAV32406	Mouse anti-verotox
43	457.5	69.5	237	23	ABP46028	Human BlyS binding
44	457.5	69.5	248	23	ABP45954	Human BlyS binding
45	457	69.5	127	22	AAU02616	Anti-adipocyte mon

ALIGNMENTS

RESULT 1	AAVS0969	standard; Protein; 125 AA.
ID	AAVS0969;	
AC	AAVS0969;	
XX	23-MAR-2000	(first entry)
DT	23-MAR-2000	
DE	Human FVIII antibody heavy chain variable region B04 protein fragment.	
DR	Human; heavy chain; antibody; factor VIII; hemostatic; variable region;	
XX	hemophilia A.	
KW	Human; heavy chain; antibody; factor VIII; hemostatic; variable region;	
KM	hemophilia A.	
OS	Homo sapiens.	
XX	MO958680-A2.	
PN	18-NOV-1999.	
XX	18-NOV-1999.	
PD	07-MAY-1999;	99WO-NL00285.
XX	07-MAY-1999;	
PF	08-MAY-1998;	98EP-0201543.
XX	08-MAY-1998;	
PR	(SANO-) STICHTING SANQUIN BLOEDVOORZIENING.	
PA	Voorberg JJ, Van Den Brink EN, Turenhout EAM;	
XX	WPI; 2000-053102/04.	
PI	N-PSDB; AAZ43866.	
DR	New polynucleotide, polypeptide and antibody useful for diagnosing the	
XX	presence of neutralizing antibodies against factor VIII and for	
PT		

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ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBT_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a
RT human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 112 AA; 12243 MW; 24PIA45EC3B84788 CRC64;

Query Match 62.1%; Score 408.5; DB 4; Length 112;
Best Local Similarity 66.9%; Pred. No. 1.1e-34;
Matches 81; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

Qy 1 EVOLVKSGEGLVYKPGSLRLSCAAGFTFRRYDIHVROTQKGLWVSSISGGNYIDY 60
Db 1 EVQLVESGGGVVQPGKSLRLSCAAGFTFYDDYGMSSVRQAPGKGLWVSGINMGSTGY 60

Qy 61 ADSVKGRTISRDNANVVYLYQNSLRADMAVYFCARDGTFGSNATWRAPDIWGRGTM 120
Db 61 ADSVKGRTISRDNANVVYLYQNSLRADMAVYFCARDGTFGSNATWRAPDIWGRGTM 120

Qy 121 V 121
Db 112 V 112

RESULT 15
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBT_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 62.0%; Score 408; DB 4; Length 116;
Best Local Similarity 65.3%; Pred. No. 1.3e-34;
Matches 81; Conservative 13; Mismatches 22; Indels 8; Gaps 1;

Qy 2 VOLVKSGEGLVYKPGSLRLSCAAGFTFRRYDIHVROTQKGLWVSSISGGNYIDYA 61
Db 1 EVQLVESGGGVVQPGKSLRLSCAAGFTFSYAMHWVRQAPGKGLWAVISYDSNKKTYA 60

Qy 62 DSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARDGTFGSNATWRAPDIWGRGTM 121
Db 61 DSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARDGTFGSNATWRAPDIWGRGTM 121

Qy 122 TVSS 125
Db 113 TVSS 116

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Search completed: December 30, 2003, 11:01:09
 Job time : 31.463 secs

09UL84
ID 09UL84 PRELIMINARY; PRT; 122 AA.
AC 09UL84;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 63.9%; Score 420.5; DB 4; Length 122;
Best Local Similarity 66.1%; Pred. No. 7.1e-36;
Matches 84; Conservative 17; Mismatches 19; Indels 7; Gaps 2;

QY 1 EVOLVSGGLVPGGSLRLSCAASGTFRRYDIHWROTQPGKLEWVSSISGSGNYIDY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAASGTFRRYDIHWROTQPGKLEWVSSISGSGNYIDY 60
QY 61 ADSVKGRFTISRDNANVVYLQNSLRADMAVYFCARD--GTIFGSAATWRAFDIWRG 118
DB 61 ADSVKGRFTISRDNANVVYLQNSLRADMAVYFCARD--GTIFGSAATWRAFDIWRG 118
QY 119 TMVTWSS 125
DB 116 TLVTWSS 122

RESULT 12
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC010327; AA010327.1; -.
DR MGD; MG1:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_3.
DR

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.6%; Score 418.5; DB 11; Length 473;
Best Local Similarity 65.1%; Pred. No. 6.4e-35;
Matches 82; Conservative 14; Mismatches 21; Indels 9; Gaps 2;

QY 1 EVOLVSGGLVPGGSLRLSCAASGTFRRYDIHWROTQPGKLEWVSSISGSGNYIDY 60
DB 20 EVOLVSGGGLVPGGSLRLSCAASGTFRRYDIHWROTQPGKLEWVSSISGSGNYIDY 79
QY 61 ADSVKGRFTISRDNANVVYLQNSLRADMAVYFCARDGTIFGSAATW--RAFDIWRG 119
DB 80 ADSVKGRFTISRDNANVTIFLQWTSLSRSEDYMYCARL-----LMLRRIDYWGQGT 131
QY 120 TMVTWSS 125
DB 132 TLVTWSS 137

RESULT 13
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotypic heavy chain variable region (fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Atkin J.D., Iape A., Jennings I.G., Horaltis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AA09421.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT 119 119
SQ SEQUENCE 119 AA; 13025 MW; F6B90404381CA7C CRC64;

Query Match 63.5%; Score 418; DB 11; Length 119;
Best Local Similarity 63.6%; Pred. No. 1.2e-35;
Matches 82; Conservative 17; Mismatches 16; Indels 14; Gaps 2;

QY 1 EVOLVSGGLVPGGSLRLSCAASGTFRRYDIHWROTQPGKLEWVSSISGSGNYIDY 60
DB 1 EVOLVSGGGLVPGGSLRLSCAASGTFRRYDIHWROTQPGKLEWVSSISGSGNYIDY 60
QY 61 ADSVKGRFTISRDNANVVYLQNSLRADMAVYFCARDGTIFGSAATWRAFDI---NG 116
DB 61 ADSVKGRFTISRDNANVTIFLQWTSLSRSEDYMYCARL-----YDVGFAVNG 110
QY 117 RGTMTWSS 125
DB 111 QGTLVTWSS 119

RESULT 14
Q9HCCI

RESULT 8

Q9NSK4 PRELIMINARY; PRT; 499 AA.
 AC O9NSK4;
 DT 01-OCT-2002 (TREMblrel. 22, Created)
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Struhsberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032249; AAH32249.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-CL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IG1; 2.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;
 Query Match 65.2%; Score 428; DB 4; Length 499;
 Best Local Similarity 66.9%; Pred. No. 5.6e-36;
 Matches 85; Conservative 13; Mismatches 27; Indels 2; Gaps 1;
 QY 1 EVOLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWSSISSGGNYIDY 60
 DB 20 EVQLVESGGGVVPRGSLRLSCISGTFTDSSGASVVRQAPGKLEWSSIMNGSTYY 79
 QY 61 ADSVKGFTISRDNANNVYVLOMNSLRADMAVYFCARDGTFGSAATWRAAF-DIWGRG 118
 DB 80 ADSVKGFTISRDNANNVYVLOMNSLRVEDTALYCARDPYCKSGSGCLGYMDVWGKG 139
 QY 119 TWTYVSS 125
 DB 140 TTYVSS 146
 RESULT 9
 Q99KA4 PRELIMINARY; PRT; 487 AA.
 AC Q99KA4;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Hypothetical 52.6 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Struhsberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004786; AAH04786.1; -.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IG; 1.

DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;

Query Match 64.7%; Score 425.5; DB 11; Length 487;
 Best Local Similarity 65.4%; Pred. No. 1.2e-35;
 Matches 83; Conservative 18; Mismatches 21; Indels 5; Gaps 2;

QY 1 EVOLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWSSISSGGNYIDY 60
 DB 20 EVQLVESGGGVVPRGSLRLSCISGTFSSYAMSWVQTEKLEWATISDGSYYTY 79
 QY 61 ADSVKGFTISRDNANNVYVLOMNSLRADMAVYFCARD--GTIFGSAATWRAFDIWRG 118
 DB 80 PDNVKGRFTISRDNANNVYVLOMNSLRKSEDTAMVYCARDMGSGPYG---YSRFDYWGCG 136
 QY 119 TWTYVSS 125
 DB 137 TTYVSS 143
 RESULT 10
 Q9UL90 PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035024; AAD56260.1; -.
 DR HSSP; P01772; 2FBJ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 64.6%; Score 425; DB 4; Length 113;
 Best Local Similarity 66.4%; Pred. No. 2.2e-36;
 Matches 83; Conservative 13; Mismatches 17; Indels 12; Gaps 1;

QY 1 EVOLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWSSISSGGNYIDY 60
 DB 1 EVQLVESGGGVVPRGSLRLSCISGTFSSYGMWVQAPGKLEWVAIFRYDGSNKYY 60
 QY 61 ADSVKGFTISRDNANNVYVLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRGTM 120
 DB 61 ADSVKGFTISRDNANNVYVLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRGTM 108
 QY 121 VTYSS 125
 DB 109 VTYSS 113
 RESULT 11

```
Db 80 ADVKGRFTISRDNSTLYLQWNSLRABDTAVYCYCKADPGYASGNTREDYWGQTL 139
QY 121 VTVSS 125
Db 140 VTVSS 144

RESULT 5
Q8WU38
ID Q8WU38 PRELIMINARY; PRT; 613 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 66.6%; Score 438.5; DB 4; Length 613;
Best Local Similarity 67.4%; Pred. No. 7.5e-37;
Matches 87; Conservative 12; Mismatches 17; Indels 13; Gaps 2;

QY 1 EVOLVSGEGVLVPGGSLRLSCAASGFTPRRDIHWYRQTPGKLEWVSSISGQNYIDY 60
Db 20 QVQLVSGGCVVPGGSLRLSCAASGFTFSYGMHWYRQAPGKLEWVAISIDGSNKTY 79
QY 61 ADVKGRFTISRDNANNNVYLQWNSLRABDMVYFCARDGITFGSAATW---RAPDIWG 116
Db 80 ADVKGRFTISRDNSTLYLQWNSLRABDTAVYCYCKAD-----WSGVTETFDIWG 130
QY 117 RGTMTVTVSS 125
Db 131 QGTMTVTVSS 139

RESULT 6
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RM MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
```

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DR EMBL; AF035043; AAD56279.1; -.
DR HSP; P01772; 2F84.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;

Query Match 66.6%; Score 438; DB 4; Length 121;
Best Local Similarity 69.8%; Pred. No. 1.1e-37;
Matches 88; Conservative 11; Mismatches 21; Indels 6; Gaps 2;

QY 1 EVOLVSGEGVLVPGGSLRLSCAASGFTPRRDIHWYRQTPGKLEWVSSISGQNYIDY 60
Db 1 EVQLVSGGCVVPGGSLRLFCASGFTPDGYAMHWYRQAPGKLEWVSLISDGSGTYY 60
QY 61 ADVKGRFTISRDNANNNVYLQWNSLRABDMVYFCARDGITFGSAAT-WRAPDIWGRT 119
Db 61 ADVKGRFTISRDNSTLYLQWNSLRABDTAVYCYCKAD-----GKTTIVDRFDIWGQGT 115
QY 120 MVTVSS 125
Db 116 MVTVSS 121

RESULT 7
Q8WU38
ID Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021276; AAH21276.1; -.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 66.0%; Score 434.5; DB 4; Length 573;
Best Local Similarity 69.8%; Pred. No. 1.8e-36;
Matches 88; Conservative 11; Mismatches 24; Indels 3; Gaps 2;

QY 1 EVOLVSGEGVLVPGGSLRLSCAASGFTPRRDIHWYRQTPGKLEWVSSISGQNYIDY 60
Db 20 EVQLVSGGCVVPGGSLRLSCAASGFTPDYAMHWYRQAPGKLEWVSGISNNSGIGY 79
QY 61 ADVKGRFTISRDNANNNVYLQWNSLRABDMVYFCARDGITFGS-AATRAPDIWGRT 119
Db 80 ADVKGRFTISRDNANSTLYLQWNSLRABDTAVYCYCKAGS--GSYIGYYGMDVWGQGT 137
QY 120 MVTVSS 125
Db 138 MVTVSS 143
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QY	121	VTVSS	125
Db	137	VTVSS	141

RESULT 2	
Q9UL91	
ID	PRELIMINARY;
Q9UL91	PRT; 118 AA

DT 01-MAY-2000 (**TREMBLrel_13**, Created)
DT 01-MAY-2000 (**TREMBLrel_13**, Last sequence update)
DT 01-MAR-2003 (**TREMBLrel_23**, Last annotation update)
DE Myosin-reactive Immunoglobulin heavy chain variable region
 (**FragmenT**).
OS Homo sapiens (Human).
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NB1 Taxid=9606;
 [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Benney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus." ;
 RL Clin. Immunol. Immunopathol. 87:164-192(1998).
DR EMBL; AF035023; MAD56259.1; -.
DR HSSP; POL1772; 2PB4.
DR InterPro: IPR007110; IG-Ilike.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig_I.
DR SMART; SM00406; IgV_I.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
ET 1
SQ SEQUENCE 118 AA; 11843 MW; D0G633949FZACI49D CRC64;

Query Match	67.7%	Score	445.5	DB	4	Length	118
Best Local Similarity	74.2%	Pred.	No. 1.7e-38				
Matches	92	Conservative	16	Indels	7	Gaps	2

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QY 1 EVQLVKSGGGLVKPGGSLRLSCAASGFTFERRDYIHWRQTPGKGLEVNSSISGGANIDY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSYMWVRQAPGKGLEVNSTISSITITITYY 60
QY 61 ADSVNGRFTISRDNANNVYLIQWNSLRABDMAYVPCARDGTIFGSAATWPAPIWGRGTM 120
Db 61 ADSVNGRFTISRDNANNSLYIQWNSLRABDTAVYYCAR---GDSS--RPFIDWGQTM 113
QY 121 VTWS 124
Db 114 VTWS 117
```

RESULT 3			
096K68			
ID	096K68	PRELIMINARY;	PRT; 494 AA.
AC	096K68;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Hypothetical protein FLJ4473.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Mammary gland;		
RA	Iisogai T., Oca T., Hayashi K., Sugiyama T., Otsubi T., Suzuki Y.		
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,		

RA Maatani M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ichida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Maehno Y.,
RA Nitomiya K., Iwayanagi T.,
RT "NBD0 human cDNA sequencing the project."
RL submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027379; BAB55072.1; -
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 494 AA; 5308 MW; 9A1D7AEB5AE84C0E CRC64;
Query Match 67.1%; Score 441.5; DB 4; Length 494;
Best Local Similarity 70.4%; Pred. No. 2.8e-37;
Matches 88; Conservative 11; Mismatches 23; Indels 3; Gaps 1;

Query Match	67.1%;	Score 441.5;	DB 4;	Length 494;
Best Local Similarity	70.4%;	Pred. No. 2.6e-37;		
Matches 88;	Conservative 11;	Mismatches 23;	Indels 3;	Gaps 1;

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QY      EVQLVKGSGEGLVYPCGSISRLLSCAASGFTPRRVDIHVROTPGKGLEWVSSISGGVYIDY 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      EVQLVKGSGGGLVYPCGSISRLLSCAASGLSGSTYAAANWRCAFGKGLEWVSSISRSDIYY 79
QY      ADSVKGRAFTISRDNANNVYLLQMSLRADMDMAVFCARDGTIFGSAATRAPFDIMRGTM 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      RDSVKGRAFTISRDNANKSLYLLQMSLRVDVTIYVYICARDSC--NKAICYGSPFMOGITL 136
QY      VTVSS 125
        |||||
Db      VTVSS 141

```

RESULT 4	
Q96BB9	
ID Q96BB9	PRELIMINARY; PRT; 597 AA

DT 01-DEC-2001 (TREMBLER, 19, Created)
DT 01-DEC-2001 (TREMBLER, 19, Last sequence update)
DT 01-MAR-2003 (TREMBLER, 23, Last annotation update)
DS Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AA15760.1; -
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003065; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 557 AA; 65039 MW; 4FC3AD8CE263D9 CRC64;

Query Match	66.7%	Score 439	DB 4	Length 597
Best Local Similarity	66.4%	Pred. No. 6	5e-37	
Matches 83	Conservative 16	Mismatches 24	Indels 0	Gaps 0

```

Qy      1 ENOLVMSGGGLVYKPGGSLRLSCAASEFTRRARDIHVYRTPGGGLEWMSISSGGNYID 60
        |||:::|||||
Db      20 EVQLLESGGGLVQPGGSLRLSCAASEFSSSIAMNRRVLRPGKGLWMSVSISSGGSTYY 79
        |||:::|||||
Qy      61 ADSVKRPTISRDNNANVVYLDQWNSLRAEEDMAVYFCARDQTITFGSAATWRAPDIWGRGTW 120
        |||:::|||||

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 30.463 Seconds
(without alignments)
1058.876 Million cell updates/sec

Title: US-09-674-752-49

Perfect score: 1 EVOLVSGSGLVKPGGSLRL.....AATWAFDIMGRTMTVSS 125

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mnc:*
8: SP organelle:*
9: SP phase:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475.5	72.3	471	4	Q8TC77
2	445.5	67.1	118	4	Q9UL91
3	441.5	67.1	494	4	Q96K68
4	439	66.7	597	4	Q96BB9
5	438.5	66.6	613	4	Q8WUK1
6	438	66.6	121	4	Q9UL71
7	434.5	66.0	573	4	Q8WU38
8	429	65.2	499	4	Q8NSK4
9	425.5	64.7	113	11	Q99KA4
10	425	64.6	487	4	Q9UL90
11	420.5	63.9	122	4	Q9UL84
12	418.5	63.6	473	11	Q91205
13	418	63.5	119	11	Q92087
14	408.5	62.1	112	4	Q9HCC1
15	408	62.0	116	4	Q9UL93
16	407	61.9	493	4	Q8NCL6

17	406.5	61.8	147	4	Q9Y509
18	402.5	61.2	118	4	Q9UL72
19	392	59.6	479	11	Q91WPS
20	383	58.2	131	4	Q9UL88
21	382	58.1	486	11	Q91207
22	380.5	57.8	469	11	Q8R3V9
23	379	57.6	480	11	Q91XE1
24	363.5	55.2	457	11	Q9R1A4
25	362	55.0	521	4	Q8N4Y9
26	360.5	54.8	124	6	Q9N0M4
27	360	54.7	95	4	Q9ULB6
28	357.5	54.3	124	6	Q9N0M6
29	357.5	54.3	288	11	Q90YF0
30	356.5	54.2	484	11	Q8VEA0
31	352	53.5	104	4	Q9UL87
32	350	53.2	112	4	Q9UGP3
33	348.5	53.0	124	4	Q9UL92
34	342	52.0	125	4	Q9UL95
35	328.5	49.9	159	4	Q96QSO
36	324	49.2	142	11	Q924Q1
37	320	48.6	473	11	Q9D8L4
38	318	48.3	614	4	Q96GA6
39	316	48.0	119	4	Q9UL94
40	315	47.9	481	11	Q91WT1
41	314	47.7	147	11	Q925S3
42	314	47.7	497	4	Q8WY24
43	313.5	47.6	613	11	Q8VCX7
44	313	47.6	168	11	Q8VDC9
45	309	47.0	117	11	Q9QXE9

ALIGNMENTS

RESULT 1

ID Q8TC77 PRELIMINARY; PRT; 471 AA.

AC Q8TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC024289; AAI24289.1; -
DR InterPro: IPR007110; IG_1ike.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 4.
DR SMART: SM00406; IG; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PSS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 72.3%; Score 475.5; DB 4; Length 471;
Best Local Similarity 74.4%; Pred. No. 7.9e-41;
Matches 93; Conservative 11; Mismatches 18; Indels 3; Gaps 1;

Qy	1	EVOLVSGSGLVKPGGSLRLSCAAGTFRRIYHWRQTPGKGLGVSSISGANYDY 60
Db	20	EVOLVSGSGLVKPGGSLRLSCAAGTFRFSSYNNWYRQAPGKGLGVSSSSSYIYY 79
Qy	61	ADVYKGRFTISRNNANVVYLVQNSLRAPDMAYVFCARQDTIGSATWTRAPDIWGRGT 120
Db	80	ADVYKGRFTISRNNANVVYLVQNSLRAPDMAYVFCARQDTIGSATWTRAPDIWGRGT 136

FT NON TER 114 114
SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4B13C4 CRC64;

Query Match 57.7%; Score 379.5; DB 1; Length 114;
Best Local Similarity 61.6%; Pred. No. 1.7e-32;

Matches 77; Conservative 15; Mismatches 22; Indels 11; Gaps 2;

QY 1 EVQLVKGSGEGLVYPGSGLRSLSCAAGFTRRYDIHMYROTPEGKLEWVSSISSGNYIDY 60

DB 1 EVQLVSGGDLVYPGSGLRSLSCVAGITPFGYDMQWROAPGKGLQKVAYFNDALSAQGY 60

QY 61 ADSVKGRTISRDNANNVYLLQNNSLRADMAVYFCARDGTIFGSAATWRAPFDINGRTM 120

DB 61 ADVKGRFTISRDNNAKDSLYLQNNSLRADTAVYYC-----APWQ-FEYWGQGITL 109

QY 121 VTSS 125

DB 110 VTSS 114

Search completed: December 30, 2003, 10:55:54
Job time : 7.70187 secs

DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region: Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; B826733FLA3CB0F1 CRC64;
 Query Match 58.4%; Score 384; DB 1; Length 117;
 Best Local Similarity 74.5%; Pred. No. 6e-33;
 Matches 73; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 EVQLVSGEGLVPGGSLRLISCAASGFTPRRDYDHWROTPGKLEWVSISGCAITYD 60
 DB 20 EVQLVSGGGLVPGGSLRLISCAASGFTFSYAMSWRAQPKGLEWVAISGGSTYY 79
 QY 61 ADSVKGFTISRDNANVLYQNNSLRAEDMAYVFCAR 98
 DB 80 GDSVKGFTISRDNANVLYQNNSLRAEDMAYVFCAR 117
 RESULT 14
 HV20_MOUSE STANDARD; PRT; 122 AA.
 ID HV20_MOUSE
 AC P01759;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region M603.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80199926; PubMed=6769593;
 RA Early P., Huang H., Davis M., Calame K., Hood L.;
 RT "An immunoglobulin heavy chain variable region gene is generated from
 three segments of DNA: VH, D and JH.";
 RL Cell 19:981-992(1980).
 RN [2]
 RP SEQUENCE OF 1-120.
 RX MEDLINE=75017346; PubMed=4213527;
 RA Rudikoff S., Potter M.;
 RT "Variable region sequence of the heavy chain from a phosphorylcholine
 binding myeloma protein.";
 RL Biochemistry 13:4033-4038(1974).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=75065510; PubMed=4530984;
 RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
 RA Davies D.R.;
 RT "The three-dimensional structure of a phosphorylcholine-binding mouse
 immunoglobulin Fab and the nature of the antigen binding site.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS PHOSPHORYLCHOLINE.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: B90795; AVMS63.
 DR PDB: 1MCP; 15-JUL-92.
 DR PDB: 2MCP; 15-JUL-92.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; 3D-structure.
 KW DOMAIN 1 121 IG-LIKE.

FT SITE 33 33 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
 FT SITE 52 52 PHORYLCHOLINE.
 FT STRAND 3 7 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
 FT STRAND 11 12 PHORYLCHOLINE.
 FT STRAND 14 15
 FT STRAND 17 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 50
 FT TURN 54 55
 FT STRAND 61 61
 FT TURN 64 69
 FT STRAND 70 75
 FT TURN 76 79
 FT STRAND 80 86
 FT HELIX 90 92
 FT STRAND 94 103
 FT STRAND 107 112
 FT STRAND 116 120
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;
 Query Match 58.1%; Score 382.5; DB 1; Length 122;
 Best Local Similarity 59.8%; Pred. No. 8.9e-33;
 Matches 76; Conservative 22; Mismatches 22; Indels 7; Gaps 4;
 QY 1 EVQLVSGEGLVPGGSLRLISCAASGFTPRRDYDHWROTPGKLEWVSISGCA--YI 58
 DB 1 EVQLVSGGGLVPGGSLRLISCAASGFTFSDFYEMWRAQPKGLEWVAISGGKYYT 60
 QY 59 DYADSVKGFTISRDNANVLYQNNSLRAEDMAYVFCARDGTFSSAATWRAFDIWRG 118
 DB 61 EYASVKGFTISRDNANVLYQNNSLRAEDMAYVFCARN--YGS--TW--YFDWAGAG 115
 QY 119 TWYTVSS 125
 DB 116 TWYTVSS 122
 RESULT 15
 HV01_CANPA STANDARD; PRT; 114 AA.
 ID HV01_CANPA
 AC P01754;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region GOM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242268; PubMed=407924;
 RA Wasserman R.L., Capra J.D.;
 RT "Primary structure of the variable regions of two canine
 immunoglobulin heavy chains.";
 RL Biochemistry 16:3160-3168(1977).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02067; AYDCGM.
 DR HSSP: P01772; 2FB4.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 112 IG-LIKE.

```

DT 21-JUL-1986 (Rel. 01, Last Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BJT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IGA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; AZHUBU.
DR HSSP: P01789; 1MCP.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;

Query Match 58.8%; Score 387; DB 1; Length 115;
Best Local Similarity 62.4%; Pred. No. 2,9e-33;
Matches 78; Conservative 16; Mismatches 21; Indels 10; Gaps 2;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTPRRDIMRWQTPKGLKLEWVSSISGCVYIDY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTVSHSWRQAPGKALZVWSAIVGGITY-Y 59
QY 61 ADSVKGRTISRDNNVYVLTQNSLRADMAVYFCARCDGTIGSATWRAFDIWRGTM 120
DB 60 ADSVKGRTISRDNSRRTVLTQNSLRADDTAVYICARSPVLDWGLYVYGGSS-----LAARLFGKGT 110
QY 121 VTWSS 125
DB 111 VTWSS 115

RESULT 12
HV3E HUMAN STANDARD; PRT; 120 AA.
ID P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
RT individual patient. II. The complete amino acid sequence of the VH
RT region of the IgM paraprotein.";
RL Immunohistochemistry 13:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM

```

```

CC TYPE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02049; M3HUBW.
DR HSSP: P01772; 2P84.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2BE410 CRC64;

Query Match 58.8%; Score 387; DB 1; Length 120;
Best Local Similarity 61.2%; Pred. No. 3e-33;
Matches 79; Conservative 18; Mismatches 14; Indels 18; Gaps 4;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTPRRDIMRWQTPKGLKLEWVSSISGCVYIDY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYNNMVRQVTSKGLKLEWVAIGTAGDQY-Y 59
QY 61 ADSVKGRTISRDNNVYVLTQNSLRADMAVYFCAR-----DGTI---FGSATWRA 111
DB 60 ADSVKGRTISRDNSRRTVLTQNSLRADDTAVYICARSPVLDWGLYVYGGSS----- 113
QY 112 PDWGRGTM 120
DB 114 --VWGQGT 120

RESULT 13
HV3C HUMAN STANDARD; PRT; 117 AA.
ID P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=8101090; PubMed=6450418;
RA Matthyseens G., Rablitz T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00236; AAA53516.1; --
CC EMBL: M35415; AAA58735.1; --
CC PIR: A02047; H3HUB26.
CC PDB: 1HOU; 23-DEC-99.
CC Genew: HGNC:5545; IGHV@.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.

```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hillemann N.;
RT "Three-dimensional structure determination of antibodies. Primary
  structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguerat M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
  immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
  and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_MHC.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Ig_v_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126
SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;
Query Match 60.1%; Score 395.5; DB 1; Length 126;
Best Local Similarity 63.5%; Pred. No. 4.2e-34;
Matches 80; Conservative 17; Mismatches 28; Indels 1; Gaps 1;
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QY 120 MVTYSS 125
Db 121 PVTYSS 126
RESULT 10
HV3U HUMAN STANDARD; PRT; 120 AA.
ID HV3U HUMAN
AC P01782;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V-II1 region DOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80020921; PubMed=114209;
RA Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT "Amino acid sequence of the heavy-chain variable region of the
  crystallizable human myeloma protein Dob.";
RL Biochemistry 18:4068-4080(1979).
RN [2]
RP CRYSTALLIZATION.
RX MEDLINE=80020920; PubMed=114208;
RA Steiner L.A., Lopes A.D.;
RT "The crystallizable human myeloma protein Dob has a hinge-region
  deletion.";
RL Biochemistry 18:4054-4067(1979).
CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
  HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
  DISULFIDE BONDS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90431; GHUDB.
DR HSBP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_MHC.
DR Pfam; PF00047; Ig_v_1.
DR SMART; SM00406; Ig_v_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;
Query Match 59.7%; Score 392.5; DB 1; Length 120;
Best Local Similarity 63.2%; Pred. No. 8.1e-34;
Matches 79; Conservative 15; Mismatches 26; Indels 5; Gaps 3;
```


RT "The rule of antibody structure. The primary structure of a
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). II. The
 RT cytochrome peptides of the H-chain, alignment of the tryptic
 RT peptides and discussion of the complete structure."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
 RP DISULFIDE BOND.
 CC MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hlischmann N.;
 RX Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A91668; GIHUNI.
 DR HSSP: P01772; 2FB4.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT MOD_RES 1 112 IG-LIKE.
 FT DISULFID 22 96 PYROLIIDONE CARBOXYLIC ACID.
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13242 MW; C96935AGE5SE165B CRC64;
 Query Match 61.2%; Score 403; DB 1; Length 119;
 Best Local Similarity 63.8%; Pred. No. 6; Ce-35;
 Matches 81; Conservative 15; Mismatches 21; Indels 10; Gaps 2;
 QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRIYDIHWROTGKGLWVSSISGNYIDY 60
 ID HV3B_HUMAN STANDARD; PRT; 114 AA.
 AC P01763;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region WEA.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=63273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated
 RT galactose in Klebsiella polysaccharides K30 and K33."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02046; M3HWE.
 DR HSSP: P01772; 2FB4.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT MOD_RES 1 112 IG-LIKE.
 FT NON_TER 114 114 PYROLIIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;
 Query Match 60.9%; Score 400.5; DB 1; Length 114;
 Best Local Similarity 64.0%; Pred. No. 1; Ce-34;
 Matches 80; Conservative 16; Mismatches 18; Indels 11; Gaps 2;
 QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRIYDIHWROTGKGLWVSSISGNYIDY 60
 ID HV3B_HUMAN STANDARD; PRT; 121 AA.
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region HIL.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT Amino acid sequence of the VH region of human myeloma
 RT cytoimmunoglobulin IgG H11."
 RL Biochemistry 18:553-560 (1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02054; GIHUL.
 DR HSSP: P01772; 2FB4.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT MOD_RES 1 112 IG-LIKE.
 FT NON_TER 1 1 PYROLIIDONE CARBOXYLIC ACID.

RESULT 2

HV16_MOUSE STANDARD; PRT; 136 AA.
 ID HV16_MOUSE
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPD family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 RN (2)
 RP SEQUENCE OF 17-136.
 RX MEDLINE=77100368; PubMed=401950;
 RA Adegungbo K., Milstein C., Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants.";
 RL Nature 265:299-304(1977).
 CC -----
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 CC -----
 DR EMBL: J00522; AAD15290.1; -;
 DR PIR: E90809; GIMS21.
 DR PDB: 1IGC; 03-JUN-95.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal; 3D-structure.
 KM IMMUNOGLOBULIN V region; Signal; 3D-structure.
 FT NON_TER 1 1
 FT SIGNAL <1 16
 FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
 FT DOMAIN 115 119 D SEGMENT.
 FT DOMAIN 120 136 JH4 SEGMENT.
 FT DISULFID 38 112
 FT CONFLICT 75 78
 FT CONFLICT 89 90
 FT CONFLICT 115 115
 FT CONFLICT 120 120
 FT NON_TER 136 136
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 62.1%; Score 408.5; DB 1; Length 136;
 Best Local Similarity 63.2%; Pred. No. 2,1e-35;
 Matches 79; Conservative 17; Mismatches 24; Indels 5; Gaps 1;
 QY 1 EVOLVSGEGVLKPGGSLRLSCAASGFTPRRDYIMHWROTQPGKLEWVSSISGGNYIDY 60
 DB 17 DVALVESGGGLVPGGSRKLSCAASGFTPSFGMHWKQAPKGLKLVAVIISGSSITLHY 76
 QY 61 ADSVKGRTTISRDNANNVYVLQNSLRRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGTM 120
 DB 77 ADTVKGRFTISRDNANNVYVLQNSLRRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGTM 120
 QY 121 VTVSS 125
 DB 132 VTVSS 136

RESULT 3

HV3H_HUMAN STANDARD; PRT; 122 AA.
 ID HV3H_HUMAN
 AC P01769;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region GA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam F.W.;
 RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
 RL Biochemistry 13:2482-2498(1974).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02052; M3HUGA.
 DR HSBP; P01772; 2PB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region; Pyrolysine carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 112 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959B84100A CRC64;

Query Match 61.8%; Score 406.5; DB 1; Length 122;
 Best Local Similarity 61.6%; Pred. No. 2,9e-35;
 Matches 77; Conservative 19; Mismatches 26; Indels 3; Gaps 1;
 QY 1 EVOLVSGEGVLKPGGSLRLSCAASGFTPRRDYIMHWROTQPGKLEWVSSISGGNYIDY 60
 DB 1 QVZLVZSSGGAVZPGRSLRLSCAASGFTPSFGMHWKQAPKGLZMLSVISYGBBZYY 60
 QY 61 ADSVKGRTTISRDNANNVYVLQNSLRRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGTM 120
 DB 61 AASVKGRTTISRDNANNVYVLQNSLRRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGTM 117
 QY 121 VTVSS 125
 DB 118 VTVSS 122
 RESULT 4
 HV3I_HUMAN STANDARD; PRT; 119 AA.
 ID HV3I_HUMAN
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region NIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponetling H., Hilschmann N.;

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.70187 Seconds

(Without alignments)
877.119 Million cell updates/sec

Title: US-09-674-752-49

Perfect score: 658
Sequence: 1 EVQLVKGSGGLVKGSSLR.....AATWPAFDIWRGCTWTVSS 125Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	438.5	66.6	122	1	HV3G_HUMAN
2	408.5	62.1	136	1	HV16_MOUSE
3	406.5	61.8	122	1	HV3H_HUMAN
4	403	61.2	119	1	HV3I_HUMAN
5	400.5	60.9	114	1	HV3B_HUMAN
6	400	60.8	121	1	HV3J_HUMAN
7	398.5	60.6	122	1	HV3A_HUMAN
8	397.5	60.4	116	1	HV3T_HUMAN
9	395.5	60.1	126	1	HV3U_HUMAN
10	392.5	59.7	120	1	HV3V_HUMAN
11	387	58.8	115	1	HV3F_HUMAN
12	387	58.8	120	1	HV3E_HUMAN
13	384	58.4	117	1	HV3C_HUMAN
14	382.5	58.1	122	1	HV20_MOUSE
15	379.5	57.7	114	1	HV01_CANPA
16	379	57.6	98	1	HV57_MOUSE
17	377	57.3	123	1	HV18_MOUSE
18	376.5	57.2	119	1	HV38_MOUSE
19	375	57.0	117	1	HV58_MOUSE
20	374	56.8	115	1	HV3D_HUMAN
21	374	56.8	123	1	HV23_MOUSE
22	373.5	56.8	97	1	HV56_MOUSE
23	373	56.7	123	1	HV19_MOUSE
24	372.5	56.6	122	1	HV21_MOUSE
25	372	56.5	117	1	HV55_MOUSE
26	371	56.4	123	1	HV23_MOUSE
27	370	56.2	123	1	HV22_MOUSE
28	370	56.2	144	1	HV26_MOUSE
29	369.5	56.1	116	1	HV05_CARAU
30	369	56.1	123	1	HV24_MOUSE
31	367	55.8	117	1	HV02_CANPA
32	362.5	55.1	119	1	HV37_MOUSE
33	362	55.0	117	1	HV17_MOUSE

34	360.5	54.8	119	1	HV3N_HUMAN
35	359.5	54.6	119	1	HV3P_HUMAN
36	359	54.6	119	1	HV3L_HUMAN
37	358.5	54.5	119	1	HV3M_HUMAN
38	358	54.4	116	1	HV3R_HUMAN
39	356	54.1	117	1	HV54_MOUSE
40	356	54.1	118	1	HV39_MOUSE
41	355	54.0	115	1	HV32_MOUSE
42	355	54.0	117	1	HV59_MOUSE
43	355	54.0	142	1	HV01_RAT
44	353	53.6	113	1	HV30_MOUSE
45	351.5	53.4	111	1	HV35_MOUSE

ALIGNMENTS

RESULT 1

ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region CAM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=61013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; MJHUM.
DR HSSP; P01772; 2F84.
DR GO; GO:000576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT MOD_RBS 1 112
FT DOMAIN 1 112
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252PIC2 CRC64;

Query Match 66.6%; Score 438.5; DB 1; Length 122;
Best Local Similarity 65.6%; Pred. No. 1.4e-38;
Matches 82; Conservative 21; Mismatches 19; Indels 3; Gaps 1;

QY	1	EVQLVKGSGGLVKGSSLRISCAAGFTFRKDYIHWRQTGKGLGVSSISGGNYIDY 60
DB	1	QVELVSSGGVAVZPGRSLRISCAAGFTFSNYAMHVRQPPGKGLGVAVISYBGBKYY 60
QY	61	ADSVKGRFTISRNNKPVYVLTQNSLRPEDMAYFPCARDCTTIGSAATRAPDIMGRTM 120
DB	61	ABSVDKRFITSRDSSKRTYLQNSLRABSTAVYCARDPVLYG--YRPFYKQGTLL 117
QY	121	VTVSS 125
DB	118	VTVSS 122

Query Match 68.1%; Score 448; DB 2; Length 119;
 Best Local Similarity 69.6%; Pred. No. 1e-34;
 Matches 87; Conservative 13; Mismatches 19; Indels 6; Gaps 1;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWVROTPGKLEWVSSISGSGNYIDY 60
 DB 1 EVOLVSGGGVLPFGSLRLSCAASGFTFSSYMSWVRQAPGKLEWVSISSGSGSTYY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAPDIMGRTM 120
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCADKRLTGT-----FDYWGQGTIL 114

QY 121 VTVSS 125
 DB 115 VTVSS 119

RESULT 11

Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31116
 R/Motif: F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
 A/Reference number: S31104; MUID:92111633; PMID:1730252
 A/Accession: S31116
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-118 <RBA>
 A/Cross-references: EMBL:X62966
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 447.5; DB 2; Length 118;
 Best Local Similarity 72.0%; Pred. No. 1.e-34;
 Matches 90; Conservative 11; Mismatches 17; Indels 7; Gaps 2;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWVROTPGKLEWVSSISGSGNYIDY 60
 DB 1 QVOLVSGGGVLPFGSLRLSCAASGFTSSYGMWVRQAPGKLEWVSISSGSGNKRY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAPDIMGRTM 120
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCADG---GKA---AFDIMGQGTM 113

QY 121 VTVSS 125
 DB 114 VTVSS 118

RESULT 12

Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
 C/Accession: S30532
 R/Motif: X
 submitted to the EMBL Data Library, October 1992
 A/Reference number: S30520
 A/Accession: S30532
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-123 <MAR>
 A/Cross-references: EMBL:Z18318
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 447; DB 2; Length 123;
 Best Local Similarity 72.2%; Pred. No. 1.3e-34;
 Matches 91; Conservative 10; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWVROTPGKLEWVSSISGSGNYIDY 60
 DB 1 EVOLVSGGGVLPFGSLRLSCAASGFTFDYAMHWVRQAPGKLEWVSISSGSGTILGY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAPDIMGRTM 119
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCADKRLTGT-----FDYWGQGTIL 117

QY 120 VTVSS 125
 DB 118 VTVSS 123

RESULT 13

Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C/Accession: S26786
 R/Motif: F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
 Eur. J. Immunol. 22, 241-245, 1992
 A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam
 A/Reference number: S26786; MUID:92111632; PMID:1730251
 A/Accession: S26786
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-128 <MOR>
 A/Cross-references: EMBL:X61014; NID:932800; PIDN:CA443348.1; PID:91335129
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 446.5; DB 2; Length 128;
 Best Local Similarity 69.5%; Pred. No. 1.5e-34;
 Matches 91; Conservative 11; Mismatches 20; Indels 9; Gaps 3;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWVROTPGKLEWVSSISGSGNYIDY 60
 DB 1 QVOLVSGGGVLPFGSLRLSCAASGFTFDYMSWVRQAPGKLEWVSISSGSGSTNY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAPDIMGRTM 114
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCAR-GLYCSSTSCYIMSNM--FDP 117

QY 115 WGRGTMTVSS 125
 DB 118 WGRGTMTVSS 128

RESULT 14

Ig heavy chain V region (W4) - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C/Accession: G36005
 R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A/Reference number: A36005; MUID:90349571; PMID:2117273
 A/Accession: G36005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-121 <SCH>
 A/Cross-references: GB:M34031
 C/Genetic8:
 A/Gene: GDB:IGH; IGHDI1
 A/Cross-references: GDB:118731; OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 68.5%; Score 451; DB 2; Length 125;
Best Local Similarity 71.2%; Pred. No. 5,7e-35;
Matches 89; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVSSISGGNYIDY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVSSISGGSTIYY 60
QY 61 ADSVKGRTTISRDNANNVYVLTQNSLRADMAVYFCARDGTFGSAATWRAFDIWRGTM 120
DB 61 ADSVKGRTTISRDNANKSLYLQNSLRADTAIVYCASSRNYSGGYSHYFDYWGQGTLL 120
QY 121 VTWSS 125
DB 121 VTWSS 125

RESULT 7

S31105
Ig heavy chain (subclass IgM) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C/Accession: S31105
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31105
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-118 <RMA>
A/Cross-references: EMBL:X63081; NID:932648; PIDN:CAA44803.1; PID:932649
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.3%; Score 449.5; DB 2; Length 118;
Best Local Similarity 73.6%; Pred. No. 7,4e-35;
Matches 92; Conservative 9; Mismatches 17; Indels 7; Gaps 2;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVSSISGGNYIDY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMHWVROAPGKLEWVSSISGGSTIYY 60
QY 61 ADSVKGRTTISRDNANNVYVLTQNSLRADMAVYFCARDGTFGSAATWRAFDIWRGTM 120
DB 61 ADSVKGRTTISRDNANKSLYLQNSLRADTAIVYCA--GQLGDD----AFDIWGQGTM 113
QY 121 VTWSS 125
DB 114 VTWSS 118

RESULT 8

S31104
Ig heavy chain (subclass IgM) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C/Accession: S31104
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31104
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-121 <RMA>
A/Cross-references: EMBL:X63080; NID:932646; PIDN:CAA44802.1; PID:932647
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 449; DB 2; Length 121;
Best Local Similarity 72.8%; Pred. No. 8,4e-35;
Matches 91; Conservative 10; Mismatches 20; Indels 4; Gaps 3;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVSSISGGNYIDY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPDYAMHWVROAPGKLEWVSGISNNSGSIY 60
QY 61 ADSVKGRTTISRDNANNVYVLTQNSLRADMAVYFCARDGTFGSAATWRAFDIWRGTM 120
DB 61 ADSVKGRTTISRDNANKSLYLQNSLRADTAIVYCAKD--VFWGSG--W-YFDLWGRGTL 116
QY 121 VTWSS 125
DB 117 VTWSS 121

RESULT 9

S31595
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31595
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31595
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <CUI>
A/Cross-references: EMBL:Z14171; NID:931007; PIDN:CAA78540.1; PID:931008
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:23-106/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 448.5; DB 2; Length 128;
Best Local Similarity 72.0%; Pred. No. 1e-34;
Matches 90; Conservative 9; Mismatches 21; Indels 5; Gaps 1;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVSSISGGNYIDY 60
DB 9 EVQLVESGGGLVQPGGSLRLSCAASGFTPDYAMHWVROAPGKLEWVSGISNNSGSIY 68
QY 61 ADSVKGRTTISRDNANNVYVLTQNSLRADMAVYFCARDGTFGSAATWRAFDIWRGTM 120
DB 69 ADSVKGRTTISRDNANKSLYLQNSLRADTAIVYCAKD----ARGDHDAFDIWRGQGTM 123
QY 121 VTWSS 125
DB 124 VTWSS 128

RESULT 10

S31108
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31108
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31108
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RMA>
A/Cross-references: EMBL:X62956
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 11.9821 Seconds

(Without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-49

Sequence: 1 EVQLVKGSGGLVPGGSLRL...AATWPAFDIMGRGTMVTS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475.5	72.3	141	2	S31669 Ig heavy chain V r
2	467.5	71.0	128	2	S26790 Ig heavy chain V r
3	454	69.0	143	2	S23624 Ig heavy chain V r
4	452.5	68.8	145	2	S11239 Ig heavy chain V r
5	452	68.7	117	2	S34012 Ig heavy chain V r
6	451	68.5	125	2	S30531 Ig heavy chain V r
7	449.5	68.3	118	2	S31105 Ig heavy chain V r
8	449	68.2	121	2	S31104 Ig heavy chain (su
9	448.5	68.2	128	2	S31595 Ig heavy chain (su
10	448	68.1	119	2	S31108 Ig heavy chain V r
11	447.5	68.0	118	2	S31116 Ig heavy chain - h
12	447	67.9	123	2	S30532 Ig heavy chain V r
13	446.5	67.9	128	2	S26786 Ig heavy chain V r
14	446	67.8	121	2	G36005 Ig heavy chain V r
15	445	67.6	119	2	G36005 Ig heavy chain V r
16	445	67.6	127	2	S19878 Ig heavy chain V r
17	445	67.6	130	2	I37783 Ig heavy chain V r
18	444	67.5	138	2	S31666 Ig variable region
19	442.5	67.2	136	2	S31587 Ig heavy chain V r
20	442	67.2	121	2	S31118 Ig heavy chain - h
21	441.5	67.1	140	2	S70442 Ig heavy chain pre
22	441	67.0	119	2	S31107 Ig heavy chain - h
23	440.5	66.9	114	2	S31120 Ig heavy chain - h
24	440.5	66.9	122	2	S31117 Ig heavy chain - h
25	440	66.9	119	2	F36005 Ig heavy chain V r
26	440	66.9	121	2	S19666 Ig heavy chain V r
27	438.5	66.6	122	1	M3HUM Ig heavy chain V-I
28	438.5	66.6	124	2	S20782 Ig heavy chain V r
29	438	66.6	120	2	S36273 Ig heavy chain V r

30	438	66.6	123	2	S26794 Ig heavy chain V r
31	437.5	66.5	120	2	S48798 Ig heavy chain V r
32	437	66.4	123	2	S31114 Ig heavy chain - h
33	436.5	66.3	122	2	S20772 Ig heavy chain V r
34	436.5	66.3	147	2	I37780 Ig variable region
35	436	66.3	127	2	S38489 Ig heavy chain - h
36	436	66.3	134	2	S31699 Ig heavy chain V r
37	435	66.1	117	2	S78486 Ig heavy chain V r
38	435	66.1	140	2	S31686 Ig heavy chain V r
39	434	66.0	140	2	S31588 Ig heavy chain V r
40	433	65.8	139	2	I37781 Ig heavy chain V r
41	431.5	65.6	110	2	PH1652 Ig variable region
42	431.5	65.6	122	2	G36005 Ig heavy chain V r
43	431	65.5	119	2	D36005 Ig heavy chain V r
44	429	65.2	135	2	S31598 Ig heavy chain V r
45	428.5	65.1	114	2	S46390 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S31669 Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_reviseion 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31669

R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31669

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-141 <CUI>

A/Cross-references: EMBL:Z14212; NID:g30959; PIND:CA478581.1; PID:g30960

C/Suprafamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

P/34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.3% Score 475.5; DB 2; Length 141;

Best Local Similarity 75.2% Pred. No. 3.4e-37;

Matches 94; Conservative 9; Mismatches 19; Indels 3; Gaps 1;

Qy 1 EVQLVKGSGGLVPGGSLRLCAASGFTPRRDYIMHWROTGPKGLEWVSISGNYIDY 60

RESULT 2

S26790 Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_reviseion 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26790

R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam

A/Reference number: S26786; MUID:92111632; PMID:1730251

A/Accession: S26790

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <MOR>

A/Cross-references: EMBL:X61013; NID:g32798; PIND:CA443347.1; PID:g1353128

C/Suprafamily: Immunoglobulin V region; immunoglobulin homology

Tue Dec 30 11:49:11 2003

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Page 7

Search completed: December 30, 2003, 11:05:35
Job time : 12.2685 secs

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-20

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Query Match	76.8%;	Score 477.5;	DB 3;	Length 125;
Best Local Similarity	74.2%;	Pred. No. 2.3e-40;		
Matches 95;	Conservative 10;	Mismatches 12;	Indels 11;	Gaps 24

Qy	1	EVQLVDSGGGLVPGKSRILRLSCVDSGLTSSSGHMTWAOAPAGLEWAVISYNGDKRY	60
Db	1	EVQLTSSGGGVVPGKSRILRLSCVSGFTFNNTGHHMTWAOAGKLEWAVIWMFGSNKY	60
Qy	61	ADSVKRFAPISRNAAKNTLYLQMSLTIEDTAVYCAKDLIESNA-----EALMGQ	112
Db	61	ADSVKRFITSRNKSQITLYLQMSLRADEDIAYITCAR---ENQIKMSRLRYTFYDYGQ	117
Qy	113	GLTLYTVSS	120
Db	118	GLTLYTVSS	125

RESULT 13
US-09-240-274-21
; Sequence 21, Application US/09240274

? PATENT NO. 6255455
 ? GENERAL INFORMATION:
 ? APPLICANT: Siegel, Donald L.
 ? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
 ? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 ? FILE REFERENCE: 09596-4202
 ? CURRENT APPLICATION NUMBER: US/09/240,274

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? SEQ ID NO 21
? LENGTH: 125
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) chain Di6
US-09-240-274-21

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Query Match	76.8%;	Score 477.5;	DB 3;	Length 125;
Best Local Similarity	74.2%;	Pred. No. 2.3e-40;		
Matches 95;	Conservative 10;	Mismatches 12;	Indels 11;	Gaps 2;

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QY      1 EVOLVSSGGGLVQPGSLSTLSCVDSGLTFSSVGMHMYQAQAGAGLEWAVSYXYGNDKXY 60
Db      1 EVQLTSSGGGVQVQPGSLSTLSCVSGFLPNNGMHMYQAQAGKLEWAVYIMFGSNKXY 60
QY      61 ADSVKRFRPISRDNAKLTLYLQMSLTETDEPTAVRYCAADLTESNIA-----EALMGQ 112
Db      61 ADSVKRFRFIISRDNSKNTLYLQMSLSRAEDTAIVYICAR--ENQIKLSRYLYFDYMGQ 117
QY      113 GILATVSS 120
Db      118 GILATVSS 125

```

RESULT 14
US-09-240-274-22
; Sequence 22, Application US/09240274

;
 ; PATENT NO. 455455
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Siegel, Donald L.
 ;
 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL.
 ;
 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 ;
 ; FILE REFERENCE: 09596-4202

```

: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/081,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 22
: LENGTH: 125
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-22

```

Query Match	76.8%;	Score 477.5;	DB 3;	Length 125;
Best Local Similarity	74.2%;	Pred. No. 2.3e-40;		
Matches 95;	Conservative 10;	Mismatches 12;	Indels 11;	Gaps 2

[illegible]

RESULT 15
US-09-240-274-24
; Sequence 24, Application US/09240274

? Patent NO. 6,255,455
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: Siegel, Donald L.
 ? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLULATED BLOOD
 ? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 ? FILE REFERENCE: 09596-4202
 ? CURRENT APPLICATION NUMBER: US/09/240,274

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? SEQ ID NO 24
? LENGTH: 125
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) chain D200
US-09-240-274-24

```

Query Match	76.1%;	Score 473.5;	DB 3;	Length 125;
Best Local Similarity	73.6%;	Pred. No. 5.6e-40;		
Matches 92;	Conservative 11;	Mismatches 17;	Indels 5;	Gaps 1

QY 1 EVQVYESGGGLVQPRSLRLSCVDSGLTFSSYGMHWNRQAPAGALEWNAVISYDGNKTY 60
Db 1 EVQLLESGGGVVQPRSLRLSCAASGFPSTYGMHWNRQAPGKLEWNAVIWPGSGNKEY 60			
QY 61 AASVYGRFPIASPDNAKNTLYLQMSLTIEDPAVYVCAKDLIESNI-----AELMGQGTLL 115			
Db 61 AASVYGRFPIISHDNSKNTLYLQMSLTIRADPAVYVCAAREVWGVILMSRKFDPYGGTLL 120			
QY 116 VTIVSS 120			
Db 121 VTIVSS 125			

GENERAL INFORMATION:
APPLICANT: Thompson, Julia E
APPLICANT: Lemhard, Simon N
APPLICANT: Wilton, Alison J
APPLICANT: Braddock, Peta SH
APPLICANT: Du Fou, Sarah L
APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for TGFbeta1
FILE REFERENCE: 28111/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,983
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-198A-4

Query Match 76.9%; Score 478.5; DB 4; Length 123;
Best Local Similarity 78.0%; Pred. No. 1.8e-40;
Matches 96; Conservative 5; Mismatches 19; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60
DB 1 EVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60
QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIEDTAVYVYCAKDLESNI---AELMCGGLTYT 117
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYVYCAKGTGEYSGYDTPDYSGGTTVT 120
QY 118 VSS 120
DB 121 VSS 123

RESULT 10
US-09-560-198A-10
Sequence 10, Application US/09560198A
Patent No. 6492497
GENERAL INFORMATION:
APPLICANT: Thompson, Julia E
APPLICANT: Lemhard, Simon N
APPLICANT: Wilton, Alison J
APPLICANT: Braddock, Peta SH
APPLICANT: Du Fou, Sarah L
APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for TGFbeta1
FILE REFERENCE: 28111/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,983
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-198A-10

Query Match 76.8%; Score 477.5; DB 4; Length 123;
Best Local Similarity 78.0%; Pred. No. 2.2e-40;
Matches 96; Conservative 5; Mismatches 19; Indels 3; Gaps 1;
QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60
DB 1 EVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60

DB 1 QVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60
QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIEDTAVYVYCAKDLESNI---AELMCGGLTYT 117
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYVYCAKGTGEYSGYDTPDYSGGTTVT 120
QY 118 VSS 120
DB 121 VSS 123

RESULT 11
US-09-240-274-8
Sequence 8, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D01
US-09-240-274-8

Query Match 76.8%; Score 477.5; DB 3; Length 125;
Best Local Similarity 74.2%; Pred. No. 2.3e-40;
Matches 95; Conservative 10; Mismatches 12; Indels 11; Gaps 2;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60
DB 1 EVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60
QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIEDTAVYVYCAKDLESNI-----BALMCO 112
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYVYCAKGTGEYSGYDTPDYSGGTTVT 117
QY 113 GTLVTVSS 120
DB 118 GTLVTVSS 125

RESULT 12
US-09-240-274-20
Sequence 20, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 125
TYPE: PRT

FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1 CL VH region"
US-09-227-693-46

Query Match 78.2%; Score 486.5; DB 3; Length 119;
Best Local Similarity 78.3%; Pred. No. 2,7e-41;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVQPGSLRLSCVDSGLTSSSGYGMHWVROAPGAGLEWVAIVSYDGNDKYY 60
DB 1 QVELVSSGGGVQPGSLRLSCAASGFTSSYAMHWVROAPGKLEWVAIVSYDGSKNTYY 60
QY 61 ADSVKGKRPATISRDNAKNTLYLQNSLTITDPAVYCAKDLISNIAEALMGCGTLTVSS 120
DB 61 ADSVKGKRPATISRDNSKNTLYLQNSLRADDTAVYCARSGARTYFD-YMGCGTLTVSS 119

RESULT 7

US-09-560-198A-2
Sequence 2, Application US/09560198A
Patent No. 6492497
GENERAL INFORMATION:
APPLICANT: Thompson, Julia E
APPLICANT: Leonard, Simon N
APPLICANT: Wilton, Allison J
APPLICANT: Bradock, Peter SH
APPLICANT: Du Fou, Sarah L
APPLICANT: McCafferty, John G
APPLICANT: Conroy, Louise A
APPLICANT: Tempest, Philip R
TITLE OF INVENTION: Specific binding members for TGFbeta1
FILE REFERENCE: 28111/35620A
CURRENT APPLICATION NUMBER: US/09/560,198A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/131,983
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-560-198A-2

Query Match 78.1%; Score 485.5; DB 4; Length 123;
Best Local Similarity 78.0%; Pred. No. 3.6e-41;
Matches 96; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGSLRLSCVDSGLTSSSGYGMHWVROAPGAGLEWVAIVSYDGNDKYY 60
DB 1 QVELVSSGGGVQPGSLRLSCAASGFTSSYGMHWVROAPGKLEWVAIVSYDGSKNTYY 60

QY 61 ADSVKGKRPATISRDNAKNTLYLQNSLTITDPAVYCAKDLISNIAEALMGCGTLTVT 117
DB 61 ADSVKGKRPATISRDNSKNTLYLQNSLRADDTAVYCARSGARTGYSYGVELMGCGTLTVT 120
QY 118 VSS 120
DB 121 VSS 123

RESULT 8

US-09-025-769B-24
Sequence 24, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ge, Yiming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOREPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-24

Query Match 77.9%; Score 484.5; DB 4; Length 117;
Best Local Similarity 80.0%; Pred. No. 4.2e-41;
Matches 96; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVQPGSLRLSCVDSGLTSSSGYGMHWVROAPGAGLEWVAIVSYDGNDKYY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTSSYAMHWVROAPGKLEWVAIVSYDGNTYY 60
QY 61 ADSVKGKRPATISRDNAKNTLYLQNSLTITDPAVYCAKDLISNIAEALMGCGTLTVSS 120
DB 61 ADSVKGKRPATISRDNSKNTLYLQNSLRADDTAVYCARSGSG---DYMGCGTLTVSS 117

RESULT 9

US-09-560-198A-4
Sequence 4, Application US/09560198A
Patent No. 6492497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,816A
 FILING DATE: 23-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.4
 FILING DATE: 02-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.8
 FILING DATE: 02-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 23-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9525004.9
 FILING DATE: 07-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9610824.6
 FILING DATE: 23-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/02240
 FILING DATE: 02-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/244,597
 FILING DATE: 01-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET INFORMATION:
 TELEPHONE: 312-474-6300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-652-816A-1

Query Match 82.5%; Score 492.5; DB 2; Length 123;
 Best Local Similarity 79.7%; Pred. No. 1.2e-43;
 Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPKSSVSKVSCKASGTFSSHAISWVRQAPGQGLEWMGDIIPILGTQNY 60
 DB 1 QVQLVQSGAEVKKPKSSVSKVSCKASGTFSSPINMLRQAPGQGLEWMGSIIPSGTANY 60
 QY 61 AAKFGQRTITADDESTAYAMELSTLTSEDYAVYIC-----ELDMFY--IWGGTMYT 111
 DB 61 AAKFGQRLITADDESTAYAMELSTLTSEDYAVYICAGSHNYELYYTYMDVMGQGTMYT 120
 QY 112 VSS 114
 DB 121 VSS 123

RESULT 5

US-08-652-816A-6
 Sequence 6, Application US/08652816A
 Patent No. 5872215

GENERAL INFORMATION:

APPLICANT: Osbourn, JK
 APPLICANT: Allen, DJ
 APPLICANT: McCaferrey, JG
 TITLE OF INVENTION: Specific binding members, materials and
 TITLE OF INVENTION: methods.
 NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,816A
 FILING DATE: 23-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.4
 FILING DATE: 02-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9125579.8
 FILING DATE: 02-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 23-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9525004.9
 FILING DATE: 07-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9610824.6
 FILING DATE: 23-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/02240
 FILING DATE: 02-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/244,597
 FILING DATE: 01-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET INFORMATION:
 TELEPHONE: 312-474-6300
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-652-816A-6

Query Match 82.5%; Score 492.5; DB 2; Length 123;
 Best Local Similarity 79.7%; Pred. No. 1.2e-43;
 Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPKSSVSKVSCKASGTFSSHAISWVRQAPGQGLEWMGDIIPILGTQNY 60
 DB 1 QVQLVQSGAEVKKPKSSVSKVSCKASGTFSSPINMLRQAPGQGLEWMGSIIPSGTANY 60
 QY 61 AAKFGQRTITADDESTAYAMELSTLTSEDYAVYIC-----ELDMFY--IWGGTMYT 111
 DB 61 AAKFGQRLITADDESTAYAMELSTLTSEDYAVYICAGSHNYELYYTYMDVMGQGTMYT 120
 QY 112 VSS 114
 DB 121 VSS 123

RESULT 6

US-08-652-816A-8
 Sequence 8, Application US/08652816A
 Patent No. 5872215

GENERAL INFORMATION:

APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-8

Query Match 82.5%; Score 492.5; DB 2; Length 123;
Best Local Similarity 79.7%; Pred. No. 1.2e-43;
Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPGQGLEWMDIIPILGTNY 60
DB 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPGQGLEWMDIIPILGTNY 60
QY 61 AQFQGRVITTADESTSTAYMELSTLSEPTAVYYC-----ELDMFY--IMGGTMT 111
DB 61 AQFQGRVITTADESTSTAYMELSTLSEPTAVYYC-----ELDMFY--IMGGTMT 111
QY 112 VSS 114
DB 112 VSS 114
QY 121 VSS 123
DB 121 VSS 123

RESULT 7
US-08-652-816A-9
Sequence 9, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-9

Query Match 82.5%; Score 492.5; DB 2; Length 123;
Best Local Similarity 79.7%; Pred. No. 1.2e-43;
Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPGQGLEWMDIIPILGTNY 60
DB 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPGQGLEWMDIIPILGTNY 60
QY 61 AQFQGRVITTADESTSTAYMELSTLSEPTAVYYC-----ELDMFY--IMGGTMT 111
DB 61 AQFQGRVITTADESTSTAYMELSTLSEPTAVYYC-----ELDMFY--IMGGTMT 111
QY 112 VSS 114
DB 112 VSS 114
QY 121 VSS 123
DB 121 VSS 123


```
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-1
```

```
Query Match      85.1%; Score 508; DB 15; Length 120;
Best Local Similarity 85.8%; Pred. No. 6,6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;
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QY      1 QVQLVSGAEVKKPKGSSVKVSCKASGCTFSSHAISWRQAPGQGLEWMGDIIPILGTGY 60
Db      1 QVQLVSGAEVKKPKGSSVKVSCKASGCTFSSVAISWRQAPGQGLEWMGDIIPILGTGY 60
QY      61 AQKFGQKRVITTADESTSTAMELSTLTSEPTAVYYCEL---DWFY---IWGGTMTVSS 114
Db      61 AQKFGQKRVITTADESTSTAMELSTLTSEPTAVYYCARWGQDGFYAMDYWGQGLTVVSS 120
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RESULT 15

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US-09-880-748-1509
; Sequence 1509, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
```

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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1509
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509
```

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Query Match      84.9%; Score 507; DB 11; Length 253;
Best Local Similarity 79.7%; Pred. No. 1.9e-42;
Matches 102; Conservative 4; Mismatches 8; Indels 14; Gaps 1;
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QY      1 QVQLVSGAEVKKPKGSSVKVSCKASGCTFSSHAISWRQAPGQGLEWMGDIIPILGTGY 60
Db      1 QVQLVSGAEVKKPKGSSVKVSCKASGCTFSSVAISWRQAPGQGLEWMGDIIPILGTGY 60
QY      61 AQKFGQKRVITTADESTSTAMELSTLTSEPTAVYYC-----ELDWFYIWGQ 106
Db      61 AQKFGQKRVITTADESTSTAMELSTLTSEPTAVYYCARWQDGFYAMDYWGQGLTVVSS 120
QY      107 GTMTVTVSS 114
Db      121 GTMTVTVSS 128
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Search completed: December 30, 2003, 11:45:25
Job time : 24.4484 secs

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; Sequence 49, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOLETTIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-19

Query Match      86.1%; Score 514; DB 15; Length 120;
Best Local Similarity 86.7%; Pred. No. 1,7e-43;
Matches 104; Conservative 4; Mismatches 6; Indels 6; Gaps 3;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGRIIPILGIANY 60

Qy      61 AAKFGQRTVITADESTSTAYMELSTLTSEDTAVYCC--ELDM-FYI--WGQGTMTVYSS 114
Db      61 AAKFGQRTVITADESTSTAYMELSLRSEDTAVYVCATSRLEMLLYLDYMGQGTLYTVSS 120

RESULT 11
US-10-308-817-191
; Sequence 191, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 119
; TYPE: PRT
; ORGANISM: human
US-10-308-817-191

Query Match      86.0%; Score 513.5; DB 12; Length 119;
Best Local Similarity 84.9%; Pred. No. 1.9e-43;
Matches 101; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGRIIPILGTANY 60

Qy      61 AAKFGQRTVITADESTSTAYMELSTLTSEDTAVYCCELDMFY----IMGQGTMTVYSS 114
Db      61 AAKFGQRTVITADESTSTAYMELSLRSEDTAVYVCARGYYIYMDVMGQGTLYTVSS 119

RESULT 12
US-10-269-805-19
; Sequence 19, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOLETTIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
```

```
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-19

Query Match      85.7%; Score 511.5; DB 15; Length 121;
Best Local Similarity 85.1%; Pred. No. 3e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 7; Gaps 1;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGRIIPILGTANY 60

Qy      61 AAKFGQRTVITADESTSTAYMELSTLTSEDTAVYCCEL-----DPMYIMGQGTMTVSS 113
Db      61 AAKFGQRTVITADESTSTAYMELSLRSEDTAVYCCARFESGYMGDAFDIMGQGTMTVSS 120

Qy      114 S 114
Db      121 S 121

RESULT 13
US-10-025-687-1
; Sequence 1, Application US/10025687
; Publication No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-1

Query Match      85.1%; Score 508; DB 14; Length 120;
Best Local Similarity 85.8%; Pred. No. 6.6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGRIIPILGTANY 60

Qy      61 AAKFGQRTVITADESTSTAYMELSTLTSEDTAVYCCEL---DMFY----IMGQGTMTVYSS 114
Db      61 AAKFGQRTVITADESTSTAYMELSLRSEDTAVYCCARGKGDGYRNDYMGQGTLYTVSS 120

RESULT 14
US-10-125-687-1
; Sequence 1, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
```

```
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent version 3.1
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-9

Query Match      86.7%; Score 517.5; DB 15; Length 121;
Best Local Similarity 86.0%; Pred. No. 7.7e-44;
Matches 104; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSYALSWVRQAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGKRVITTADESTSTAYMELSTLTSEDTAVYYC-----ELDMFYIMGQGMVTVS 113
DB      61 AOKFGKRVITTADESTSTAYMELSLNSEDTAVYYCAAFSPETETDAFDIMGQGMVTVS 120
QY      114 S 114
DB      121 S 121

RESULT 7
US-10-269-805-35
; Sequence 35, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent version 3.1
; SEQ ID NO 35
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-35

Query Match      86.5%; Score 516.5; DB 15; Length 125;
Best Local Similarity 83.2%; Pred. No. 1e-43; Indels 11; Gaps 1;
Matches 104; Conservative 3; Mismatches 7; Indels 11; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSYALSWVRQAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGKRVITTADESTSTAYMELSTLTSEDTAVYYC-----LDMFYIMGQGMVTVS 109
DB      61 AOKFGKRVITTADESTSTAYMELSLNSEDTAVYYCAAFSPETETDAFDIMGQGMVTVS 120
QY      110 VTSS 114
DB      121 VTSS 125

RESULT 8
US-09-976-118-2
; Sequence 2, Application US/09976118
; Patent No. US2002005803A1
; GENERAL INFORMATION:
; APPLICANT: Ratsch, Kevin Paul
; APPLICANT: Curjel, David T.
; APPLICANT: Bonner, James Allen
```

```
; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 270
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of anti-EGFR ecfv
; OTHER INFORMATION: clone pSEX01-63
US-09-976-118-2

Query Match      86.4%; Score 516; DB 9; Length 270;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSYALSWVRQAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGKRVITTADESTSTAYMELSTLTSEDTAVYYCELD-----WFIYMGQGT 108
DB      61 AOKFGKRVITTADESTSTAYMELSLNSEDTAVYYCARDPDYSGSYRPMFDPWQGT 120
QY      109 MVTSS 114
DB      121 LVTVSS 126

RESULT 9
US-10-269-805-3
; Sequence 3, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-3

Query Match      86.2%; Score 514.5; DB 15; Length 123;
Best Local Similarity 83.7%; Pred. No. 1.5e-43; Indels 9; Gaps 2;
Matches 103; Conservative 4; Mismatches 7; Indels 9; Gaps 2;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSYALSWVRQAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGKRVITTADESTSTAYMELSTLTSEDTAVYYC-----ELDM---FIYMGQGMVT 111
DB      61 AOKFGKRVITTADESTSTAYMELSLNSEDTAVYYCARGVGDPMISFPDYMGQGMVT 120
QY      112 VSS 114
DB      121 VSS 123

RESULT 10
US-10-269-805-49
```

```

: APPLICANT: Watkins, Jeffrey D.
: TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
: FILE REFERENCE: P-IX 5519
: CURRENT APPLICATION NUMBER: US/10/300,675
: CURRENT FILING DATE: 2002-11-19
: PRIOR APPLICATION NUMBER: US 09/989,901
: PRIOR FILING DATE: 2001-11-19
: NUMBER OF SEQ ID NOS: 59
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 118
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Recombinant variant
US-10-300-675-10

```

[illegible]

```

RESULT 3
US-10-300-675-12
; Sequence 12, Application US/10300675
; Publication No. US20030198638A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
PRIOR FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Recombinant variant
US-10-300-675-12

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[illegible]

RESULT 4
US-10-300-675-14
; Sequence 14, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519

```

: CURRENT APPLICATION NUMBER: US/10/300,675
: CURRENT FILING DATE: 2002-11-19
: PRIOR APPLICATION NUMBER: US 09/988,901
: PRIOR FILING DATE: 2001-11-19
: NUMBER OF SEQ ID NOS: 59
: SOFTWARE: PastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 118
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Recombinant variant
US-10-300-675-14

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```

Qy      1 QVQLVDSGAELVKPKGGSSVVKVSCKASGGTFFSSHAISWVROAPGQGLLEWNGDIIPIILGCTGY 60
Db      1 QVQLVDSGAELVKPKGGSSVVKVSCKASGGTFFSYAISWVROAPGQGLLEWNGDIIPIILGCTANY 60

Qy      61 AQKFGKRVITITADSTSTAYMELSTLTSSBDTAVYYCELD---NFYIWGQSTMTVSS 114
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 AQKFGKRVITITADSTSTAYMELSTLTSSBDTAVYYCARBDNSGMYHWYGGQTLTVSS 118

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RESULT 5
US-10-269-805-25
; Sequence 25, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 124
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-269-805-25

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[illegible]

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RESULT 6
US-10-269-805-9
; Sequence 9, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; PIDS REFERENCE: A-172
; CURRENT APPLICATION NUMBER: US/10/269,805

```

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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 24.484 Seconds

(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	87.1	118	12	US-10-300-675-6
2	520	87.1	118	12	US-10-300-675-10
3	520	87.1	118	12	US-10-300-675-12
4	520	87.1	118	12	US-10-300-675-14
5	520	87.1	124	15	US-10-269-805-25
6	517.5	86.7	121	15	US-10-269-805-9
7	516.5	86.5	125	15	US-10-269-805-35
8	516	86.4	270	9	US-09-976-118-2
9	514.5	86.2	123	15	US-10-269-805-3
10	514	86.0	120	15	US-10-269-805-49
11	513.5	85.7	121	15	US-10-308-817-191
12	511.5	85.7	121	15	US-10-269-805-19
13	508	85.1	120	15	US-10-025-687-1
14	508	85.1	120	15	US-10-125-687-1
15	507	84.9	253	11	US-09-880-748-1509

16	506.5	84.8	248	11	US-09-880-748-1733	Sequence 1733, Ap
17	506.5	84.8	248	11	US-09-880-748-1734	Sequence 1734, Ap
18	506	84.7	120	15	US-10-269-805-37	Sequence 37, Appl
19	505.5	84.7	244	11	US-09-880-748-1891	Sequence 1891, Ap
20	505.5	84.7	248	11	US-09-880-748-1718	Sequence 1718, Ap
21	505.5	84.7	248	11	US-09-880-748-1879	Sequence 1879, Ap
22	504.5	84.5	627	14	US-10-047-542-47	Sequence 47, Appl
23	504	84.4	244	11	US-09-880-748-1866	Sequence 1866, Ap
24	502.5	84.2	248	11	US-09-880-748-1719	Sequence 1719, Ap
25	502.5	84.2	248	11	US-09-880-748-1732	Sequence 1732, Ap
26	502.5	84.2	248	11	US-09-880-748-1737	Sequence 1737, Ap
27	502	84.1	120	15	US-10-269-805-15	Sequence 15, Appl
28	501.5	84.0	248	11	US-09-880-748-1741	Sequence 1741, Ap
29	500.5	83.8	253	11	US-09-880-748-1880	Sequence 1880, Ap
30	499.5	83.7	248	11	US-09-880-748-1727	Sequence 1727, Ap
31	499.5	83.7	248	11	US-09-880-748-1728	Sequence 1728, Ap
32	499	83.6	257	11	US-09-880-748-1553	Sequence 1553, Ap
33	498.5	83.5	219	15	US-10-184-508A-7	Sequence 7, Appl1
34	498.5	83.5	219	15	US-10-184-508A-7	Sequence 7, Appl1
35	498.5	83.5	222	15	US-10-184-508A-6	Sequence 6, Appl1
36	498.5	83.5	222	15	US-10-184-508A-6	Sequence 6, Appl1
37	498.5	83.5	245	15	US-10-151-882-15	Sequence 15, Appl
38	497.5	83.3	218	15	US-10-184-508A-8	Sequence 8, Appl1
39	497.5	83.3	218	15	US-10-186-186-8	Sequence 8, Appl1
40	496	83.1	120	15	US-10-269-805-5	Sequence 5, Appl1
41	496	83.1	256	11	US-09-880-748-1600	Sequence 1600, Ap
42	495.5	83.0	246	11	US-09-880-748-2062	Sequence 2062, Ap
43	495.5	83.0	246	11	US-09-880-748-1717	Sequence 1717, Ap
44	495	82.9	252	11	US-09-880-748-1666	Sequence 1666, Ap
45	494.5	82.8	123	15	US-10-269-805-17	Sequence 17, Appl

ALIGNMENTS

```
RESULT 1
US-10-300-675-6
; Sequence 6, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-300-675-6

Query Match      87.1%; Score 520; DB 12; Length 118;
Best Local Similarity 85.6%; Pred. No. 4,2e-44;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPKSSVAVSCASGCTFSSHAISWRQAPQGLEMGGIIPILGTVNY 60
DB      1 QVQLVQSGAEVKKPKSSVAVSCASGCTFSSVAISWRQAPQGLEMGGIIPFTNAY 60
QY      61 AAKPQGRVITTADEGSTAYMEISLITSDTAIVYCELD---WFIWGCTMTVSS 114
DB      61 AAKPQGRVITTADEGSTAYMEISLITSDTAIVYCARBDSGGMHYWGCTLTVSS 118

RESULT 2
US-10-300-675-10
; Sequence 10, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
```

Db 61 AAGFQGRVTTTAADESTSTAYMELSSLRSEDTAYYCARWGSGDFYANDYMGQGLTVTSS 120

RESULT 14
ABJ18672
ID ABJ18672 standard; Protein; 120 AA

DT 06-MAR-2003 (first entry)
yy

DE Antibody library related heavy variable chain protein region seq ID No 1
XX
KM Library; recombinant antibody; clustering variable region; in silico;
KM immunogenicity; antibody therapeutic.

Unidentified.

PN WO200284277-A1.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US12202.

PR 17-APR-2001; 2001US-284407P.

PA (ABMA-) ABMAXIS INC.

PI Luo P;

DR WPI; 2003-093043/08.

PT Constructing a library of recombinant antibodies useful as source of
PT antibody candidates for screening antigens comprises clustering
PT variable regions of antibodies having known 3-dimensional structures
PT into structural ensembles -

PS Disclosure; Page 98-99; 119pp; English.

CC The invention relates to a novel method for the construction of a library
CC of recombinant antibodies. The novel method comprises clustering variable
CC regions of a collection of antibodies having known 3D structures into at
CC least two families of structural ensembles, each comprising at least two
CC different antibody sequences but with substantially identical main chain
CC conformations. The method is useful for constructing a library of
CC artificial antibodies in silico which provides a structurally diverse and
CC yet functionally more relevant source of antibody candidates which can
CC then be screened for binding a wide variety of target molecules,
CC including small molecules, and biomacromolecules such as proteins,
CC peptides and nucleic acids. The libraries constructed are useful as a
CC source of antibody candidates for further screening for novel antibodies
CC with high affinity against a wide range of antigens and having no or
CC minimum immunogenicity to human subjects treated with antibody
CC therapeutics. This sequence represents a protein region of an antibody
CC relating to the novel antibody library construction method of the
CC invention.

SQ Sequence 120 AA;

Query Match	85.1%;	Score 508;	DB 24;	Length 120;
Best Local Similarity	85.8%;	Pred. No. 3.9e-37;		
Matches 103; Conservative	3;	Mismatches 8;	Indels 6;	Gaps 2

Qy 1 QVQLVSGAEVKKPGSSVKVSCASGGTSSHAISWRAPGGGLEMMGDIIPILGTGNY 600

Db 1 QVQLVSGAEVKKPGSSVKVSCASGGTSSHAISWRAPGGGLEMMGDIIPILGTGNY 600

```

Qy      61 A QKFGQRVTITADESTSTAYNELSTLSEDTAYYCEL--DMFY---IMGGIMVTYSS 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 A QKFGQRVTITADESTSTAYNELSLSEDTAYYCARWGSDGFYAMDYMGQGLVTYSS 120

```

RESULT 15.
ABJ18718
ID ABJ18718 standard; Protein; 120 AA

AC	ABJ18718;
XX	
DT	06-MAR-2003 (first entry)
..	

DE Antibody library related VH protein region 1DHA

KM Library; recombinant antibody; clustering variable region; in silico;
KM immunogenicity; antibody therapeutic.

OS Unidentified.

PN WO200284277-A1.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US12202.

PR 17-APR-2001; 2001US-284407P.

PA (ABMA-) ABMAXIS INC.

Luo P.

DR WPI; 2003-093043/08.

Constructing a library of recombinant antibodies useful as source of antibody candidates for screening antigens comprises clustering variable regions of antibodies having known 3-dimensional structures into structural ensembles -

PS Disclosure; Fig 13B; 119pp; English.

The invention relates to a novel method for the construction of a library of recombinant antibodies. The novel method comprises clustering variable regions of a collection of antibodies having known 3D structures into at least two families of structural ensembles, each comprising at least two different antibody sequences but with substantially identical main chain conformations. The method is useful for constructing a library of artificial antibodies *in silico* which provides a structurally diverse and yet functionally more relevant source of antibody candidates which can then be screened for binding a wide variety of target molecules, including small molecules, and biomacromolecules such as proteins, peptides and nucleic acids. The libraries constructed are useful as a source of antibody candidates for further screening for novel antibodies with high affinity against a wide range of antigens and having no or minimum immunogenicity to human subjects treated with antibody therapeutics. This sequence represents a protein region of an antibody relating to the novel antibody library construction method of the invention.

SQ Sequence 120 AA;

Query Match 85.1%; Score 508; DB 24; Length 120;
 Best Local Similarity 85.8%; Pred. No. 3.9e-37;
 Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2

QY	Db	QY	Db
1 QVQLVQSGAEVKKPKSSSVVVSCKAGCGTSSSHAIISNVRCAPOGLEMDMDIIPILQITGNY	1 QVQLVQSGAEVKKPKSSSVVSCKAGCGTSSSHAIISNVRCAPOGLEMDMDIIPILQITGNY	61 AOKPGGRITITDEESTSTRAMELSTLTSEEDIVVYCYEL---DMFY---IMGOSTMTVVS	61 AOKPGGRITITDEESTSTRAMELSTLTSEEDIVVYCYEARAGGQDFAMNDIVGQGITLVTS
60	60	120	120

Search completed: December 30, 2003, 10:54:37
Job time : 37.756 sec

Search completed: December 30, 2003, 10:54:37
Job time : 37.756 secs

CC TWP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostatic hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
 CC chain regions of a human anti-TIMP-1 antibody of the invention.
 CC
 SQ Sequence 225 AA;
 Query Match 85.2%; Score 508.5; DB 24; Length 225;
 Best Local Similarity 85.1%; Pred. No. 6.5e-37;
 Matches 103; Conservative 3; Mismatches 8; Indels 7; Gaps 2;
 QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVRQAPGGGLEWMGDIIPILGTGY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSVAISWVRQAPGGGLEWMGDIIPILGTANY 60
 QY 61 AQRFGRRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDW-----FYIMGGTMYTVSS 113
 DB 61 AQRFGRRVITTADESTSTAYMELSLRSEDTAVYYCARGLYMAVYPIFDPMGGTLTVSS 120
 QY 114 S 114
 DB 121 S 121
 RESULT 12
 AAB67618 standard; Protein; 245 AA.
 XX ID AAB67618 standard; Protein; 245 AA.
 XX AC AAB67618;
 XX DT 29-MAY-2001 (first entry)
 XX DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_2.
 XX KM Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
 XX KW miscarriage; abortion; preclasis; antibody; HLA phenotyping; ss.
 XX OS Homo sapiens.
 XX PN MO200114558-A1.
 XX PD 01-MAR-2001.
 XX PF 28-AUG-2000; 2000MO-EP08388.
 XX PR 26-AUG-1999; 99EP-0116691.
 XX PA (MORP-) MORPHOSYS AG.
 XX PI Kretschmar T, Tesar M, Marget M, Kroenke M;
 XX DR WPI; 2001-218451/22.
 XX PT Novel isolated human immunoglobulin or functional immunoglobulin
 XX fragment specific for human leukocyte antigen Cw6, useful for treatment
 XX of humans and for human leukocyte antigen phenotyping -
 XX Claim 3; Fig 1; 23pp; English.
 CC AAB67617-23 represent single chain antibody (scFv) fragments which
 CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
 CC derived from a synthetic human combinatorial antibody library based on
 CC molecular consensus frameworks and CDRs randomised with trinucleotides.
 CC The specification describes a human immunoglobulin fragments specific

CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
 CC studies of natural killer cell silencing as well as miscarriages.
 CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
 CC Preclasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
 CC fragments are useful for the preparation of a pharmaceutical for the
 CC treatment of humans. They are also useful for HLA phenotyping.
 CC
 SQ Sequence 245 AA;
 Query Match 85.2%; Score 508.5; DB 22; Length 245;
 Best Local Similarity 87.2%; Pred. No. 7.1e-37;
 Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 2;
 QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVRQAPGGGLEWMGDIIPILGTGY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSVAISWVRQAPGGGLEWMGDIIPILGTANY 60
 QY 61 AQRFGRRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDWYF--IWGGTMYTVSS 114
 DB 61 AQRFGRRVITTADESTSTAYMELSLRSEDTAVYYCARGFDFPMDFGGTLTVSS 117
 RESULT 13
 AAM27550 standard; Protein; 120 AA.
 XX ID AAM27550 standard; Protein; 120 AA.
 XX AC AAM27550;
 XX DT 23-JAN-1998 (first entry)
 XX DE Human Ab heavy chain variable region VH1A consensus.
 XX KM Human; antibody; preparation; library; VH1A; variable region;
 XX KW heavy chain; consensus.
 XX OS Homo sapiens.
 XX PN WO9708320-A1.
 XX PD 06-MAR-1997.
 XX PF 19-AUG-1996; 96MO-EP03647.
 XX PR 18-AUG-1995; 95EP-0113021.
 XX PA (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 XX PI Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
 XX DR WPI; 1997-179277/16.
 XX DR N-PSDB; AAT87948.
 XX PT Preparation of human derived antibody gene library - using synthetic
 XX PT consensus sequences, and signal consensus antibody gene as universal
 XX PT framework for highly diverse antibody libraries
 XX PS Example 1; Fig 5A; 436pp; English.
 XX CC The present sequence is the human antibody heavy chain
 XX CC variable region synthetic sequence VH1A, used in the preparation of
 XX CC a human derived antibody gene library.
 SQ Sequence 120 AA;
 Query Match 85.1%; Score 508; DB 18; Length 120;
 Best Local Similarity 85.8%; Pred. No. 3.9e-37;
 Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;
 QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVRQAPGGGLEWMGDIIPILGTGY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSVAISWVRQAPGGGLEWMGDIIPILGTANY 60
 QY 61 AQRFGRRVITTADESTSTAYMELSTLTSEDTAVYYCEL---DMFY---IWGGTMYTVSS 114

Oy	1	OVOLVOSAEVKKPSSSVVSKKGGCTSSHAISWVRAPOGGLMMGDIIPIILGATGY	60
Db	1	OVOLVOSAEVKKPSSSVVSKKGGCTSSHAISWVRAPOGGLMMGGIIPFIATAY	60
Oy	61	AQPFQGRVTITADESTSTAYMELSTLTSIEDTAVYYC-ELDFEYI--WGQGTMTVSS	114
Db	61	AQPFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARDFSLDYWGQGTLTAVSS	117
RESULT 10			
ID	ABB57559	standard; Peptide; 115 AA.	
XX	ABB57559;		
DT	18-MAR-2002	(first entry)	
DE	HLA-DR-specific protein MS-GPCS VH sequence.		
XX			
XX	Immunomodulatory human MHC class II antigen-binding protein; HLA;		
XX	human leukocyte antigen; immune system, immunosuppression; antibody;		
XX	major histocompatibility complex; antirheumatic; antiarthritic;		
XX	neuroprotective; antiinflammatory; antidiabetic; antiporiatic;		
XX	immunosuppressive; dermatological; antihypoid; nephrotoxic; psoriasis;		
XX	thyromimetic; hepatotropic; immune response suppressor; narcolepsy;		
XX	rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulin;		
XX	grave's disease; insulin-dependent diabetes; Hashimoto's disease;		
XX	systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;		
XX	transplant rejection; graft versus host disease; pemphigus vulgaris;		
XX	glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;		
XX	irritable bowel disease; Sjogren's syndrome.		
OS	Homo sapiens.		
DS	Synthetic.		
XX	WO200187338-A1.		
XX	22-NOV-2001.		
XX	14-MAY-2001; 2001WO-US15626.		
XX	12-MAY-2000; 2000EP-0110063.		
PR	06-OCT-2000; 2000US-238762P.		
XX	(GPCB-) GPC BIOTECH AG.		
PA	(MORP-) MORPHOSYS AG.		
PI	Nagy Z, Tesar M, Thomassen-Wolf E;		
XX	WPI; 2002-0755289/10.		
DR			
PT	Composition for suppressing immune response, treating diseases of		
PT	immune system, has polypeptide comprising antibody-based		
PT	antigen-binding domain of human composition, which binds antigen		
PT	expressed on a cell surface -		
XX	Example; Fig 15; 139pp; English.		
PS			
XX	The present invention describes a composition (I), comprising a		
CC	polypeptide comprising an antibody-based antigen-binding domain of human		
CC	composition with binding specificity for an antigen expressed on the		
CC	surface of a cell, where treating cells expressing the antigen with the		
CC	polypeptide leads to suppression of an immune response, and the IC50 for		
CC	the suppression of immune response is 1 microM or less. (I) has		
CC	antirheumatic, antiarthritic, neuroprotective, antiinflammatory,		
CC	antidiabetic, antiporiatic, immunosuppressive, dermatological,		
CC	antihypoid, nephrotoxic, thyromimetic and hepatotropic activities, and		
CC	can be used as a suppressor of immune response. (I) is useful for		
CC	suppressing activation or proliferation of a cell of the immune system,		
CC	suppressing IL-2 secretion by a cell, the interaction of a cell of the		
CC	immune system with another cell, immunosuppressing a patient and for		
CC	killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR		

	CC	on the surface of the cell, where neither cytotoxic entities nor immunological mechanisms are needed to cause or lead to the killing.
	CC	(1) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritic, multiple sclerosis, Grave's disease,
	CC	insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus erythematosus, ankylosing spondylitis, transplant rejection, graft versus host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,
	CC	glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.
	CC	AA92469 to AB92474 and AB857457 to AB857590 represent sequence used in the exemplification of the present invention.
XX	SQ	Sequence 115 AA;
	Query Match	85.2%; Score 508.5; DB 23; Length 115;
	Best Local Similarity	87.8%; Pred. NO. 3.4e-37;
	Matches 101; Conservative	4; Mismatches 9; Indels 1; Gaps 1
QY		1 QVQLVSGAEVKKPGSSVYKVCCKASGCTPSSHAIISWRAQAGGLEMGDIIPLIGTGYNT 60
DB		1 QVQLVSGAEVKKPGSSVYKVCCKASGCTPSSVAIISWRQAQGGLFMWGGIPIFGTANY 60
QY		61 AQKEGRVTITADESTRAWMLSTLTSBDTRAVYCELDWFY-ITGGGTMYTVSS 114
DB		61 AQKPGRVTITADESTRAWMLSLRSBEDRAVYICARHSFFDYGGGITLVTVSS 115
RESULT 11		
ID	ABR01510	ABR01510 standard; Protein; 225 AA.
AC	ABR01510;	
XX	DT	16-Apr-2003 (first entry)
DE		Human anti-TIMP-1 antibody heavy chain #8.
XX	XX	Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VCDDR3;
KM		matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;
KM		variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
KM		alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KM		lupus nephritis; glomerulosclerotic renal disease; lung cancer;
XX		idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.
OS		Homo sapiens.
PX		WO200286085-A2.
PD		31-OCT-2002.
PF		24-APR-2002; 2002MO-US12801.
PR		24-APR-2001; 2001US-285683P.
PA		(FARB) BAYER CORP.
PA		(MORP-) MORPHOSYS AG.
PI		Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;
DR		WPI; 2003-129114/12.
N-PSDB;		ABZ74781.
PT		New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)
PT		antibodies, for diagnosing or ameliorating the symptoms of a disorder
PT		in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
PT		hypertrophy or lung cancer -
PS		Claim 20; Page 153; 228pp; English.
XX		The invention relates to a novel purified preparation of a human
XX		antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
XX		and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of

CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 220 AA;

Query Match 86.3%; Score 515; DB 24; Length 220;

Best Local Similarity 87.1%; Pred. No. 1.7e-37;

Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEMMGDIIPILGTANY 60

Db 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEMMGDIIPILGTANY 60

Qy 61 AQRQGRVTITADESTSTAYMELSTLTSEDPAVYVCEDMFIY--WGQGTMTVYSS 114

Db 61 AQRQGRVTITADESTSTAYMELSTLTSEDPAVYVCEDMFIY--WGQGTMTVYSS 116

RESULT 8

ABR01538 ID ABR01538 standard; Protein; 220 AA.

XX ABR01538;

DT 16-APR-2003 (first entry)

XX Human anti-TIMP-1 antibody heavy chain #36.

XX Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;

XX matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;

XX variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;

XX alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;

XX lupus nephritis; glomerulosclerotic renal disease; lung cancer;

XX idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX Homo sapiens.

XX WO200286085-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-US12801.

XX 24-APR-2001; 2001US-285683P.

XX (FARB) BAYER CORP.

XX (MORP-) MORPHOSYS AG.

XX Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;

XX WPI; 2003-129114/12.

XX N-PSDB; ABZ74809.

XX New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)

XX antibody, for diagnosing or ameliorating the symptoms of a disorder

XX in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate

XX hypertrophy or lung cancer

XX Claim 20; Page 173; 228pp; English.

XX The invention relates to a novel purified preparation of a human

XX antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)

XX and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of

XX TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and

XX a variable light chain (VLC)DR3 region. An antibody preparation of the

XX invention has hepatotropic, cytosolic, nephrotropic and cardiac

XX activity. The human antibody is useful for decreasing an MMP-inhibiting

XX activity of a TIMP-1. It is especially useful for ameliorating the

XX symptoms of a disorder in which TIMP-1 is elevated, e.g. liver

XX fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary

XX syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic

CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 220 AA;

Query Match 85.4%; Score 510; DB 24; Length 220;

Best Local Similarity 87.1%; Pred. No. 4.7e-37;

Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEMMGDIIPILGTANY 60

Db 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEMMGDIIPILGTANY 60

Qy 61 AQRQGRVTITADESTSTAYMELSTLTSEDPAVYVCEDMFIY--WGQGTMTVYSS 114

Db 61 AQRQGRVTITADESTSTAYMELSTLTSEDPAVYVCEDMFIY--WGQGTMTVYSS 116

RESULT 9

ABR67617 ID ABR67617 standard; Protein; 245 AA.

XX ABR67617;

DT 29-MAY-2001 (first entry)

XX Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_1.

XX Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;

XX miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.

XX Homo sapiens.

XX WO200114558-A1.

XX 01-MAR-2001.

XX 28-AUG-2000; 2000WO-EP08388.

XX 26-AUG-1999; 99EP-0116691.

XX (MORP-) MORPHOSYS AG.

XX Kretzschmar T, Tassar M, Marget M, Kroecke M;

XX WPI; 2001-218451/22.

XX Novel isolated human immunoglobulin or functional immunoglobulin

XX fragment specific for human leukocyte antigen Cw6, useful for treatment

XX of humans and for human leukocyte antigen phenotyping

XX Claim 3; Fig 1; 23pp; English.

XX AAB67617-23 represent single chain antibody (scFv) fragments which

XX are specific for human leukocyte antigen (HLA)-Cw6. The fragments are

XX derived from a synthetic human combinatorial antibody library based on

XX molecular consensus frameworks and CDRs randomised with trinucleotides.

XX The specification describes a human immunoglobulin fragments specific

XX for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in

XX studies of natural killer cell silencing as well as miscarriages.

XX HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.

XX Polaris may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin

XX fragments are useful for the preparation of a pharmaceutical for the

XX treatment of humans. They are also useful for HLA phenotyping.

XX Sequence 245 AA;

XX Query Match 85.3%; Score 509.5; DB 22; Length 245;

XX Best Local Similarity 87.2%; Pred. No. 5.8e-37;

XX Matches 102; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

RESULT 6
 AAR24442
 ID AAR24442 standard; Protein; 481 AA.
 XX
 AC AAR24442;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-JAN-1992 (first entry)
 XX
 DE Sequence of antibody molecule IgG.
 XX
 KW Antibody; immunoglobulin G.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 308 /label= N
 FT /note= "Substrn. to create glycan addition site"
 FT Misc-difference 310 /label= S
 FT /note= "see above"
 FT Misc-difference 321 /label= N
 FT /note= "see above"
 FT Misc-difference 329 /label= N
 FT /note= "see above"
 FT Misc-difference 331 /label= S
 FT /note= "see above"
 FT Misc-difference 356 /label= N
 FT /note= "see above"
 FT Misc-difference 369 /label= N
 FT /note= "see above"
 FT /label= N
 FT /note= "see above"
 MO9209293-A1.
 XX
 PD 11-JUN-1992.
 XX
 PF 18-NOV-1991; 91WO-US08605.
 XX
 PR 23-NOV-1990; 90US-0618314.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Seed B, Walz G;
 XX
 DR WPI; 1992-216789/26.
 DR N-PSDB; AAQ25443.
 XX
 PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
 PT - used in treating chronic inflammation, rheumatoid arthritis,
 PT psoriasis, etc.
 XX
 PS Disclosure; Fig 1; 46pp; English.
 XX
 CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
 CC inventors designed a molecule including several such sites for
 CC attachment of sialyl-Lex side chains (see AAR24442, FT). The
 CC additional N-linked glycosylation sites are introduced at locations
 CC which impair complement fixing and Fc receptor binding ability. They
 CC are preferably located in the CH2 region of the Ig molecule.
 CC Antibodies bearing multiple sialyl-Lex determinants are useful for
 CC disrupting undesirable interactions between cells or proteins.
 CC Disrupting this interaction has therapeutic applications, for
 CC example, in minimizing inflammation following tissue injury.
 CC (updated on 25-MAR-2003 to correct PN field.)
 CC

SQL Sequence 481 AA;
 Query Match 86.3%; Score 515.5; DB 13; Length 481;
 Best Local Similarity 81.1%; Pred. No. 3; 4e-37;
 Matches 103; Conservative 3; Mismatches 8; Indels 13; Gaps 1;
 QY 1 QVQLVQSGAEVKKPSSSVKSCKASGTFPSSHAISWVRQAPQGLEMMGDIIPILQTCGY 60
 DB 25 QVQLVQSGAEVKKPSSSVKSCKASGTFPSSHAISWVRQAPQGLEMMGDIIPILQTCGY 84
 QY 61 AQPFGQRTVITADESTAYMELSTLTSEDYAVYCELD-----WPYIWGGQ 107
 DB 85 AQPFGQRTVITADESTAYMELSLRSEDTAVYCYCARDNGAYVCSGSCYSGMFDPMGGQ 144
 QY 108 TMVTVSS 114
 DB 145 TLVTVSS 151
 RESULT 7
 ABR01512
 ID ABR01512 standard; Protein; 220 AA.
 XX
 AC ABR01512;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human anti-TIMP-1 antibody heavy chain #10.
 XX
 KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
 KW matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatocytic;
 KW variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200286085-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 24-APR-2002; 2002WO-US12801.
 XX
 PR 24-APR-2001; 2001US-285683P.
 XX
 PA (FARB) BAYER CORP.
 PA (MORP-) MORPHOSYS AG.
 XX
 PI Pan C, Knorr AM, Schauer M, Hirsch-dietrich C, Kraft S, Krebs B;
 XX
 DR WPI; 2003-129114/12.
 DR N-PSDB; AB274783.
 XX
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
 PT hypertrophy or lung cancer.
 XX
 PS Claim 20; Page 154; 228pp; English.
 XX
 CC The invention relates to a novel purified preparation of a human
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
 CC and neutralizes a matrix metalloproteinase (MMP)-inhibiting activity of
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytosolic, nephrotropic and cardiac
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon

CC fragment.
XX
SQ Sequence 271 AA;
Query Match 87.2%; Score 520.5; DB 23; Length 271;
Best Local Similarity 87.2%; Pred. No. 7e-38;
Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 1;
QY 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIPIPLGTGY 60
DB 5 EVQLVSGAEVKKRQSSVKVSCKASGCTFSSVAISWVROAPGQGLEWMGDIPIPLGTANY 64
QY 61 AQRKQGRVTTTADSTSTAYMELSTLTSEDPAVYCCD---LDMFYIMGGGTMTVYSS 114
DB 65 AQRKQGRVTTTADSTSTAYMELSLNSSEDTAVYCCARDSDYGMQGLTVYSS 121
RESULT 4
ID AAY99558 standard; Protein; 118 AA.
AC AAY99558;
XX
DT 20-SEP-2000 (first entry)
XX
DE Human LH13 monoclonal antibody heavy chain variable region.
XX
KM Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;
KM cytotoxic; cytotoxic; heavy chain variable region.
OS Homo sapiens.
XX
PN WO200032635-A2.
PD 08-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US28485.
XX
PR 02-DEC-1998; 98US-0203768.
XX
PA (IXSY-) IXSYS INC.
PI Watkins JD, Huse WD;
XX
DR WPI; 2000-412293/35.
DR N-PSDB; AAA48411.
XX
PT New tumor-specific human monoclonal antibody, useful for the treatment
PT and diagnosis of cancer, comprises at least one complementarity
PT determining region -
XX
PS Claim 10; Page 82-83; 84pp; English.
XX
CC The present sequence is the heavy chain variable region of a human
CC tumour-specific monoclonal antibody. Neoplastic cells selectively express
CC antigens which are not present on normal cells. Thus monoclonal
CC antibodies can be produced that are specifically directed against
CC tumour-specific antigens. The antibodies can be conjugated to cytotoxic
CC or cytostatic agents and used to selectively target cancer cells for the
CC elimination of tumours. They can also be linked to diagnostic moieties
CC that allow the imaging of neoplastic cells. Nucleic acids encoding human
CC tumour-specific monoclonal antibodies can be used to express the
CC antibodies and can be recombinantly engineered to produced modified
CC antibodies with higher affinity or higher selectivity for tumour cells.
CC Tumour-specific antibodies were produced by hybridomas that were
CC generated by in vitro immunisation of human spleen cell cultures with
CC breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
CC was then isolated from the hybridoma by RT-PCR. The present sequence
CC was produced by LH13 hybridoma cell line.
XX
SQ Sequence 118 AA;
Query Match 87.1%; Score 520; DB 21; Length 118;

Best Local Similarity 85.6%; Pred. No. 3.4e-38;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;
QY 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIPIPLGTGY 60
DB 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSVAISWVROAPGQGLEWMGDIPIPLGTANY 60
QY 61 AQRKQGRVTTTADSTSTAYMELSTLTSEDPAVYCCD---WIFYIMGGGTMTVYSS 114
DB 61 AQRKQGRVTTTADSTSTAYMELSLNSSEDTAVYCCARDSDYGMQGLTVYSS 118
RESULT 5
ID AAU97198 standard; Protein; 270 AA.
AC AAU97198;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human anti-EGFR single-chain antibody isolated from clone pSEX1-63.
XX
KM Human; anti-epidermal growth factor receptor single-chain antibody;
KM anti-EGFR-scFv; IgM; cancer; tumour growth; clone pSEX1-63; cytostatic.
OS Homo sapiens.
XX
PN WO200230984-A1.
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US11857.
XX
PR 13-OCT-2000; 2000US-240353P.
XX
PA (UABR-) UAB RES FOUND.
PI Ralsch KP, Curiel DT, Bonner JA;
XX
DR WPI; 2002-463261/49.
XX
PT Novel human anti-epidermal growth factor receptor single-chain antibody
PT useful for diagnostic location and assessment of tumour growth, and in
PT treating cancer -
XX
PS Claim 3; Fig 2; 51pp; English.
XX
CC The present invention relates to human anti-epidermal growth factor
CC receptor single-chain antibodies (anti-EGFR-scFv) isolated from a
CC human IgM phage display library using EGFR as antigen. Two isolates
CC with different amino acid sequences were identified. The
CC anti-EGFR-scFvs are useful for treating cancer, and for the
CC diagnostic location and assessment of tumour growth, where the
CC anti-EGFR-scFv is radiolabelled. The present sequence represents
CC human anti-EGFR single-chain antibody isolated from clone pSEX1-63.
XX
SQ Sequence 270 AA;
Query Match 86.4%; Score 516; DB 23; Length 270;
Best Local Similarity 81.7%; Pred. No. 1.7e-37;
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;
QY 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIPIPLGTGY 60
DB 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSVAISWVROAPGQGLEWMGDIPIPLGTANY 60
QY 61 AQRKQGRVTTTADSTSTAYMELSTLTSEDPAVYCCD---WIFYIMGGGTMTVYSS 108
DB 61 AQRKQGRVTTTADSTSTAYMELSLNSSEDTAVYCCARDSDYGMQGLTVYSS 120
QY 109 MVTYSS 114
DB 121 LTVYSS 126

PT treatment of hemophilia A patients with these antibodies -
XX
XX Example 9; Fig 11B; 61pp; English.
XX
CC This invention describes a novel polynucleotide (1) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (1) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents a fragment
CC of the human factor VIII antibody heavy chain variable region protein
CC DP-10 which is used in the method of the invention.
XX
SQ Sequence 114 AA;
Query Match 100.0%; Score 597; DB 21; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.1e-45;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 QVQLVSGAEVKKPKSSVKVSCKASGTFSSHAISWVRQAPGQGLEWMGDIIPILGIGNY 60
QY 61 AOKFGRRVITTADESTSTAYMELSTLTSEDTAYVYCELDWFIYWGQGMVTVSS 114
DB 61 AOKFGRRVITTADESTSTAYMELSTLTSEDTAYVYCELDWFIYWGQGMVTVSS 114
RESULT 2
AAV50971
ID AAV50971 standard; Protein; 116 AA.
XX
XX AAV50971;
AC
XX 23-MAR-2000 (first entry)
DT
XX Human FVIII antibody A2 scFv heavy chain protein DP-10 #2.
DE
XX Human; heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; scFv; A2.
XX
XX Homo sapiens.
OS
XX WO958680-A2.
PN
XX 18-NOV-1999.
PD
XX 07-MAY-1999; 99WO-NL00285.
PF
XX 08-MAY-1998; 98EP-0201543.
PR
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
PA
XX Voorberg JJ, Van Den Brink EN, Turenhout EAM;
PI WPI; 2000-053102/04.
DR
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
XX Example 9; Fig 11A; 61pp; English.
XX
CC This invention describes a novel polynucleotide (1) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (1) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents a human

CC factor VIII antibody A2 specific scFv protein DP-10 which is used
CC in the method of the invention.
XX
XX Sequence 116 AA;
SQ
Query Match 98.2%; Score 586; DB 21; Length 116;
Best Local Similarity 98.3%; Pred. No. 5.7e-44;
Matches 114; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
Db 1 QVQLVSGAEVKKPKSSVKVSCKASGTFSSHAISWVRQAPGQGLEWMGDIIPILGIGNY 60
QY 61 AOKFGRRVITTADESTSTAYMELSTLTSEDTAYVYCELDWFIYWGQGMVTVSS 114
DB 61 AOKFGRRVITTADESTSTAYMELSTLTSEDTAYVYCELDWFIYWGQGMVTVSS 116
RESULT 3
AAG66039
ID AAG66039 standard; Protein; 271 AA.
XX
XX AAG66039;
AC
XX 27-FEB-2002 (first entry)
DT
XX scFv 1b4 antibody fragment.
DE
XX
XX Ryk protein; angiogenesis; variant; receptor tyrosine kinase; cytostatic;
KM anti-diabetic; ophthalmological; cardiac; vulnery; antiangiogenic;
KW gene therapy; fusion protein.
XX
XX Synthetic.
OS
XX WO200185789-A2.
PN
XX 15-NOV-2001.
PD
XX 09-MAY-2001; 2001WO-US15043.
PF
XX 10-MAY-2000; 2000US-0568783.
PR
XX (FARB) BAYER CORP.
PA
XX Rocznak S, Dubois-Stringfellow NA, Zolotorev A;
PI WPI; 2002-049443/06.
DR N-PSDB; AAI67770.
XX
XX Modulating angiogenesis at a site, for treating or preventing cancer,
PT metastasis, diabetic retinopathy, cardiovascular disease, wound by
PT supplying composition comprising variant Ryk protein to the site -
XX
XX Examples; Page 79-80; 81pp; English.
XX
XX The invention relates to modulating angiogenesis at a site by supplying
CC a composition comprising a variant Ryk protein (1) (a member of the
CC receptor tyrosine kinase family), or modulating formation of cells into
CC capillary-like structures by contacting the cells with a composition
CC comprising (1). The method is useful modulating angiogenesis at a site
CC (preferably, within a human) or modulating the formation of cells
CC (endothelial cells of human origin) into capillary-like structure. The
CC condition e.g., cancer, metastasis, diabetic retinopathy, macular
CC degeneration, cardiovascular disease, wound, pregnancy, or a clinical
CC condition involving angiogenesis in the reproductive system, including
CC regulation of placental vascularization in an individual. The variant
CC protein is supplied to the individual as a source of polynucleotide
CC encoding the protein and expressing the protein in vivo. (1) is used
CC as an immunogen to produce an antibody against it. The antibodies are
CC useful for modulating angiogenesis at a site. Polynucleotides encoding
CC (1) is useful in gene therapy technique for treating above mentioned
CC medical conditions. The present sequence represents the scFv 1b4 antibody

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 / Search time 36.6726 Seconds

(without alignments)
493.415 Million cell updates/sec

Title: US-09-674-752-51

Sequence: 1 QVQLVSGAEVKKKSGSSVKV.....YCELDWPFYWGQGTMTVSS 114

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	100.0	114	21	AAV50974 Human FVIII heavy
2	586	98.2	116	21	AAV50971 Human FVIII antibo
3	520.5	87.2	271	23	AA666039 scFv 1b4 antibody
4	520	87.1	118	21	AAV99558 Human Lh13 monoclo
5	516	86.4	270	23	AAU97198 Human anti-RGR 81
6	515.5	86.3	481	13	AAAR24442 Sequence of antibo
7	515	86.3	220	24	ABR01512 Human anti-TIMP-1
8	510	85.4	220	24	ABR01538 Human anti-TIMP-1
9	509.5	85.3	245	22	AA67617 Human leukocyte an

10	508.5	85.2	115	23	ABBS7559
11	508.5	85.2	225	24	ABR01510 Human anti-TIMP-1
12	508.5	85.2	245	22	AA67618 Human leukocyte an
13	508	85.1	120	18	AA67550 Human Ab heavy cha
14	508	85.1	120	24	ABJ18672 Antibody library r
15	508	85.1	120	24	ABJ18718 Antibody library r
16	507	84.9	253	23	ABP45498 Human Blys binding
17	506.5	84.8	229	24	ABR01512 Human anti-TIMP-1
18	506.5	84.8	248	23	ABP45722 Human Blys binding
19	506.5	84.8	248	23	ABP45723 Human Blys binding
20	505.5	84.7	125	22	AAU02555 Anti-adipocyte mon
21	505.5	84.7	219	22	ABR01523 Human anti-TIMP-1
22	505.5	84.7	223	24	ABR01535 Human anti-TIMP-1
23	505.5	84.7	244	23	ABP45870 Human Blys binding
24	505.5	84.7	248	23	ABP45707 Human Blys binding
25	505.5	84.7	248	23	ABP45868 Human Blys binding
26	504	84.4	222	24	ABR01531 Human anti-TIMP-1
27	504	84.4	254	23	ABP45855 Human Blys binding
28	503.5	84.3	249	21	AAAB36083 Recombinant human
29	502.5	84.2	248	23	ABP45708 Human Blys binding
30	502.5	84.2	248	23	ABP45721 Human Blys binding
31	502.5	84.2	248	23	ABP45726 Human Blys binding
32	501.5	84.0	231	24	ABR01524 Human anti-TIMP-1
33	501.5	84.0	248	23	ABP45730 Human Blys binding
34	500.5	83.8	253	23	ABP45869 Human Blys binding
35	499.5	83.7	248	23	ABP45716 Human Blys binding
36	499.5	83.6	257	23	ABP45717 Human Blys binding
37	499	83.6	257	23	ABP45542 Synthetic antibody
38	498.5	83.5	222	22	AAU04972 Synthetic antibody
39	498.5	83.5	223	22	AAU04973 APRIL binding scFv
40	498.5	83.5	245	24	ABP40521 Synthetic antibody
41	497.5	83.3	222	22	AAU04974 Synthetic antibody
42	497.5	83.3	222	22	AAU04976 Synthetic antibody
43	496	83.1	256	23	ABP45589 Human Blys binding
44	495.5	83.0	246	23	ABP46051 Human Blys binding
45	495.5	83.0	248	23	ABP45706 Human Blys binding

ALIGNMENTS

RESULT 1
AAV50974 standard; Protein: 114 AA.
AAV50974:
AC AAV50974;
XX 23-MAR-2000 (first entry)
DT XX Human FVIII heavy chain variable region protein fragment.
XX DE Human FVIII heavy chain; antibody; factor VIII; hemostatic; variable region;
XX KM Human, heavy chain; antibody; factor VIII; hemostatic; variable region;
XX KW hemophilia A.
XX OS Homo sapiens.
XX PN WO955680-A2.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99WO-NL00285.
XX PR 08-MAY-1998; 98EP-0201543.
XX PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX PI Voorberg JJ, Van Den Brink EN, Turehout EM;
XX WPI: 2000-053102/04.
XX DR N-PSDB; AA243867.
XX PT New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 11.576 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597
Sequence: 1 QVQLVQSGAEVKKRQSSVKV.....YCELDFWFIWGQGTMTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	85.1	120	4	US-09-025-769B-35
2	508	85.1	120	4	US-09-025-769B-57
3	503.5	84.3	119	4	US-09-025-769B-21
4	492.5	82.5	123	2	US-08-652-816A-1
5	492.5	82.5	123	2	US-08-652-816A-6
6	492.5	82.5	123	2	US-08-652-816A-8
7	492.5	82.5	123	2	US-08-652-816A-9
8	476.5	79.8	121	2	US-08-232-081B-41
9	474.5	79.5	119	3	US-08-983-607-50
10	474.5	79.5	120	2	US-08-428-197-12
11	474.5	79.5	120	5	PCT-US93-10555-12
12	474.5	79.5	120	5	PCT-US93-10555-13
13	474.5	79.5	120	5	PCT-US93-10555-13
14	471.5	78.0	123	2	US-08-378-919-10
15	470.5	78.8	123	2	US-08-652-816A-7
16	461	77.2	147	1	US-08-217-918-4
17	455	76.2	102	1	US-07-834-539A-55
18	455	76.2	102	1	US-08-053-111-63
19	455	76.2	102	1	US-08-645-641-63
20	455	76.2	102	1	US-07-853-408B-63
21	455	76.2	102	2	US-08-096-762-63
22	455	76.2	102	2	US-08-800-353-55
23	455	76.2	102	2	US-08-308-865-63
24	455	76.2	102	5	PCT-US92-06185-55
25	455	76.2	102	5	PCT-US92-10983-63
26	455	76.2	117	3	US-09-042-353-232
27	455	76.2	117	4	US-08-758-417A-80

28	452	75.7	128	1	US-08-202-047-22	Sequence 22, Appl
29	452	75.7	128	3	US-08-364-690-22	Sequence 22, Appl
30	452	75.7	128	4	US-08-635-109-3	Sequence 3, Appl
31	449.5	75.3	125	3	US-09-199-149-3	Sequence 3, Appl
32	441.5	74.0	129	2	US-08-561-521-45	Sequence 45, Appl
33	441.5	74.0	129	4	US-08-525-539A-77	Sequence 77, Appl
34	441.5	74.0	129	5	PCT-US95-01219-45	Sequence 45, Appl
35	435.5	72.9	122	5	PCT-US95-00067-2	Sequence 2, Appl
36	432.5	72.4	119	1	US-08-458-516-10	Sequence 10, Appl
37	432.5	72.4	232	1	US-08-458-516-22	Sequence 22, Appl
38	432.5	72.4	235	1	US-08-458-516-23	Sequence 23, Appl
39	432.5	72.4	449	1	US-08-458-516-13	Sequence 13, Appl
40	432	72.4	118	2	US-08-428-257A-78	Sequence 78, Appl
41	432	72.4	118	3	US-07-987-264-60	Sequence 60, Appl
42	431.5	72.3	117	1	US-07-634-278-105	Sequence 105, App
43	431.5	72.3	117	1	US-08-477-728-105	Sequence 105, App
44	431.5	72.3	117	1	US-08-474-040-105	Sequence 105, App
45	431.5	72.3	117	1	US-08-487-200-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-09-025-769B-35
Sequence 35, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Illig, Vlc
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-09-025-769B-35

Query Match 85.1%; Score 508; DB 4; Length 120;
Best Local Similarity 85.8%; Pred. No. 2.8e-45;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60
DB 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60
QY 61 AOKFGKRTITADESTSTAYMELSTLTSEDTAVYYCEL---DMFY---IMGGTAVYVSS 114
DB 61 AOKFGKRTITADESTSTAYMELSLRSEDIAVYYCARWGSGDFYANDYWGQGLTVYVSS 120

RESULT 2

US-09-025-769B-57
; Sequence 57, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 120 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-025-769B-57

Query Match 85.1%; Score 508; DB 4; Length 120;

Best Local Similarity 85.8%; Pred. No. 2.8e-45;

Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60
DB 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60
QY 61 AOKFGKRTITADESTSTAYMELSTLTSEDTAVYYCEL---DMFY---IMGGTAVYVSS 114
DB 61 AOKFGKRTITADESTSTAYMELSLRSEDIAVYYCARWGSGDFYANDYWGQGLTVYVSS 120

RESULT 3

US-09-025-769B-21

; Sequence 21, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-025-769B-21

Query Match 84.3%; Score 503.5; DB 4; Length 119;
Best Local Similarity 84.9%; Pred. No. 8.1e-45;
Matches 101; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60
DB 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60
QY 61 AOKFGKRTITADESTSTAYMELSTLTSEDTAVYYCEL---LDMFYIMGGTAVYVSS 114
DB 61 AOKFGKRTITADESTSTAYMELSLRSEDIAVYYCARAPYCSGDFYMGQGLTVYVSS 119

RESULT 4

US-08-652-816A-1

; Sequence 1, Application US/08652816A

; Patent No. 5872215

; GENERAL INFORMATION:

; APPLICANT: Oebourn, JK

; APPLICANT: Allen, DJ

; APPLICANT: McCafferty, JG

; TITLE OF INVENTION: Specific binding members, materials and

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

CC fragment.
XX
SQ Sequence 271 AA;

Query Match 87.2%; Score 520.5; DB 23; Length 271;
Best Local Similarity 87.2%; Pred. No. 7e-38; Mismatches 4; Indels 3; Gaps 1;
Matches 102; Conservative

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGCTFSSHAISMVRQAPQGLMMGDIPIIGTQNY 60
DB 5 EVQLVQSGAEVKKPSSSVKVCCKASGCTFSSHAISMVRQAPQGLMMGDIPIIGTQNY 64

QY 61 AOKFGRTVITADESTSTAYMELSTLTSEDPAVYCE---LDWFIWGGTMTVSS 114
DB 65 AOKFGRTVITADESTSTAYMELSLRSEDTAVYVCARSYDWFPMWGGTLTVSS 121

RESULT 4
ID AAY99558 standard; protein; 118 AA.
XX AAY99558;

AC AAY99558;
DT 20-SEP-2000 (first entry)

DE Human LH13 monoclonal antibody heavy chain variable region.

XX Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;
KM cytostatic; cytotoxic; heavy chain variable region.

XX Homo sapiens.

PN WO200032635-A2.

PD 08-JUN-2000.

PF 01-DEC-1999; 99WO-US28485.

XX 02-DEC-1999; 98US-0203768.

XX (IXSY-) IXSYS INC.

PI Watkins JD, Huse WD;

XX MPI, 2000-412293/35.

DR N-PSDB; AAA48411.

XX New tumour-specific human monoclonal antibody, useful for the treatment
PT and diagnosis of cancer, comprises at least one complementarity
PT determining region -

XX Claim 10; Page 82-83; 84pp; English.

XX The present sequence is the heavy chain variable region of a human
CC tumour-specific monoclonal antibody. Neoplastic cells selectively express
CC antigens which are not present on normal cells. Thus monoclonal
CC antibodies can be produced that are specifically directed against
CC tumour-specific antigens. The antibodies can be conjugated to cytotoxic
CC or cytostatic agents and used to selectively target cancer cells for the
CC elimination of tumours. They can also be linked to diagnostic moieties
CC that allow the imaging of neoplastic cells. Nucleic acids encoding human
CC tumour-specific monoclonal antibodies can be used to express the
CC antibodies and can be recombinantly engineered to produce modified
CC antibodies with higher affinity or higher selectivity for tumour cells.
CC Tumour-specific antibodies were produced by hybridomas that were
CC generated by in vitro immunisation of human spleen cell cultures with
CC breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
CC was then isolated from the hybridoma by RT-PCR. The present sequence
CC was produced by LH13 hybridoma cell line.

XX Sequence 118 AA;

Query Match 87.1%; Score 520; DB 21; Length 118;

Best Local Similarity 85.6%; Pred. No. 3.4e-39;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGCTFSSHAISMVRQAPQGLMMGDIPIIGTQNY 60
DB 1 QVQLVQSGAEVKKPSSSVKVCCKASGCTFSSHAISMVRQAPQGLMMGDIPIIGTQNY 60

QY 61 AOKFGRTVITADESTSTAYMELSTLTSEDPAVYCELD---WFIWGGTMTVSS 114
DB 61 AOKFGRTVITADESTSTAYMELSLRSEDTAVYVCAREDSGWHYWGCGTLTVSS 118

RESULT 5
ID AAU97198 standard; protein; 270 AA.
XX AAU97198;

AC AAU97198;

DT 27-AUG-2002 (first entry)

DE Human anti-EGFR single-chain antibody isolated from clone pSEX81-63.

XX Human; anti-epidermal growth factor receptor single-chain antibody;
KM anti-EGFR-scFv; IGM; cancer; tumour growth; clone pSEX81-63; cytostatic.

XX Homo sapiens.

PN WO200230984-A1.

PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-US31857.

XX 13-OCT-2000; 2000US-240353P.

XX (UABR-) UAB RES FOUND.

PI Ralech KP, Curriel DT, Bonner JA;

XX MPI, 2002-463261/49.

XX Novel human anti-epidermal growth factor receptor single-chain antibody
PT useful for diagnostic location and assessment of tumour growth, and in
PT treating cancer -

XX Claim 3; Fig 2; 51pp; English.

XX The present invention relates to human anti-epidermal growth factor
CC receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a
CC human IGM phage display library using EGFR as antigen. Two isolates
CC with different amino acid sequences were identified. The
CC anti-EGFR-scFvs are useful for treating cancer, and for the
CC diagnostic location and assessment of tumour growth, where the
CC anti-EGFR-scFv is radiolabelled. The present sequence represents
CC human anti-EGFR single-chain antibody isolated from clone pSEX81-63.

XX Sequence 270 AA;

Query Match 86.4%; Score 516; DB 23; Length 270;
Best Local Similarity 81.7%; Pred. No. 1.7e-37;
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGCTFSSHAISMVRQAPQGLMMGDIPIIGTQNY 60
DB 1 QVQLVQSGAEVKKPSSSVKVCCKASGCTFSSHAISMVRQAPQGLMMGDIPIIGTQNY 60

QY 61 AOKFGRTVITADESTSTAYMELSTLTSEDPAVYCELD-----WFIWGGT 108
DB 61 AOKFGRTVITADESTSTAYMELSLRSEDTAVYICADPDYVSGSYPMWFGGCT 120

QY 109 MVTVSS 114

DB 121 LTVSS 126

CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX
SQ Sequence 220 AA;

Query Match 86.3%; Score 515; DB 24; Length 220;
Best Local Similarity 87.1%; Pred. No. 1, 7e-37;
Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSHAISWVROAPGGLEMMGDIIPILCTGNY 60
DB 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSVAISWVROAPGGLEMMGDIIPILCTGNY 60
QY 61 AOKFGCRVTITADESTSTAYMELSTLTSEDTAVYVCELDWFI--WGQTMVTSS 114
DB 61 AOKFGCRVTITADESTSTAYMELSLRSEDTAVYVCELDWFI--WGQTMVTSS 116

RESULT 8

ABR01538
ID ABR01538 standard; Protein; 220 AA.

XX
AC ABR01538;

XX
DT 16-APR-2003 (first entry)

XX
DE Human anti-TIMP-1 antibody heavy chain #36.

XX
KM Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;
KM matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;
KM variable light chain; cytotactic; nephrotropic; cardiant; liver fibrosis;
KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KM lupus nephritis; glomerulosclerotic renal disease; lung cancer;
KM idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX
OS Homo sapiens.

XX
PN WO200286085-A2.

XX
PD 31-OCT-2002.

XX
PF 24-APR-2002; 2002WO-US12801.

XX
PR 24-APR-2001; 2001US-285683P.

XX
PA (FARB) BAYER CORP.

XX
PI (MORP-) MORPHOSYS AG.

XX
PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;

XX
DR WPI; 2001-129114/12.

XX
DR N-PSDB; AB274809.

XX
PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)
PT antibodies, for diagnosing or ameliorating the symptoms of a disorder
PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate
PT hypertrophy or lung cancer.

XX
PS Claim 20; Page 173; 228pp; English.

XX
CC The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)
CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of
CC TIMP-1. The antibody comprises a variable heavy chain (VHCDR3 region and
CC a variable light chain (VLCDR3 region). An antibody preparation of the
CC invention has hepatotropic, cytotactic, nephrotropic and cardiant
CC activity. The human antibody is useful for decreasing an MMP-inhibiting
CC activity of a TIMP-1. It is especially useful for ameliorating the
CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic

CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX
SQ Sequence 220 AA;

Query Match 85.4%; Score 510; DB 24; Length 220;
Best Local Similarity 87.1%; Pred. No. 4, 7e-37;
Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSHAISWVROAPGGLEMMGDIIPILCTGNY 60
DB 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSVAISWVROAPGGLEMMGDIIPILCTGNY 60
QY 61 AOKFGCRVTITADESTSTAYMELSTLTSEDTAVYVCELDWFI--WGQTMVTSS 114
DB 61 AOKFGCRVTITADESTSTAYMELSLRSEDTAVYVCELDWFI--WGQTMVTSS 116

RESULT 9

AAB67617
ID AAB67617 standard; Protein; 245 AA.

XX
AC AAB67617;

XX
DT 29-MAY-2001 (first entry)

XX
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_1.

XX
KM Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
KM miscarriage; abortion; psoriasis; antibody; HLA phenotyping; 88.

XX
OS Homo sapiens.

XX
PN WO200114558-A1.

XX
PD 01-MAR-2001.

XX
PF 28-AUG-2000; 2000WO-EP08388.

XX
PR 26-AUG-1999; 99EP-0116691.

XX
PA (MORP-) MORPHOSYS AG.

XX
PI Kretschmar T, Tesar M, Margot M, Kroenke M;

XX
DR WPI; 2001-218451/22.

XX
PT Novel isolated human immunoglobulin or functional immunoglobulin
PT fragment specific for human leukocyte antigen Cw6, useful for treatment
PT of humans and for human leukocyte antigen phenotyping.

XX
PS Claim 3; Fig 1; 23pp; English.

XX
CC AAB67617-23 represent single chain antibody (scFv) fragments which
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
CC derived from a synthetic human combinatorial antibody library based on
CC molecular consensus frameworks and CDRE randomized with trinucleotides.
CC The specification describes a human immunoglobulin fragments specific
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
CC studies of natural killer cell silencing as well as miscarriages.
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
CC Posttrans may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
CC fragments are useful for the preparation of a pharmaceutical for the
CC treatment of humans. They are also useful for HLA phenotyping.

XX
SQ Sequence 245 AA;

Query Match 85.3%; Score 509.5; DB 22; Length 245;
Best Local Similarity 87.2%; Pred. No. 5, 8e-37;
Matches 102; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

CC TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting
 CC activity of a TIMP-1. It is especially useful for ameliorating the
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 225 AA;

Query Match 85.2%; Score 508.5; DB 24; Length 225;
 Best Local Similarity 85.1%; Pred. No. 6.5e-37;
 Matches 103; Conservative 3; Mismatches 8; Indels 7; Gaps 2;

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWRQAPGQLEWMGDIIPILGTGNY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWRQAPGQLEWMGDIIPILGTGNY 60
 QY 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDW----FTYMGQSTMTVSS 113
 DB 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCARGLYMAVYPPDFMGQSTLTVSS 120
 QY 114 S 114
 DB 121 S 121

RESULT 12

ID AAB67618 standard; Protein; 245 AA.

XX AAB67618;

DT 29-MAY-2001 (first entry)

XX Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_2.

KM Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
 KM miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.

OS Homo sapiens.

PN WO200114558-A1.

PD 01-MAR-2001.

PF 28-AUG-2000; 2000WO-EP08388.

PR 26-AUG-1999; 99EP-0116691.

XX (MORP-) MORPHOSYS AG.

PI Kretzschmar T, Teear M, Marget M, Kroenke M;

DR WPI; 2001-218451/22.

XX Novel isolated human immunoglobulin or functional immunoglobulin

PT fragment specific for human leukocyte antigen Cw6, useful for treatment

PS of humans and for human leukocyte antigen phenotyping -

XX Claim 3; Fig 1; 23pp; English.

CC AAB67617-23 represent single chain antibody (scFv) fragments which
 CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
 CC derived from a synthetic human combinatorial antibody library based on
 CC molecular consensus frameworks and CDRs randomised with trinucleotides.
 CC The specification describes a human immunoglobulin fragments specific

CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
 CC studies of natural killer cell silencing as well as miscarriages.
 CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
 CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
 CC fragments are useful for the preparation of a pharmaceutical for the
 CC treatment of humans. They are also useful for HLA phenotyping.

XX Sequence 245 AA;

Query Match 85.2%; Score 508.5; DB 22; Length 245;
 Best Local Similarity 87.2%; Pred. No. 7.1e-37;
 Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWRQAPGQLEWMGDIIPILGTGNY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWRQAPGQLEWMGDIIPILGTGNY 60
 QY 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDWRY--ITGQSTMTVSS 114
 DB 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCARGPDYPMDFMGQSTLTVSS 117

RESULT 13

ID AAM27550 standard; Protein; 120 AA.

XX AAM27550;

DT 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH1A consensus.

XX Human; antibody; preparation; library; VH1A; variable region;

KM heavy chain; consensus.

OS Homo sapiens.

PN WO9708320-A1.

PD 06-MAR-1997.

PF 19-AUG-1996; 96WO-EP03647.

PR 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

PI Ge L, Ilaag V, Knappik A, Moroney S, Pack P, Plueckthun A;

DR N-PSDB; AAT67948.

PF 1997-179277/16.

XX Preparation of human derived antibody gene library - using synthetic

PT consensus sequences, and signal consensus antibody gene as universal

XX framework for highly diverse antibody libraries

PS Example 1; Fig 5A; 436pp; English.

XX The present sequence is the human antibody heavy chain

CC variable region synthetic sequence VH1A, used in the preparation of

XX a human derived antibody gene library.

XX Sequence 120 AA;

Query Match 85.1%; Score 508; DB 18; Length 120;
 Best Local Similarity 85.8%; Pred. No. 3.9e-37;
 Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;
 QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWRQAPGQLEWMGDIIPILGTGNY 60
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWRQAPGQLEWMGDIIPILGTGNY 60
 QY 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYGEL--DWFY--ITGQSTMTVSS 114

; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-9

Query Match 86.7%; Score 517.5; DB 15; Length 121;
Best Local Similarity 86.0%; Pred. No. 7.7e-44;
Matches 104; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

Oy 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Db 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Oy 61 AOKFGRTVITADESTSTAYMELSTLTSEDYAVYCC-----ELDMFYIMGGTMYV 113
Db 61 AOKFGRTVITADESTSTAYMELSLRSBEDTAVYCCAFSPETETDADIMGGTMYV 120
Oy 114 S 114
Db 121 S 121

RESULT 7
US-10-269-805-35
; Sequence 35, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-35

Query Match 86.5%; Score 516.5; DB 15; Length 125;
Best Local Similarity 83.2%; Pred. No. 1e-43;
Matches 104; Conservative 3; Mismatches 7; Indels 11; Gaps 1;

Oy 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Db 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Oy 61 AOKFGRTVITADESTSTAYMELSTLTSEDYAVYCC-----LDMFYIMGGTMY 109
Db 61 AOKFGRTVITADESTSTAYMELSLRSBEDTAVYCCARSPIYDILTGTIDAFDIWGGTMY 120
Oy 110 VTSS 114
Db 121 VTSS 125

RESULT 8
US-09-976-118-2
; Sequence 2, Application US/09976118
; Patent No. US20020058033A1
; GENERAL INFORMATION:
; APPLICANT: Raiech, Kevin Paul
; APPLICANT: Curiel, David T.
; APPLICANT: Bonner, James Allen

; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 270
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFv
; OTHER INFORMATION: clone pSEX81-63
US-09-976-118-2

Query Match 86.4%; Score 516; DB 9; Length 270;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;

Oy 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Db 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Oy 61 AOKFGRTVITADESTSTAYMELSTLTSEDYAVYCC-----WFIYMGCT 108
Db 61 AOKFGRTVITADESTSTAYMELSLRSBEDTAVYCCARDPDYVSGSYRPMFDPMGCT 120
Oy 109 MYVSS 114
Db 121 LVTVSS 126

RESULT 9
US-10-269-805-3
; Sequence 3, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-3

Query Match 86.2%; Score 514.5; DB 15; Length 123;
Best Local Similarity 83.7%; Pred. No. 1.5e-43;
Matches 103; Conservative 4; Mismatches 7; Indels 9; Gaps 2;

Oy 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Db 1 OVQLVQSGAEVKKPGSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60
Oy 61 AOKFGRTVITADESTSTAYMELSTLTSEDYAVYCC-----ELDM--FYIMGGTMY 111
Db 61 AOKFGRTVITADESTSTAYMELSLRSBEDTAVYCCARGVGDMDLSPDYMGCTLYT 120
Oy 112 VSS 114
Db 121 VSS 123

RESULT 10
US-10-269-805-49

4	492.5	123	2	US-08-428-197-12
5	492.5	121	3	US-08-428-1055-13
6	492.5	119	2	US-08-428-1055-13
7	492.5	120	2	PCT-US93-1055-10
8	476.5	120	5	PCT-US93-939-7
9	474.5	120	5	US-08-652-816A-4
10	474.5	120	2	US-08-217-918-55
11	474.5	123	2	US-08-217-918-63
12	474.5	147	1	US-08-645-408B-63
13	471.5	102	1	US-08-851-762-55
14	461	102	1	US-08-800-353-63
15	455	102	2	US-08-800-865-55
16	455	102	2	US-08-308-06185-63
17	455	102	2	PCT-US92-10983-63
18	455	102	2	PCT-US92-353-232
19	455	102	5	PCT-US92-353-232
20	455	102	5	US-08-758-417A-80
21	455	102	3	US-08-758-417A-80
22	455	117	4	US-08-758-417A-80
23	455	117	4	US-08-758-417A-80
24	455	117	4	US-08-758-417A-80
25	455	117	4	US-08-758-417A-80
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27	455	117	4	US-08-758-417A-80

Sequence 4, Appl
 Sequence 55, Appl
 Sequence 63, Appl
 Sequence 63, Appl
 Sequence 63, Appl
 Sequence 63, Appl
 Sequence 55, Appl
 Sequence 63, Appl
 Sequence 55, Appl
 Sequence 63, Appl
 Sequence 232, Appl
 Sequence 80, Appl

MUR-5-10-
 US-09-0225-10-
 Query Match Similarity
 Best Loc 1001
 Matches

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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 12.3883 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642
Sequence: 1 EVOLVESGDLVQPGSLRL.....GKYYGMDVMGQITTVSS 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	81.8	120	4	US-09-025-769B-38 Sequence 38, Appl
2	525	81.8	120	4	US-09-025-769B-63 Sequence 63, Appl
3	525	81.8	281	4	US-09-025-769B-178 Sequence 178, App
4	524.5	81.7	249	4	US-10-039-785-53 Sequence 53, Appl
5	518	80.7	122	2	US-07-934-373C-21 Sequence 21, Appl
6	518	80.7	122	3	US-08-437-642B-21 Sequence 21, Appl
7	518	80.7	122	4	US-08-146-206C-21 Sequence 21, Appl
8	518	80.7	122	5	PCR-US93-07832-21 Sequence 21, Appl
9	513	79.9	140	3	US-08-983-607-32 Sequence 32, Appl
10	510	79.4	263	4	US-09-069-821-3 Sequence 3, Appl
11	510	79.4	283	4	US-09-420-592A-6 Sequence 6, Appl
12	506.5	78.9	125	2	US-08-428-197-1 Sequence 1, Appl
13	506.5	78.9	125	3	PCR-US93-10555-1 Sequence 1, Appl
14	501.5	78.1	113	3	US-08-974-899-6 Sequence 99, Appl
15	499.5	77.8	125	1	US-08-478-039-99 Sequence 99, Appl
16	499.5	77.8	125	1	US-08-476-348A-99 Sequence 99, Appl
17	498	77.6	120	2	US-07-934-373C-4 Sequence 4, Appl
18	498	77.6	120	3	US-08-437-642B-4 Sequence 4, Appl
19	498	77.6	120	4	US-08-146-206C-4 Sequence 4, Appl
20	497	77.4	120	5	PCR-US93-07832-4 Sequence 4, Appl
21	497	77.4	124	3	US-08-983-607-47 Sequence 28, Appl
22	497	77.4	131	3	US-08-983-607-28 Sequence 28, Appl
23	495	77.1	124	3	US-08-983-607-51 Sequence 51, Appl
24	491.5	76.6	117	3	US-08-983-607-46 Sequence 46, Appl
25	489	76.2	112	5	PCR-US93-08435-12 Sequence 12, Appl
26	488.5	76.1	117	4	US-09-025-769B-14 Sequence 24, Appl
27	488.5	76.1	123	2	US-08-665-202-30 Sequence 30, Appl

28	488.5	76.1	123	4	US-09-315-574-30 Sequence 30, Appl
29	487	75.9	116	2	US-08-428-197-2 Sequence 2, Appl
30	487	75.9	116	5	PCT-US93-10555-2 Sequence 2, Appl
31	487	75.9	122	5	PCT-US93-08435-43 Sequence 43, Appl
32	486	75.7	115	3	US-08-983-607-36 Sequence 36, Appl
33	485.5	75.6	117	3	US-09-157-370-1 Sequence 1, Appl
34	485	75.5	126	3	US-08-983-607-48 Sequence 48, Appl
35	484.5	75.5	119	2	US-07-988-925-11 Sequence 11, Appl
36	484.5	75.5	119	2	US-08-362-780-11 Sequence 11, Appl
37	484	75.4	122	5	PCT-US93-08435-14 Sequence 14, Appl
38	481.5	75.0	120	2	US-08-428-197-20 Sequence 20, Appl
39	481.5	75.0	120	2	PCT-US93-10555-20 Sequence 20, Appl
40	481	74.9	118	2	US-08-958-201-2 Sequence 2, Appl
41	481	74.9	118	2	US-08-958-201-4 Sequence 4, Appl
42	481	74.9	144	1	US-08-026-320A-2 Sequence 2, Appl
43	480.5	74.8	115	5	US-08-428-197-42 Sequence 42, Appl
44	480.5	74.8	115	5	PCT-US93-10555-42 Sequence 42, Appl
45	480.5	74.8	120	2	US-08-428-197-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-38
Sequence 38, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-09-025-769B-38
Query Match 81.8%; Score 525; DB 4; Length 120;
Best Local Similarity 82.0%; Pred. No. 1.9e-43;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVOLVESGDLVOPGSLRLSCAAGFTFSPNPMWVRQAPGKGLWVAIIGRSGTTFY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSSYAMSWVRQAPGKGLWVAISGSGSTTY 60
QY 61 ADVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 120
DB 61 ADVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 118
QY 121 SS 122
DB 119 SS 120

RESULT 2
US-09-025-769B-63
; Sequence 63, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly) peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-63

Query Match 81.8%; Score 525; DB 4; Length 120;
Best Local Similarity 82.0%; Pred. No. 1.9e-43;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVOLVESGDLVOPGSLRLSCAAGFTFSPNPMWVRQAPGKGLWVAIIGRSGTTFY 60
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSSYAMSWVRQAPGKGLWVAISGSGSTTY 60
QY 61 ADVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 120
DB 61 ADVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 118
QY 121 SS 122

DB 119 SS 120

RESULT 3
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly) peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 81.8%; Score 525; DB 4; Length 281;
Best Local Similarity 82.0%; Pred. No. 4.9e-43;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVOLVESGDLVOPGSLRLSCAAGFTFSPNPMWVRQAPGKGLWVAIIGRSGTTFY 60
DB 26 EVOLVESGGGLVOPGSLRLSCAAGFTFSSYAMSWVRQAPGKGLWVAISGSGSTTY 85
QY 61 ADVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 120
DB 86 ADVKGRFTISRDNKNTLYLQNMNLSRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 143
QY 121 SS 122
DB 144 SS 145

RESULT 4
US-10-039-785-53
; Sequence 53, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.

```

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53

Query Match      81.7%; Score 524.5; DB 4; Length 249;
Best Local Similarity 80.0%; Pred. No. 4,8e-43;
Matches 100; Conservative 12; Mismatches 10; Indels 3; Gaps 1;

Qy      1 EVOLVESGGLVOPGSGSLRLSCAASGFTFSNFAAMSWVRQAPGKGLIEWVAALGSGSGTFF 60
Db      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSTAMSWVRQAPGKGLIEWVAISGSGSGTFF 60
Qy      61 ADSVKGRTISRDSKNTLVYLEMNSLRAPDAIYYCAKRGGRGKYKGM-DVWGCGTTVT 117
Db      61 ADSVKGRTISRDSKNTLVLYQMNSLRAPDAIYYCAKRGGRGKYKGM-DVWGCGTTVT 120
Qy      118 VTVSS 122
Db      121 VTVSS 125

RESULT 5
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
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; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-21

Query Match      80.7%; Score 518; DB 2; Length 122;
Best Local Similarity 82.1%; Pred. No. 9,1e-43;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

Qy      1 EVOLVESGGLVOPGSGSLRLSCAASGFTFSNFAAMSWVRQAPGKGLIEWVAALGSGSGTFF 60
Db      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSTAMSWVRQAPGKGLIEWVAISGSGSGTFF 60
Qy      61 ADSVKGRTISRDSKNTLVYLEMNSLRAPDAIYYCAKRGGRGKYKGM-DVWGCGTTVT 119
Db      61 ADSVKGRTISRDSKNTLVLYQMNSLRAPDAIYYCAKRGVGVISGLVDYWGCGTILVT 119
Qy      120 VSS 122
Db      120 VSS 122

RESULT 6
US-08-437-642B-21
; Sequence 21, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-21

Query Match
Best Local Similarity 80.7%; Score 518; DB 3; Length 122;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

QY 1 EVOLVESGGDLVQPGSLRLSCAASGFTFSNFMAMSVWROAPGKLEWVAIGRSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMSVWROAPGKLEWVSISGDGSGTTY 60
QY 61 ADVKGRFTISRNSKNTLYLEENSLRAEDTAIYYCAKRGGRGYKYYGM-DVWGQGTLYT 119
DB 61 ADVKGRFTISRNSKNTLYLQMSLRAEDTAIYYCA-RGRVGYSLSLGLDYWGQGTLYT 119
QY 120 VSS 122
DB 120 VSS 122

RESULT 7
US-08-146-206C-21
Sequence 21, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
US-08-146-206C-21

Query Match
Best Local Similarity 80.7%; Score 518; DB 4; Length 122;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

QY 1 EVOLVESGGDLVQPGSLRLSCAASGFTFSNFMAMSVWROAPGKLEWVAIGRSGTTY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTFSYAMSVWROAPGKLEWVSISGDGSGTTY 60
QY 61 ADVKGRFTISRNSKNTLYLEENSLRAEDTAIYYCAKRGGRGYKYYGM-DVWGQGTLYT 119
DB 61 ADVKGRFTISRNSKNTLYLQMSLRAEDTAIYYCA-RGRVGYSLSLGLDYWGQGTLYT 119
QY 120 VSS 122
DB 120 VSS 122

RESULT 8
PCT-US93-07832-21
Sequence 21, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: Linear
PCT-US93-07832-21

Query Match
Best Local Similarity 80.7%; Score 518; DB 5; Length 122;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

QY 1 EVOLVESGGDLVQPGSLRLSCAASGFTFSNFMAMSVWROAPGKLEWVAIGRSGTTY 60

Db 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLIEWTVISGGGSTRY 60
QY 61 ADVSKGRFTISRDNSKNTVLYEMNSLRADDTAIYYCARGRGKYTKGH-DWVGQGTYYT 119
Db 61 ADVSKGRFTISRDNSKNTVLYEMNSLRADDTAVYYCA-RGRVGSLSGLYDYGQGTLYT 119
QY 120 VSS 122
119
Db 120 VSS 122

RESULT 9

US-08-983-607-32
; Sequence 32, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Klinek
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; CLONE: V86
; FEATURE:
; NAME/KEY: heavy chain and linker
; US-08-983-607-32

Query Match 79.9%; Score 513; DB 3; Length 140;
Best Local Similarity 80.2%; Pred. No. 3,2e-42;
Matches 101; Conservative 11; Mismatches 8; Indels 6; Gaps 3;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSNPAWSVRQAPGKGLIEWVAALIGRSGTYY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLIEWVAALISGSGSTRY 60
QY 61 ADVSKGRFTISRDNSKNTVLYEMNSLRADDTAIYYCAK----RGRGKYTKGMDVGQGT 116
Db 61 ADVSKGRFTISRDNSKNTVLYEMNSLRADDTAVYYCAKGMGRGEG-DYY-MDVGKGT 118
QY 117 TTVTSS 122
119
Db 119 MVTWSS 124

RESULT 10

US-09-069-821-3
; Sequence 3, Application US/09069821
; Patent No. 6323322
; GENERAL INFORMATION:
; APPLICANT: FILIPILA, DAVID
; APPLICANT: MANG, MAOLIANG
; APPLICANT: SHOR, ROBERT
; APPLICANT: WHITLOW, MARC
; APPLICANT: LEE, LHSYNG S.
; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
; TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,821
; FILING DATE: 30-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,449
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KIM, JUDITH U.
; REGISTRATION NUMBER: 40,679
; REFERENCE/DOCKET NUMBER: 0977, 2280003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-09-069-821-3

Query Match 79.4%; Score 510; DB 4; Length 263;
Best Local Similarity 77.1%; Pred. No. 1,3e-41;
Matches 101; Conservative 11; Mismatches 9; Indels 10; Gaps 3;

CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howell, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
PCT-US93-10555-1

Query Match 78.9%; Score 506.5; DB 5; Length 125;
Best Local Similarity 77.3%; Pred. No. 1.2e-41;
Matches 99; Conservative 9; Mismatches 11; Indels 9; Gaps 2;

QY 1 EVQLVESGGDLVOPGSGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYAAIGRSGTTFY 60
DB 1 EVQLVESGGDLVOPGSGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYAAIGRSGTTFY 60
QY 61 ADVSKGRFTISRDNKNTLYLQNSLRADDTAVYYCAR--GQVLYSGSGTHMFDPMWQ 114
DB 61 ADVSKGRFTISRDNKNTLYLQNSLRADDTAVYYCTK---GQVLYSGSGTHMFDPMWQ 117
QY 115 GTTVVSS 122
DB 118 GTTVVSS 125

RESULT 14
US-08-974-899-6
Sequence 6, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardeau, Paula M.
TITLE OF INVENTION: Humanized Anti-CD1a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-6

Query Match 78.1%; Score 501.5; DB 3; Length 113;
Best Local Similarity 78.7%; Pred. No. 3.2e-41;
Matches 96; Conservative 9; Mismatches 8; Indels 9; Gaps 1;

QY 1 EVQLVESGGDLVOPGSGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYAAIGRSGTTFY 60
DB 1 EVQLVESGGDLVOPGSGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYVSISSGSGTTFY 60
QY 61 ADVSKGRFTISRDNKNTLYLQNSLRADDTAVYYCAR--GQVLYSGSGTHMFDPMWQ 120
DB 61 ADVSKGRFTISRDNKNTLYLQNSLRADDTAVYYCAR-----GQVLYSGSGTHMFDPMWQ 111
QY 121 SS 122
DB 112 SS 113

RESULT 15
US-08-478-039-99
Sequence 99, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teekin Eeq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-478-039-99

Query Match 77.8%; Score 499.5; DB 1; Length 125;
Best Local Similarity 77.3%; Pred. No. 5.6e-41;
Matches 99; Conservative 8; Mismatches 12; Indels 9; Gaps 2;

QY	1	EVQLVESGGDLVQPGSGSLRLSCAASGFTFSNFMPSWVRQAPGKGLEWVAIAIGRSQTTFY	60
DB	1	EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAIAISGSGSTYY	60
QY	61	ADSVKGRFTISRDNKNTVYLEMNSLRAPDAIYYCAKRGSGYKYYG-----MDVMGQ	114
DB	61	ADSVKGRFTISRDNKNTVLYIQMNSLRAPDAIYYCAK---GQVLYYGGSGYHMFDPMGQ	117
QY	115	GTTVTWSS	122
DB	118	GTLVTWSS	125

Search completed: December 30, 2003, 11:05:37
Job time: 13.4716 secs

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 11.576 Seconds
(without alignments)
416.677 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597

Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....YCELDWFYWGQGTMTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/6C COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/6D COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	85.1	120	4	US-09-025-769B-35
2	508	85.1	120	4	US-09-025-769B-57
3	503.5	84.3	119	4	US-09-025-769B-21
4	492.5	82.5	123	2	US-08-652-816A-1
5	492.5	82.5	123	2	US-08-652-816A-6
6	492.5	82.5	123	2	US-08-652-816A-8
7	492.5	82.5	123	2	US-08-652-816A-9
8	476.5	79.8	121	2	US-08-232-081B-41
9	474.5	79.5	119	3	US-08-383-607-50
10	474.5	79.5	120	2	US-08-428-197-12
11	474.5	79.5	120	2	US-08-428-197-13
12	474.5	79.5	120	5	PCT-US93-10555-12
13	474.5	79.5	120	5	PCT-US93-10555-13
14	471.5	79.0	476	2	US-08-378-939-10
15	470.5	78.8	123	2	US-08-652-816A-7
16	461	77.2	147	1	US-08-217-918-4
17	455	76.2	102	1	US-07-834-539A-55
18	455	76.2	102	1	US-08-653-131-63
19	455	76.2	102	1	US-08-645-641-63
20	455	76.2	102	1	US-07-853-408B-63
21	455	76.2	102	2	US-08-096-762-63
22	455	76.2	102	2	US-08-800-353-55
23	455	76.2	102	2	US-08-308-865-63
24	455	76.2	102	5	PCT-US92-06185-55
25	455	76.2	102	5	PCT-US92-10983-63
26	455	76.2	117	3	US-09-042-353-232
27	455	76.2	117	4	US-08-758-417A-80

28 452 75.7 128 1 US-08-202-047-22 Sequence 22, Appl
29 452 75.7 128 3 US-08-964-690-22 Sequence 22, Appl
30 452 75.7 128 4 US-08-635-109-3 Sequence 3, Appl
31 449.5 75.3 125 3 US-09-199-149-3 Sequence 3, Appl
32 441.5 74.0 129 2 US-08-561-521-45 Sequence 45, Appl
33 441.5 74.0 129 4 US-08-525-539A-77 Sequence 77, Appl
34 441.5 74.0 129 5 PCT-US95-01219-45 Sequence 45, Appl
35 435.5 72.9 122 5 PCT-US95-00067-2 Sequence 10, Appl
36 432.5 72.4 119 1 US-08-458-516-10 Sequence 22, Appl
37 432.5 72.4 222 1 US-08-458-516-22 Sequence 22, Appl
38 432.5 72.4 235 1 US-08-458-516-23 Sequence 13, Appl
39 432.5 72.4 449 1 US-08-458-516-13 Sequence 78, Appl
40 432 72.4 118 2 US-08-428-257A-78 Sequence 60, Appl
41 432 72.4 118 3 US-07-987-264-60 Sequence 105, App
42 431.5 72.3 117 1 US-07-634-278-105 Sequence 105, App
43 431.5 72.3 117 1 US-08-477-728-105 Sequence 105, App
44 431.5 72.3 117 1 US-08-474-040-105 Sequence 105, App
45 431.5 72.3 117 1 US-08-487-200-105 Sequence 105, App

ALIGNMENTS

RESULT 1
US-09-025-769B-35
; Sequence 35, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-35

Query Match 85.1%; Score 508; DB 4; Length 120;
Best Local Similarity 85.8%; Pred. No. 2.8e-45;
Matches 103; Conservative 8; Mismatches 6; Gaps 2;


```

QY 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
QY 61 AOKFQGRVTITADESTSTAYMELSLTSTEDTAVVYCEL---DWFY---IMGGQTMVTVSS 114
DB 61 AOKFQGRVTITADESTSTAYMELSLRSEDSTAVVYCARWGGDGFYAMDYWGQGLTVTVSS 120

```

RESULT 2

```

US-09-025-769B-57
; Sequence 57, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-57

```

```

Query Match 85.1%; Score 508; DB 4; Length 120;
Best Local Similarity 85.8%; Pred. No. 2.8e-45;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
QY 61 AOKFQGRVTITADESTSTAYMELSLTSTEDTAVVYCEL---DWFY---IMGGQTMVTVSS 114
DB 61 AOKFQGRVTITADESTSTAYMELSLRSEDSTAVVYCARWGGDGFYAMDYWGQGLTVTVSS 120

```

RESULT 3

```

US-09-025-769B-21
; Sequence 21, Application US/09025769B
; Patent No. 6300064

```

```

; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-21

```

```

Query Match 84.3%; Score 503.5; DB 4; Length 119;
Best Local Similarity 84.9%; Pred. No. 8.1e-45;
Matches 101; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
QY 61 AOKFQGRVTITADESTSTAYMELSLTSTEDTAVVYCE-----LDMFYIWGGQTMVTVSS 114
DB 61 AOKFQGRVTITADESTSTAYMELSLRSEDSTAVVYCARAPGVCSGFDYWGQGLTVTVSS 119

```

RESULT 4

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US-08-652-816A-1
; Sequence 1, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

```

```

; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 427
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-427

```

```

Query Match      80.9%; Score 519.5; DB 12; Length 313;
Best Local Similarity 78.9%; Pred. No. 2.9e-40;
Matches 101; Conservative 9; Mismatches 11; Indels 7; Gaps 2;

Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGTTFY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGTTFY 120

Qy 61 ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAKRGK-----GYKYGMVWGQ 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKSHFGYYYDSGYSY-FDYWGQ 179

Qy 115 GTTVTVSS 122
   |||:|||||
Db 180 GTLVTVSS 187

```

```

RESULT 15
US-10-001-934-39
; Sequence 39, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
; TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/001,934
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-39

```

```

Query Match      80.8%; Score 519; DB 15; Length 118;
Best Local Similarity 81.1%; Pred. No. 1.2e-40;
Matches 99; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGTTFY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGTTFY 60

Qy 61 ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAKRGKGYKYGMVWGQTTVTY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR----GYGRYSPDLWGQTLVTY 116

Qy 121 SS 122
   |||:
Db 117 SS 118

```

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Search completed: December 30, 2003, 11:45:25
Job time : 26.1641 secs

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Db      121 GTMTVSS 128
      || |||||
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

RESULT 11
US-09-811-123-3
; Sequence 3, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT-073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

Query Match      81.2%; Score 521.5; DB 9; Length 119;
Best Local Similarity 83.6%; Pred. No. 7e-41;
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

Qy      1 EVLVESGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAATIGRSGTTFY 60
Db      1 EVLVESGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAATIGRSGTTFY 60
      |||||
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
      |||||
Qy      121 SS 122
Db      118 SS 119

Query Match      81.2%; Score 521.5; DB 15; Length 119;
Best Local Similarity 83.6%; Pred. No. 7e-41;
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

RESULT 12
US-10-268-501-6
; Sequence 6, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Slikowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain consensus sequence
US-10-268-501-6

Query Match      81.2%; Score 521.5; DB 15; Length 119;
Best Local Similarity 83.6%; Pred. No. 7e-41;
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

RESULT 13
US-09-880-748-1974
; Sequence 1974, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1974
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1974

Query Match      81.0%; Score 520; DB 11; Length 248;
Best Local Similarity 78.7%; Pred. No. 2.1e-40;
Matches 96; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy      1 EVLVESGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAATIGRSGTTFY 60
Db      1 EVLVQSGGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVSYISSSGTTIY 60
      |||||
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
      |||||
Qy      121 SS 122
Db      121 SS 122

RESULT 14
US-10-291-265-427
; Sequence 427, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
```

```

Db      121 VTVSS 125
|||||
RESULT 8
US-10-039-785-53
; Sequence 53, Application US/10039785
; Publication No. US2002006746A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T106F07 scFv
US-10-039-785-53

```

```

Query Match      81.7%; Score 524.5; DB 13; Length 249;
Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3; Gaps 1;

Qy      1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60
      |||||
Db      1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60
      |||||

Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG---GRGKYKYMGMVWGQTT 117
      |||||
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG---GRGKYKYMGMVWGQTT 120
      |||||

Qy      118 VTVSS 122
      |||||
Db      121 VTVSS 125
      |||||

```

```

RESULT 9
US-09-880-748-1605
; Sequence 1605, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816

```

```

; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1605
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1605

```

```

Query Match      81.7%; Score 524.5; DB 11; Length 251;
Best Local Similarity 80.0%; Pred. No. 8.1e-41;
Matches 100; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

Qy      1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60
      |||||
Db      1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60
      |||||

Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG---CYKYYGMDVMWGQTT 117
      |||||
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG---CYKYYGMDVMWGQTT 120
      |||||

Qy      118 VTVSS 122
      |||||
Db      121 VTVSS 125
      |||||

```

```

RESULT 10
US-09-880-748-1701
; Sequence 1701, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1701
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1701

```

```

Query Match      81.3%; Score 522; DB 11; Length 254;
Best Local Similarity 78.1%; Pred. No. 1.4e-40;
Matches 100; Conservative 11; Mismatches 11; Indels 6; Gaps 1;

Qy      1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60
      |||||
Db      1 EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60
      |||||

Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG-----RGKYKYMGMVWGQ 114
      |||||
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG-----RGKYKYMGMVWGQ 120
      |||||

Qy      115 GTTVTVSS 122

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; ORGANISM: Homo sapiens
US-09-840-459-76

Query Match      82.8%; Score 531.5; DB 10; Length 125;
Best Local Similarity 82.5%; Pred. No. 8.8e-42;
Matches 104; Conservative 8; Mismatches 9; Indels 5; Gaps 2;

Qy 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCAK-----RGRGGYKYYGMDVWGQGT 116
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCAKDIETAMFPY--YFGMDVWGQGT 119
Qy 117 TVTVSS 122
Db 120 TVTVSS 125

RESULT 5
US-10-025-687-4
; Sequence 4, Application US/10025687
; Publication No. US2002014225A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-4

Query Match      81.8%; Score 525; DB 14; Length 120;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Qy 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCAKRGGRGKYYKYYGMDVWGQGT 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCARWGGDG--FYAMDYWGQGT 118
Qy 121 SS 122
Db 119 SS 120

RESULT 6
US-10-125-687-4
; Sequence 4, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-4

Query Match      81.8%; Score 525; DB 15; Length 120;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Qy 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCAKRGGRGKYYKYYGMDVWGQGT 120
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCARWGGDG--FYAMDYWGQGT 118
Qy 121 SS 122
Db 119 SS 120

RESULT 7
US-10-139-785-53
; Sequence 53, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006F07 scFv
US-10-139-785-53

Query Match      81.7%; Score 524.5; DB 12; Length 249;
Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3; Gaps 1;

Qy 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPQGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCAKRGGRGKYYKYYGMDVWGQGT 117
Db 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAIYYCAREPSFOQMGHYSYGMVWGQGT 120
Qy 118 VTVSS 122
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Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;
Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKRG-----GGYKYYGMDVWGQ 114
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKRRNYDFWSGXYYYYGMDVWGQ 120
Qy 115 GTTVTVSS 122
Db 121 GTTVTVSS 128

RESULT 2
US-09-840-459-79
; Sequence 79, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-79

Query Match 85.5%; Score 549; DB 10; Length 128;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;
Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;
Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKRG-----GGYKYYGMDVWGQ 114
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKRRNYDFWSGXYYYYGMDVWGQ 120
Qy 115 GTTVTVSS 122
Db 121 GTTVTVSS 128

RESULT 3
US-09-840-459-84
; Sequence 84, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-79

Query Match 85.5%; Score 549; DB 10; Length 128;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;
Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;
Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKRG-----GGYKYYGMDVWGQ 114
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKRRNYDFWSGXYYYYGMDVWGQ 120
Qy 115 GTTVTVSS 122
Db 121 GTTVTVSS 128

RESULT 4
US-09-840-459-76
; Sequence 76, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(125)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-84
```

```
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-012
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US/09/840,459
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-84

Query Match 85.3%; Score 547.5; DB 10; Length 125;
Best Local Similarity 84.0%; Pred. No. 3e-43;
Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSCTFF 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAK---RGRGGYKYYGMDVWGQ 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAIYCAKAVVRGVISYYYYGMDVWGQ 120
Qy 118 VTVSS 122
Db 121 VTVSS 125

RESULT 4
US-09-840-459-76
; Sequence 76, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(125)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-76
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 26.1641 Seconds
(without alignments)
927.994 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642

Sequence: 1 EVQLVDSGDLVQPGGSLRL.....GKYIGMDVWGQGTTVTVSS 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	85.5	128	10	US-09-840-459-77
2	549	85.5	128	10	US-09-840-459-77
3	547.5	85.3	125	10	US-09-840-459-84
4	531.5	82.8	125	10	US-09-840-459-76
5	525	81.8	120	14	US-10-025-687-4
6	525	81.8	120	15	US-10-125-687-4
7	524.5	81.7	249	12	US-10-139-785-53
8	524.5	81.7	249	13	US-10-039-785-53
9	524.5	81.7	251	11	US-09-880-748-1605
10	522	81.3	254	11	US-09-880-748-1701
11	521.5	81.2	119	9	US-09-811-123-3
12	521.5	81.2	119	15	US-10-268-501-6
13	520	81.0	248	11	US-09-880-748-1974
14	519.5	80.9	313	12	US-10-291-265-427
15	519	80.8	118	15	US-10-001-934-39

16	518	80.7	253	12	US-10-120-414-76
17	517	80.5	124	10	US-09-840-459-81
18	516	80.4	124	15	US-10-040-244-16
19	515.5	80.3	224	11	US-09-372-656-68
20	515.5	80.3	253	11	US-09-880-748-989
21	515	80.2	248	11	US-09-880-748-1965
22	515	80.2	251	11	US-09-880-748-908
23	514	80.1	136	12	US-10-045-674-487
24	514	80.1	367	12	US-10-045-674-453
25	513.5	80.0	119	12	US-10-044-896-6
26	511	79.6	128	10	US-09-840-459-78
27	511	79.6	252	11	US-09-880-748-1431
28	510.5	79.5	248	11	US-09-880-748-913
29	510	79.4	248	11	US-09-880-748-921
30	510	79.4	251	11	US-09-880-748-1456
31	510	79.4	251	11	US-09-880-748-1740
32	510	79.4	252	11	US-09-880-748-1637
33	510	79.4	254	11	US-09-880-748-1739
34	510	79.4	263	10	US-09-956-086-3
35	510	79.4	263	10	US-09-956-087-3
36	510	79.4	283	10	US-09-983-580-6
37	510	79.4	283	10	US-09-985-442-6
38	509.5	79.4	244	12	US-10-322-673-45
39	509.5	79.4	251	11	US-09-880-748-1171
40	508.5	79.2	121	10	US-09-840-459-92
41	508.5	79.2	123	10	US-09-840-459-82
42	508	79.1	124	10	US-09-840-459-89
43	508	79.1	124	12	US-10-308-817-190
44	508	79.1	245	12	US-10-322-673-43
45	507.5	79.0	431	12	US-10-045-674-588

ALIGNMENTS

RESULT 1
US-09-840-459-77
; Sequence 77, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-77

Query Match 85.5%; Score 549; DB 10; Length 128;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;

XX CC This invention relates to a novel humanised, chimeric or human
 CC monoclonal antibody or its antigen binding portion that specifically
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
 CC The antibodies may also be useful for increasing IGF-IR activity and
 CC thus restoring IGF-IR activity in a condition characterised by low
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
 CC invention is also useful for inducing apoptosis of specific cells in a
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,
 CC gigantism, priortias and atherosclerosis. Fully human anti-IGF-IR
 CC antibodies minimise the immunogenic and allergic responses intrinsic to
 CC mouse or mouse-derived monoclonal antibodies and thus increase the
 CC efficacy and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention.

XX SQ Sequence 124 AA;
 Query Match 81.5%; Score 523.5; DB 23; Length 124;
 Best Local Similarity 80.6%; Pred. No. 1.7e-41;
 Matches 100; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

Qy 2 VOLVESGGDLVOPGGSLRLSCAASGFTFSNFMNSWVRQAPGKLEWVAALGGRSGTTFYA 61
 Db 1 VOLLESGLVQPGGSLRLSCTASGFTFSYANWVRQAPGKLEWVAISGSGGTTFYA 60
 Qy 62 DSVKGRFTISRDNKNTVYLEMNSLRADDTAIYYCAKR---GRGGYKYGYMDVWGQGTTV 118
 Db 61 DSVKGRFTISRDNKNTVLYQMNSLRADDTAVYYCAKDLGHSDSYIYYGMDVWGQGTTV 120
 Qy 119 TVSS 122
 Db 121 TVSS 124

RESULT 15
 ABP56504
 ID ABP56504 standard; Protein; 121 AA.

XX AC ABP56504;

XX DT 20-MAR-2003 (first entry)

XX DE Human anti-Fc-epsilon-R1 alpha autoantibody heavy chain LTM-alpha-15.

XX KW Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;
 KW allergic disease; urticaria; late phase allergic reaction; malignancy;
 KW intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;
 KW conditional autoimmunity; IgE mediated disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200202085-A2.

XX PD 17-OCT-2002.

XX PF 03-APR-2002; 2002WO-EP03660.

XX PR 04-APR-2001; 2001US-281024P.

XX PA (ZLBB-) ZLB BIOPLASMA AG.

XX FI Miescher S;

XX DR WPI; 2003-103348/09.

XX PT Identifying and obtaining inhibitor of a pathological process for
 PT treating e.g. autoimmunity comprises determining if a compound is
 PT capable of modulating the binding of the Fc-epsilon-R1 receptor and an
 PT autoantibody against its alpha-chain -
 XX Claim 20; Page 22; 29pp; English.

XX CC The present invention describes a method for identifying and obtaining
 CC an inhibitor of a pathological process. The method comprises determining
 CC if a compound is capable of modulating the binding of the Fc-epsilon-R1
 CC receptor alpha-chain and an autoantibody against its alpha-chain. Also
 CC described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor
 CC alpha-chain for identifying and obtaining an inhibitor of a pathological
 CC process; (2) use of the identified inhibitor for inhibiting activity of
 CC the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and
 CC (3) a compound identified by the method, which binds but does not
 CC activate the receptor; and (4) a polypeptide capable of specific binding
 CC to the Fc-epsilon-R1 receptor alpha-chain. The method is useful for
 CC obtaining an inhibitor of a pathological process e.g. imbalance between
 CC cell-bound and free IgE e.g. allergic disease (urticaria, late phase
 CC allergic reactions, intrinsic asthma, drug intolerance and food
 CC intolerance), IgE mediated disease or malignancy. The compound is useful
 CC for treating a pathological process, particularly conditional
 CC autoimmunity. The present sequence represents a human recombinant
 CC anti-Fc-epsilon-R1 alpha autoantibody heavy chain protein sequence from
 CC the present invention.

XX SQ Sequence 121 AA;

Query Match 81.4%; Score 522.5; DB 24; Length 121;
 Best Local Similarity 82.8%; Pred. No. 2.1e-41;
 Matches 101; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDLVOPGGSLRLSCAASGFTFSNFMNSWVRQAPGKLEWVAALGGRSGTTFY 60
 Db 1 EVQLVESGGGLVQPGGSLRLSCTASGFTFSYANWVRQAPGKLEWVAISGSGGTTFY 60
 Qy 61 ADSVKGRFTISRDNKNTVYLEMNSLRADDTAIYYCAKRGGYKYGYMDVWGQGTTVTV 120
 Db 61 ADSVKGRFTISRDNKNTVLYQMNSLRADDTAVYYCAKGERWLPSTY-MDVWKGKGTTVTV 119
 Qy 121 SS 122
 Db 120 SS 121

Search completed: December 30, 2003, 10:54:38
 Job time : 40.3295 secs

XX The present sequence is the consensus single chain fragment
CC VH3-V-kappa-2. VH3-V-kappa-2, which comprises the human antibody
CC heavy and light chain variable region consensus sequences VH3 and
CC V-kappa-2, was used in the preparation of a human derived antibody
CC gene library.

XX SQ Sequence 281 AA;
Query Match 81.8%; Score 525; DB 10; Length 281;
Best Local Similarity 82.0%; Pred. No. 3e-41;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIAIGRSSTTFY 60
DB 26 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIAIGRSSTTFY 85
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIYCAKRGVYKYGMDVWGQGTITV 120
DB 86 ADSVKGRFTISRDNKNTLYLQNSLRADTAIYCAKRGVYKYGMDVWGQGTITV 143
QY 121 SS 122
DB 144 SS 145

RESULT 13
ABP45594
ID ABP45594 standard; Protein; 251 AA.
XX AC ABP45594;
XX DT 19-AUG-2002 (first entry)
XX DE Human BlyS binding scFv SEQ ID 1605.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX KW anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US19110.
XX PR 16-JUN-2000; 2000US-212210P.
XX PR 17-OCT-2000; 2000US-240816P.
XX PR 16-MAR-2001; 2001US-276248P.
XX PR 21-MAR-2001; 2001US-277379P.
XX PR 25-MAY-2001; 2001US-293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PF Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX PI WPI; 2002-114799/15.
XX DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX PT the diagnosis and treatment of cancers and immune disorders -
XX PS Claim 1; Page 2318-2319; 3148pp; English.
XX CC This invention describes novel antibodies that immunospecifically bind to
XX CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and anti-AIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX SQ Sequence 251 AA;
Query Match 81.7%; Score 524.5; DB 23; Length 251;
Best Local Similarity 80.0%; Pred. No. 3e-41;
Matches 100; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIAIGRSSTTFY 60
DB 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIAIGRSSTTFY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIYCAKRGVYKYGMDVWGQGTITV 117
DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTAIYCAKRGVYKYGMDVWGQGTITV 120
QY 118 VTVSS 122
DB 121 VTVSS 125

RESULT 14
ABG77138
ID ABG77138 standard; Protein; 124 AA.
XX AC ABG77138;
XX DT 24-OCT-2002 (first entry)
XX DE Anti-IGF-IR antibody (2.13.2) variable region heavy chain protein.
XX KW Insulin-like growth factor I receptor; antibody; human;
XX KW cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;
XX KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
XX KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
XX KW atherosclerosis.
XX OS Homo sapiens.
XX PN WO200253596-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-US51113.
XX PR 05-JAN-2001; 2001US-259927P.
XX PA (PFIZ) PFIZER INC.
XX PA (ABGE-) ABGENIX INC.
XX PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX DR WPI; 2002-575410/61.
XX DR N-FSDB; ABS62700.
XX PT Novel humanized, chimeric monoclonal antibody that specifically binds
XX PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
XX PT binding of IGF-I or IGF-II to receptor and for treating cancer in
XX PT humans -
XX PS Claim 13; Page 127; 172pp; English.

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DR N-PSDB; AAT87951.
XX
PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX
PS Example 1; Fig 5D; 436pp; English.
XX
CC The present sequence is the human antibody heavy chain
CC variable region synthetic sequence VH3, used in the preparation of
CC a human derived antibody gene library.
XX
SQ Sequence 120 AA;
    Query Match      81.8%; Score 525; DB 18; Length 120;
    Best Local Similarity 82.0%; Pred. No. 1.2e-41;
    Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVQLVESGGDLVQPQGSRLRLSCAASGFTFSNFMAMSWVRQAPKGLEWVAIAIGRSGTTFY 60
DB 1 EVQLVESGGGLVQPQGSRLRLSCAASGFTFSYAMSWVRQAPKGLEWVAISGSGSTYY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGCGYKYGYGMDVWGQGTTFVTV 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIYYCARWGGD--FYAMDYWGQGTFLVTV 118

QY 121 SS 122
DB 119 SS 120

RESULT 11
ABJ18675
ID ABJ18675 standard; Protein; 120 AA.
XX
AC ABJ18675;
XX
DT 06-MAR-2003 (first entry)
XX
DE Antibody library related heavy variable chain protein region SEQ ID No 4.
XX
KW Library; recombinant antibody; clustering variable region; in silico;
KW immunogenicity; antibody therapeutic.
XX
OS Unidentified.
XX
PN WO200284277-A1.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US12202.
XX
PR 17-APR-2001; 2001US-284407P.
XX
PA (ABMA-) ABMAXIS INC.
XX
PI Luo P;
XX
WPI; 2003-093043/08.
XX
CC Constructing a library of recombinant antibodies useful as source of
PT antibody candidates for screening antigens comprises clustering
PT variable regions of antibodies having known 3-dimensional structures
PT into structural ensembles -
XX
PS Disclosure; Page 101; 119pp; English.
XX
CC The invention relates to a novel method for the construction of a library
CC of recombinant antibodies. The novel method comprises clustering variable
CC regions of a collection of antibodies having known 3D structures into at
CC least two families of structural ensembles, each comprising at least two
CC different antibody sequences but with substantially identical main chain
CC conformations. The method is useful for constructing a library of

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CC artificial antibodies in silico which provides a structurally diverse and
CC yet functionally more relevant source of antibody candidates which can
CC then be screened for binding a wide variety of target molecules,
CC including small molecules, and biomacromolecules such as proteins,
CC peptides and nucleic acids. The libraries constructed are useful as a
CC source of antibody candidates for further screening for novel antibodies
CC with high affinity against a wide range of antigens and having no or
CC minimum immunogenicity to human subjects treated with antibody
CC therapeutics. This sequence represents a protein region of an antibody
CC relating to the novel antibody library construction method of the
XX invention.
XX
SQ Sequence 120 AA;
    Query Match      81.8%; Score 525; DB 24; Length 120;
    Best Local Similarity 82.0%; Pred. No. 1.2e-41;
    Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVQLVESGGDLVQPQGSRLRLSCAASGFTFSNFMAMSWVRQAPKGLEWVAIAIGRSGTTFY 60
DB 1 EVQLVESGGGLVQPQGSRLRLSCAASGFTFSYAMSWVRQAPKGLEWVAISGSGSTYY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGCGYKYGYGMDVWGQGTTFVTV 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNSLRADTAIYYCARWGGD--FYAMDYWGQGTFLVTV 118

QY 121 SS 122
DB 119 SS 120

RESULT 12
AAW27560
ID AAW27560 standard; Protein; 281 AA.
XX
AC AAW27560;
XX
DT 23-JAN-1998 (first entry)
XX
DE Consensus single chain fragment VH3-V-kappa-2.
XX
KW Human; antibody; preparation; library; VH3; variable region;
KW light chain; heavy chain; V-kappa-2; single chain; consensus.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /label= sig_peptide
FT Peptide 22..281 /label= mat_peptide
XX
PN WO9708320-A1.
XX
PD 06-MAR-1997.
XX
PF 19-AUG-1996; 96WO-EP03647.
XX
PR 18-AUG-1995; 95EP-0113021.
XX
PA (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
XX
PI Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
XX
WPI; 1997-179277/16.
XX
N-PSDB; AAT87958.
XX
CC Preparation of human derived antibody gene library - using synthetic
CC consensus sequences, and signal consensus antibody gene as universal
CC framework for highly diverse antibody libraries
XX
PS Example 2; Fig 8; 436pp; English.

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CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is human heavy chain variable (VH) region, 038064.
 XX
 SQ Sequence 125 AA;

Query Match 82.8%; Score 531.5; DB 22; Length 125;
 Best Local Similarity 82.5%; Pred. No. 3.1e-42;
 Matches 104; Conservative 8; Mismatches 9; Indels 5; Gaps 2;
 QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMVSRQAPGKLEWVAIGRSSTTFY 60
 DB 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMVSRQAPGKLEWVAISGGSTYY 60
 QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAK---RGRGGYKYGMVWGQGT 116
 DB 61 ADSVKGRFTISRDNKNTLYLQMNLSLRADTAIYYCAKDIEDTAMFFY-YIGMDVWGQGT 119

QY 117 TVTVSS 122
 DB 120 TVTVSS 125

RESULT 9
 ABG77157
 ID ABG77157 standard; Protein; 470 AA.

AC ABG77157;
 XX
 DT 24-OCT-2002 (first entry)

XX Amino acid sequence of anti-IGF-IR antibody 2.13.2 Vh domain.

XX Insulin-like growth factor I receptor; antibody; human;
 KW cytosolic; osteoplastic; antiatherosclerotic; antipsoriatic;
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
 KW atherosclerosis.

XX Homo sapiens.

XX WO200253596-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-US51113.

XX 05-JAN-2001; 2001US-259927P.

XX (PFIZ) PFIZER INC.

XX (ABGE-) ABGENIX INC.

XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;

XX WPI; 2002-575410/61.

XX Novel humanized, chimeric monoclonal antibody that specifically binds

PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting

PT binding of IGF-I or IGF-II to receptor and for treating cancer in

PT humans
 XX Claim 16; Figure 19B; 172pp; English.
 XX This invention relates to a novel humanised, chimeric or human
 CC monoclonal antibody or its antigen binding portion that specifically
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
 CC The antibodies may also be useful for increasing IGF-IR activity and
 CC thus restoring IGF-IR activity in a condition characterised by low
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
 CC invention is also useful for inducing apoptosis of specific cells in a
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,
 CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
 CC antibodies minimise the immunogenic and allergic responses intrinsic to
 CC mouse or mouse-derived monoclonal antibodies and thus increase the
 CC efficacy and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention.
 XX

SQ Sequence 470 AA;
 Query Match 82.3%; Score 528.5; DB 23; Length 470;
 Best Local Similarity 80.8%; Pred. No. 2.5e-41;
 Matches 101; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMVSRQAPGKLEWVAIGRSSTTFY 60
 DB 20 EVLVESGGGLVQPGGSLRLSCTASGFTFSYAMVSRQAPGKLEWVAISGGSTTFY 79

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAK---RGRGGYKYGMVWGQGT 117
 DB 80 ADSVKGRFTISRDNKNTLYLQMNLSLRADTAIYYCAKDLGWSDSYIYGMVWGQGT 139

QY 118 TVTVSS 122
 DB 140 TVTVSS 144

RESULT 10
 AAW27553
 ID AAW27553 standard; Protein; 120 AA.

XX AAW27553;

XX 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH3 consensus.

XX Human; antibody; preparation; library; VH3; variable region;

KW heavy chain; consensus.

XX Homo sapiens.

XX WO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96WO-EP03647.

XX 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;

XX WPI; 1997-179277/16.

Query Match 84.0%; Score 539.5; DB 23; Length 125;
 Best Local Similarity 84.0%; Pred. No. 5.5e-43;
 Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 2;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAALIGRSCTTFY 60
 DB 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAALIGRSCTTFY 60
 QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAK-RGRGG--YKYGMQDVWGQTT 117
 DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAKDLGVDFYFYGGYGGMDVWGQTT 120

QY 118 VTSS 122
 DB 121 VTSS 125

RESULT 7
 ID AAM24101 standard; Protein; 384 AA.
 AC AAM24101;
 XX 12-OCT-2001 (first entry)
 DE Human EST encoded protein SEQ ID NO: 1626.
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 OS Homo sapiens.
 XX WO200154477-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02687.
 XX 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werthman T;
 XX WPI: 2001-476164/51.
 DR N-PSDB; AAH98760.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 PS Claim 20; Page 1102-1103; 1275pp; English.
 XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX Sequence 384 AA;
 SQ Query Match 83.7%; Score 537.5; DB 22; Length 384;
 Best Local Similarity 78.2%; Pred. No. 2.9e-42;
 Matches 104; Conservative 9; Mismatches 9; Indels 11; Gaps 2;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAALIGRSCTTFY 60
 DB 20 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVSGISGSGSTYY 79
 QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAK-----GRGGYK-----YKGM 109
 DB 80 ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAKHPAYYYGSGYSSHHYYYYYGM 139

QY 110 DVMCGQTTVTSS 122
 DB 140 DVMCGQTTVTSS 152

RESULT 8
 ID AAE07013 standard; Protein; 125 AA.
 XX AAE07013;
 AC AAE07013;
 XX 16-OCT-2001 (first entry)
 DE Human heavy chain variable (VH) region, 038064.
 XX Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
 KW neointimal hyperplasia; VH; heavy chain variable region.
 OS Homo sapiens.
 XX Location/Qualifiers
 FH Key 31..35
 FT Region /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT Region 50..66
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT Region 99..114
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 XX WO200157226-A1.
 XX 09-AUG-2001.
 XX 02-FEB-2001; 2001WO-US03537.
 XX 03-FEB-2000; 2000US-0497625.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX WPI: 2001-488888/53.
 DR Humanized immunoglobulin for treating a CC-chemokine receptor
 XX 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 XX Disclosure; Page 168; 183pp; English.
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of

RESULT 5
 ABG77158
 ID ABG77158 standard; Protein; 470 AA.
 AC ABG77158;
 XX
 DT 24-OCT-2002 (first entry)
 DE
 XX Germline protein sequence of anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6.
 KW Insulin-like growth factor I receptor; antibody; human;
 KW cytotatic; osteopathic; antiatherosclerotic; antiaporiatic;
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200253596-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-US51113.
 XX
 PR 05-JAN-2001; 2001US-259927P.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX
 DR WPI; 2002-575410/61.
 XX
 PT Novel humanized, chimeric monoclonal antibody that specifically binds
 PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in
 PT humans -
 XX
 PS Disclosure; Figure 19B; 172pp; English.
 XX
 CC This invention relates to a novel humanised, chimeric or human
 CC monoclonal antibody or its antigen binding portion that specifically
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
 CC The antibodies may also be useful for increasing IGF-IR activity and
 CC thus restoring IGF-IR activity in a condition characterised by low
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
 CC invention is also useful for inducing apoptosis of specific cells in a
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,
 CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
 CC antibodies minimise the immunogenic and allergic responses intrinsic to
 CC mouse or mouse-derivatised monoclonal antibodies and thus increase the
 CC efficacy and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention.
 XX
 SQ Sequence 470 AA;
 Query March 84.8%; Score 544.5; DB 23; Length 470;
 Best Local Similarity 83.2%; Pred. No. 8e-43;
 Matches 104; Conservative 9; Mismatches 9; Indels 3; Gaps 1;
 1 EVQLVESGGDLVPGGSLRLSCAASGTPFSNFMVSRQAPKGLVWVAATIGRSGLTTFY 60
 20 EVQLTESGGGLVPGGSLRLSCAASGTPFSSTAMVSRQAPKGLVWVAISGGSGSIYY 79

61 ADSVKGRFTISRDNKNTVYVLENNLSRAEDTAIYYCAKRGSG--YKYGMVMDVWGOTT 117
 80 ADSVKGRFTISRDNKNTVYVLENNLSRAEDTAIYYCAKGYSSGWYIYYGMVMDVWGOTT 139
 118 VTSS 122
 140 VTSS 144
 RESULT 6
 ABG77142
 ID ABG77142 standard; Protein; 125 AA.
 AC ABG77142;
 XX
 DT 24-OCT-2002 (first entry)
 DE
 XX Anti-IGF-IR antibody (4.9.2) variable region heavy chain protein.
 KW Insulin-like growth factor I receptor; antibody; human;
 KW cytotatic; osteopathic; antiatherosclerotic; antiaporiatic;
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200253596-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-US51113.
 XX
 PR 05-JAN-2001; 2001US-259927P.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
 XX
 DR WPI; 2002-575410/61.
 XX
 PT Novel humanized, chimeric monoclonal antibody that specifically binds
 PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in
 PT humans -
 XX
 PS Claim 13; Page 130; 172pp; English.
 XX
 CC This invention relates to a novel humanised, chimeric or human
 CC monoclonal antibody or its antigen binding portion that specifically
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.
 CC The antibodies may also be useful for increasing IGF-IR activity and
 CC thus restoring IGF-IR activity in a condition characterised by low
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the
 CC invention is also useful for inducing apoptosis of specific cells in a
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,
 CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR
 CC antibodies minimise the immunogenic and allergic responses intrinsic to
 CC mouse or mouse-derivatised monoclonal antibodies and thus increase the
 CC efficacy and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention.
 XX
 SQ Sequence 125 AA;

DR WPI; 2001-48888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor

PT 2-mediated disorder in a patient, comprises a binding specificity for

PT CCR2, and a non-human antigen binding region and human immunoglobulin

PT -

XX Disclosure; Page 168; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding

CC fragment, having binding specificity for CC-chemokine receptor 2

CC (CCR2), comprising an antigen binding region of non-human origin

CC and at least a portion of an immunoglobulin of human origin. The

CC humanised antibodies are useful for inhibiting the interaction of

CC a cell expressing CCR2. They are useful for inhibiting or treating

CC HIV infection. The proteins of the invention are useful for inhibiting

CC leukocyte trafficking, for treating CCR2-mediated disorders such as

CC inflammatory disorder, autoimmune disorders such as rheumatoid

CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,

CC and for inhibiting restenosis. They are useful in therapy or diagnosis,

CC and in the manufacture of a medicament for treating CCR-2 mediated

CC disease. They are also useful for treating allergy, anaphylaxis,

CC malignancy, chronic and acute inflammation, histamine and IgE-

CC mediated allergic reaction, shock, stenosis, allograft rejection,

CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired

CC immune deficiency syndrome (AIDS), restenosis associated with vascular

CC intervention, including angioplasty and/or stent placement in a mammal.

CC Humanised antibodies are also useful for inhibiting narrowing of the

CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of

CC a vessel in a mammal, preferably associated with vascular intervention.

CC The present sequence is human heavy chain variable (VH) region, 038062.

XX

XX Sequence 128 AA;

Query Match 85.5%; Score 549; DB 22; Length 128;

Best Local Similarity 82.0%; Pred. No. 7.3e-44;

Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;

QY 1 EVQLVESGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKLEWVAIAIGRSGTTFY 60

Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAISGSGSTYY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKGR-----GGYKYYGMDVWGQ 114

Db 61 ADSVKGRFTISRDNKNTVLYQMNSLRADTAIYYCAKDRNDFWSGYKYYGMDVWGQ 120

QY 115 GTTVTVSS 122

Db 121 GTTVTVSS 128

RESULT 4

AAE07021

ID AAE07021 standard; Protein; 125 AA.

XX

XX AAE07021;

XX

XX 16-OCT-2001 (first entry)

XX Human heavy chain variable (VH) region, 4G12.

XX Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

KW neuroprotective; immunosuppressive; human immunodeficiency virus;

KW HIV infection; cytotoxic; vasotropic; leukocyte trafficking; allergy;

KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;

KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;

KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;

KW AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;

KW neointimal hyperplasia; VH; heavy chain variable region.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT 31..35

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT 50..66

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT 99..114

FT /label= CDR3

FT /note= "Complementarity determining region 3"

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US03537.

XX 03-FEB-2000; 2000US-0497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX WPI; 2001-48888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor

PT 2-mediated disorder in a patient, comprises a binding specificity for

PT CCR2, and a non-human antigen binding region and human immunoglobulin

PT -

XX Disclosure; Page 171; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding

CC fragment, having binding specificity for CC-chemokine receptor 2

CC (CCR2), comprising an antigen binding region of non-human origin

CC and at least a portion of an immunoglobulin of human origin. The

CC humanised antibodies are useful for inhibiting the interaction of

CC a cell expressing CCR2. They are useful for inhibiting or treating

CC HIV infection. The proteins of the invention are useful for inhibiting

CC leukocyte trafficking, for treating CCR2-mediated disorders such as

CC inflammatory disorder, autoimmune disorders such as rheumatoid

CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,

CC and for inhibiting restenosis. They are useful in therapy or diagnosis,

CC and in the manufacture of a medicament for treating CCR-2 mediated

CC disease. They are also useful for treating allergy, anaphylaxis,

CC malignancy, chronic and acute inflammation, histamine and IgE-

CC mediated allergic reaction, shock, stenosis, allograft rejection,

CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired

CC immune deficiency syndrome (AIDS), restenosis associated with vascular

CC intervention, including angioplasty and/or stent placement in a mammal.

CC Humanised antibodies are also useful for inhibiting narrowing of the

CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of

CC a vessel in a mammal, preferably associated with vascular intervention.

CC The present sequence is human heavy chain variable (VH) region, 4G12.

XX

XX Sequence 125 AA;

Query Match 85.3%; Score 547.5; DB 22; Length 125;

Best Local Similarity 84.0%; Pred. No. 9.9e-44;

Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 EVQLVESGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKLEWVAIAIGRSGTTFY 60

Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVAISGSGSTYY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAK---RGRGGYKYYGMDVWGQTT 117

Db 61 ADSVKGRFTISRDNKNTVLYQMNSLRADTAIYYCAKAVVRGVISYYYGMDVWGQTT 120

QY 118 VTVSS 122

Db 121 VTVSS 125

XX PS Example 9; Fig 11A; 61pp; English.

XX CC This invention describes a novel polynucleotide (I) (and complements and

XX CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

XX CC coding for a human antibody with factor VIII specificity which has

XX CC hemostatic activity. (I) is useful a primer or probe for detecting the

XX CC presence of inhibitory antibodies directed against factor VIII. The

XX CC polypeptides of the invention and the antibodies generated from them

XX CC are useful in compositions for neutralizing factor VIII inhibiting

XX CC antibodies in hemophilia A patients. This sequence represents a human

XX CC factor VIII antibody A2 specific scFv protein DP-47 which is used

XX CC in the method of the invention.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 642; DB 21; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.4e-52;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

DB 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQTTTV 120

DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQTTTV 120

QY 121 SS 122

DB 121 SS 122

RESULT 2

AA50975

ID AAY50975 standard; Protein; 122 AA.

XX AC AAY50975;

XX DT 23-MAR-2000 (first entry)

XX DE Human FVIII heavy chain variable region DP-47 protein fragment.

XX KW Human; heavy chain; antibody; factor VIII; hemostatic; variable region;

XX KW hemophilia A.

XX OS Homo sapiens.

XX PN WO9958680-A2.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-NL00285.

XX PR 08-MAY-1998; 98EP-0201543.

XX PA (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.

XX PI Voorberg JJ, Van Den Brink EN, Turenhout EM;

XX DR WPI; 2000-053102/04.

XX DR N-PSDB; AA243868.

XX PT New polynucleotide, polypeptide and antibody useful for diagnosing the

XX PT presence of neutralizing antibodies against factor VIII and for

XX PT treatment of hemophilia A patients with these antibodies -

XX PS Example 9; Fig 11c; 61pp; English.

XX CC This invention describes a novel polynucleotide (I) (and complements and

XX CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

XX CC coding for a human antibody with factor VIII specificity which has

XX CC hemostatic activity. (I) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents a fragment

CC of the human factor VIII antibody heavy chain variable region protein

CC DP-47 which is used in the method of the invention.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 642; DB 21; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.4e-52;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

DB 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQTTTV 120

DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQTTTV 120

QY 121 SS 122

DB 121 SS 122

RESULT 3

AAE07014

ID AAE07014 standard; Protein; 128 AA.

XX AC AAE07014;

XX DT 16-OCT-2001 (first entry)

XX DE Human heavy chain variable (VH) region, 038062.

XX KW Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

XX KW neuroprotective; immunosuppressive; human immunodeficiency virus;

XX KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;

XX KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

XX KW multiple sclerosis; atherosclerosis; stenosis; allograft rejection;

XX KW anaphylaxis; malignancy; inflammation; stenosis; acquired immune deficiency syndrome;

XX KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;

XX KW AIDS; inflammatory glomerulopathy; vascular intervention; LD9 antibody;

XX KW neointimal hyperplasia; VH; heavy chain variable region.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT Region 50..66

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT Region 99..117

FT /label= CDR3

FT /note= "Complementarity determining region 3"

FT Misc-difference 109

FT /label= Unknown

XX PN WO200157226-A1.

XX PD 09-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US03537.

XX PR 03-FEB-2000; 2000US-0497625.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 39.2461 Seconds
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493.415 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	642	100.0	122	21	AAV50973 Human FVIII antibo
2	642	100.0	122	21	AAV50975 Human FVIII heavy
3	549	85.5	128	22	AAE07014 Human heavy chain
4	547.5	85.3	125	22	AAE07021 Human heavy chain
5	544.5	84.8	470	23	ABG77158 Germline protein s
6	539.5	84.0	125	23	ABG77142 Anti-IGF-IR antibo
7	537.5	83.7	384	22	AA24101 Human EST encoded
8	531.5	82.8	125	22	AAE07013 Human heavy chain
9	528.5	82.3	470	23	ABG77157 Amino acid sequenc

10	525	81.8	120	18	AAW27553	Human Ab heavy cha
11	525	81.8	120	24	ABJ18675	Antibody library r
12	525	81.8	281	18	AAW27560	Consensus single c
13	524.5	81.7	251	23	ABP45594	Human BlyS binding
14	523.5	81.5	124	23	ABG77138	Human anti-IGF-IR antibo
15	522.5	81.4	121	24	ABP56504	Human anti-Fc-epsi
16	522.5	81.4	121	24	ABP56506	Human anti-Fc-epsi
17	522	81.3	254	23	ABP45690	Human BlyS binding
18	521.5	81.2	117	22	AAE12061	Human anti-tissue
19	521.5	81.2	119	22	AAE2088	Human Vh consensus
20	521.5	81.2	119	22	AAE60401	Consensus human he
21	521.5	81.2	119	22	AAE61586	Human variable hea
22	521.5	81.2	119	23	AAU74541	Human subgroup V H
23	521	81.2	222	24	ABR01515	Human anti-TIMP-1
24	520	81.0	248	23	ABP45963	Human BlyS binding
25	519.5	80.9	313	22	AAU14320	Human novel protei
26	519	80.8	118	23	AAU83803	MS-GPC-6 heavy cha
27	519	80.8	118	23	ABBS7561	HLA-DR-specific pr
28	518	80.7	253	24	ABJ19830	Human VEGF-2 relat
29	517	80.5	124	22	AAE07018	Human heavy chain
30	516.5	80.5	121	24	ABP56507	Human anti-Fc-epsi
31	516	80.4	177	24	ABJ36939	Anti-CD40 monoclon
32	515.5	80.3	221	24	ABR01534	Human anti-TIMP-1
33	515.5	80.3	253	23	ABP44978	Human BlyS binding
34	515	80.2	248	23	ABP45954	Human BlyS binding
35	515	80.2	251	23	ABP44897	Human BlyS binding
36	514	80.1	136	24	ABP55473	Synthetic 3-23 VH
37	514	80.1	367	24	ABP55467	MAliA3 protein seq
38	513.5	80.0	119	23	AAE28151	Human consensus an
39	513.5	80.0	245	22	AAE67620	Human leukocyte an
40	513	79.9	128	18	AAW06242	Heavy chain variab
41	513	79.9	140	18	AAW13524	Anti-melanoma anti
42	511	79.6	122	14	AAE30773	Consensus humanise
43	511	79.6	128	22	AAE07015	Human heavy chain
44	511	79.6	252	23	ABP45420	Human BlyS binding
45	510.5	79.5	121	19	AAW47180	Variable heavy (VH

ALIGNMENTS

RESULT 1
AAV50973
ID AAV50973 standard; Protein; 122 AA.
XX
AC AAV50973;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human FVIII antibody A2 scFv heavy chain protein DP-47 #2.
XX
KW Human; heavy chain; antibody; factor VIII; hemostatic;
KW hemophilia A; scFv; A2.
XX
OS Homo sapiens.
XX
PN WO9958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
(SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -

Query Match 68.4%; Score 439; DB 11; Length 487;
Best Local Similarity 68.8%; Pred. No. 1.4e-35;
Matches 86; Conservative 14; Mismatches 21; Indels 4; Gaps 2;
QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNFMWSVRQAPGKLEWVAALIGRSGLTTFY 60
DB 20 EVOLVESGDLVOPGSLRLSCAASGFTFSNFMWSVRQAPGKLEWVAALIGRSGLTTFY 79
QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYVG---MDVWGQTT 117
DB 80 PDNVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYVG---MDVWGQTT 138
QY 118 VTVSS 122
DB 139 ITVSS 143

Search completed: December 30, 2003, 11:01:10
Job time : 30.7319 secs

RESULT 14
Q91WPS PRELIMINARY; PRT; 479 AA.
AC Q91WPS
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;
Query Match 69.9%; Score 448.5; DB 11; Length 479;
Best Local Similarity 70.5%; Pred. No. 1.6e-36;
Matches 86; Conservative 15; Mismatches 14; Indels 7; Gaps 2;
QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNFMWSVRQAPGKLEWVAALIGRSGLTTFY 60
DB 20 EVOLVESGDLVOPGSLRLSCAASGFTFSNFMWSVRQAPGKLEWVAALIGRSGLTTFY 79
QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYVGMDVWGQTTTV 120
DB 80 SDTMKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYVGMDVWGQTTTV 132
QY 121 SS 122
DB 133 SS 134
RESULT 15
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

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Db 116 S 116

RESULT 11
Q8N5K4 PRELIMINARY; PRT; 499 AA.
AC Q8N5K4; 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -.
DR InterPro; IPR003599; IG.
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DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003596; IG_MHC.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00407; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 71.3%; Score 457.5; DB 4; Length 499;
Best Local Similarity 70.0%; Pred. No. 2.1e-37;
Matches 91; Conservative 12; Mismatches 16; Indels 11; Gaps 2;

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Db 20 EVQLVESGGGVVPRPGSRLSLSCATSTGFTFDGASVVRQAPGKLEWVSSINWNGGSTNY 79
QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKY-----YGMVYV 112
Db 80 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKY-----YGMVYV 112
QY 113 GQGTIVTVSS 122
Db 137 GQGTIVTVSS 146

RESULT 12
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AC Q9HCC1;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Teujimoto Y., Aaeda S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme :Isolation from a
human synthetic phage display library and characterization."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSP; P01772; 2FB4.

Query Match 70.6%; Score 453; DB 4; Length 122;
Best Local Similarity 74.6%; Pred. No. 1e-37;
Matches 91; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 1 EVQLVESGDDLVPQGSRLSLCAASGFTFSNFAMSVVRQAPGKLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGGVVPRPGSRLSLSCATSTGFTFSNYGMHVRQAPGKLEWVAIAISNDGSNKFY 60
QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWQGTIVTV 120
Db 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWQGTIVTV 120
QY 121 SS 122
Db 121 SS 122
```

ID	Q9Y509	PRELIMINARY:	PRT:	147 AA.
AC	Q9Y509			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	WH3 protein (Fragment).			
GN	WH3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96071149; PubMed=7475288;			
RA	Cao J., Vassio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,			
RA	Lichtenstein A.K., Berenson J.R.;			
RT	"A CD10-positive subset of malignant cells is identified in multiple			
RT	myeloma using PCR with patient-specific immunoglobulin gene primers."			
RL	Leukemia 9:1948-1953(1995).			
DR	EMBL; S80860; AAD14339.1; -.			
DR	HSSP; P01772; 2FB4.			
DR	InterPro; IPR007110; IG-1like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON TER			
SQ	SEQUENCE 147 AA; 15768 MW; 8489FCMAA7BC925C CRC64;			
Query Match	71.8%;	Score 461;	DB 4;	Length 147;
Best Local Similarity	71.4%;	Pred. No. 2e-38;		
Matches	90;	Conservative	9;	Mismatches 23; Indels 4; Gaps 1
QY	1	EVQLVESGGDVLVQPGSGSLRLSCAASGFTFSNFMASWVRQAPGKGLVWVAIGRSGTTFY	60	
DB	1	QVHLVESGGGVQVQPKSLRLSCAASGFTFSNFMASWVRQAPGKGLVWVAIGRSGTTFY	60	
QY	61	ADSVKGRFTISRDNSKNTVYLEMNSLRADITAIYCAKGR---GGIKYIGMDWGQGT	116	
DB	61	AGSVKGRFTISRDNSKNTVYLEMNSLRADITAIYCAKGR---GGIKYIGMDWGQGT	120	
QY	117	TYTVSS 122		
DB	121	LVTWSS 126		
RESULT 9				
Q9UL90	PRELIMINARY:	PRT:	113 AA.	
AC	Q9UL90			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Myosin-reactive immunoglobulin heavy chain variable region			
DE	(Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035024; AAD56260.1; -.			
DR	HSSP; P01772; 2FB4.			

```

DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv_1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD1906ED07F CRC64;

Query Match 71.6%; Score 459.5; DB 4; Length 113;
Best Local Similarity 73.8%; Pred. No. 2.1e-38;
Matches 90; Conservative 9; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVOLVESGGDLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSGITTFY 60
Db 1 EVOLVESGGGVVQPGSLRLSCAASGFTFSYGMAMVRQAPGKLEWVAIFRIYDGNKITY 60
QY 61 ADVSKGFTTISRDNKNTVYLEMNSLRAPEDTAIYYCAKRGGRGYKYYGMVDWGGITTVT 120
Db 61 ADVSKGFTTISRDNKNTVLYLQNSLRAPEDTAIYYCAK-----DLNVMGGTLVTV 111
QY 121 SS 122
Db 112 SS 113

RESULT 10
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel_13, Created)
DT 01-MAY-2000 (TrEMBLrel_13, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel_23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv_1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Query Match 71.6%; Score 459.5; DB 4; Length 116;
Best Local Similarity 76.0%; Pred. No. 2.1e-38;
Matches 92; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

QY 2 VOLVESGGDLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSGITTFY 61
Db 1 VOLVESGGGVVQPGSLRLSCAASGFTFSYGMAMVRQAPGKLEWVAISYDGSNKITY 60
QY 62 DSVKGRFTTISRDNKNTVYLEMNSLRAPEDTAIYYCAKRGGRGYKYYGMVDWGGITTVT 121
Db 61 DSVKGRFTTISRDNKNTVLYLQNSLRAPEDTAIYYCA--GGGG---LGIYGGGGTLVTVS 115
QY 122 S 122

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Qy 119 TVSS 122
 Db 140 TVSS 143

RESULT 2

Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strauberg R.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8EC263D9 CRC64;

Query Match 76.9%; Score 493.5; DB 4; Length 597;
 Best Local Similarity 76.0%; Pred. No. 6.5e-41;
 Matches 95; Conservative 13; Mismatches 14; Indels 3; Gaps 1;

Qy 1 EVOLVESGGLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSSTTFY 60
 Db 20 EVOLVESGGGLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSSTTFY 79
 Qy 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGSGYKYYGMDVWGCTTV 117
 Db 80 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGSGYKYYGMDVWGCTTV 139
 Qy 118 TVSS 122
 Db 140 TVSS 144

RESULT 3

Q9UL71 PRELIMINARY; PRT; 121 AA.
 AC Q9UL71;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=964934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -

DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 75.0%; Score 481.5; DB 4; Length 121;
 Best Local Similarity 76.2%; Pred. No. 1.4e-40;
 Matches 93; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EVOLVESGGLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSSTTFY 60
 Db 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSSTTFY 60
 Qy 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGSGYKYYGMDVWGCTTV 120
 Db 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGSGYKYYGMDVWGCTTV 119
 Qy 121 SS 122
 Db 120 SS 121

RESULT 4

Q8TC77 PRELIMINARY; PRT; 471 AA.
 AC Q8TC77;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strauberg R.;
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC024289; AAH24289.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 51791 MW; 388FTF4CF58660E CRC64;

Query Match 73.2%; Score 470; DB 4; Length 471;
 Best Local Similarity 72.1%; Pred. No. 1.1e-38;
 Matches 88; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVESGGLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSSTTFY 60
 Db 20 EVOLVESGGGLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSSTTFY 79
 Qy 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGSGYKYYGMDVWGCTTV 120
 Db 80 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGSGYKYYGMDVWGCTTV 139
 Qy 121 SS 122
 Db 140 SS 141

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 29.7319 Seconds
(without alignment)
1058.876 Million cell updates/sec

Title: US-09-674-752-53

Sequence: 1 EVQLVESGGDLVQPQSGSLRL.....GKRYGMDVWGQGTITVSS 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_ricket:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	80.2	573	4	Q8WU38
2	493.5	76.9	597	4	Q96BB9
3	481.5	75.0	121	4	Q9UL71
4	470	73.2	471	4	Q8TC77
5	464	72.3	613	4	Q8WU38
6	463	72.1	118	4	Q9UL91
7	463	72.1	494	4	Q96K68
8	461	71.8	147	4	Q9Y509
9	459.5	71.6	113	4	Q9UL90
10	459.5	71.6	116	4	Q9UL93
11	457.5	71.3	499	4	Q8NSK4
12	456	71.0	112	4	Q9HCC1
13	453	70.6	122	4	Q9UL84
14	448.5	69.9	479	11	Q91WPS
15	439	68.4	487	11	Q99K44
16	438.5	68.3	119	11	Q920E7

17	435	67.8	118	4	Q9UL72	Q9UL72 homo sapien
18	433	67.4	473	11	Q91Z05	Q91Z05 mus musculu
19	418.5	65.2	493	4	Q8NCL6	Q8NCL6 homo sapien
20	417.5	65.0	480	11	Q91XE1	Q91XE1 mus musculu
21	416	64.8	469	11	Q8R3V9	Q8R3V9 mus musculu
22	413.5	64.4	131	4	Q9UL88	Q9UL88 homo sapien
23	402.5	62.7	486	11	Q91Z07	Q91Z07 mus musculu
24	399.5	62.2	521	4	Q8N4Y9	Q8N4Y9 homo sapien
25	395	61.5	484	11	Q8VEA0	Q8VEA0 mus musculu
26	394	61.4	95	4	Q9UL86	Q9UL86 homo sapien
27	391	60.9	298	11	Q9QYF0	Q9QYF0 mus musculu
28	384.5	59.8	112	4	Q9GCP3	Q9GCP3 homo sapien
29	384	59.8	159	4	Q9GQ50	Q9GQ50 homo sapien
30	381	59.3	437	11	Q9RI14	Q9RI14 mus musculu
31	375.5	58.5	104	4	Q9UL87	Q9UL87 homo sapien
32	369	57.5	124	4	Q9UL92	Q9UL92 homo sapien
33	368	57.3	124	6	Q9N0M4	Q9N0M4 oryctolagus
34	365	56.9	124	6	Q9N0M6	Q9N0M6 oryctolagus
35	359.5	56.0	125	4	Q9UL95	Q9UL95 homo sapien
36	356	55.5	500	4	Q9BRV0	Q9BRV0 homo sapien
37	352.5	54.9	119	4	Q9UL94	Q9UL94 homo sapien
38	351.5	54.8	484	11	Q9ULA6	Q9ULA6 mus musculu
39	349.5	54.4	473	11	Q9D8L4	Q9D8L4 mus musculu
40	347.5	54.1	117	11	Q9QXE9	Q9QXE9 mus musculu
41	342	53.3	145	11	Q924P7	Q924P7 mus musculu
42	339	52.8	116	4	Q9UL89	Q9UL89 homo sapien
43	338	52.6	145	11	Q924R1	Q924R1 mus musculu
44	338	52.6	145	11	Q924R4	Q924R4 mus musculu
45	336	52.3	121	11	Q99NG4	Q99NG4 mus musculu

ALIGNMENTS

RESULT 1

Q8WU38 ID Q8WU38 PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=tonsil;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC021276; AAH21276.1;
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_4.
DR SMART: SM00406; IG_1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; PD072344033AC530 CRC64;

Query Match 80.2%; Score 515; DB 4; Length 573;

Best Local Similarity 79.8%; Pred. No. 4.4e-43; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVQLVESGGDLPVQPGSRLRLSCAASGFTSNFAMSWVRQAPGKLEWYAAIGRSGTTFY 60
Db EVQLVESGGGLVQPGSRLRLSCAASGFTDDYAMHWVRQAPGKLEWYSGISWNSIGY 79
QY 61 ADVYKGRFTISRDNKSTLYLENSLRAPEDTRAIYCARGGGY--KRYGMDVWGQGTIV 118
Db 80 ADVYKGRFTISRDNKSTLYLENSLRAPEDTRAIYCARGGGSYIGYGYGMDVWGQGTIV 139

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RESULT 14
ID HV21_MOUSE STANDARD; PRT; 122 AA.
AC P01790;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
(MOPC 511).";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 65.7%; Score 422; DB 1; Length 122;
Best Local Similarity 67.7%; Pred. No. 2.2e-36;
Matches 84; Conservative 15; Mismatches 21; Indels 4; Gaps 2;

QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNFMASWVRQAPGKLEWVAIGRSG--TT 58
DB 1 EVKLVESSGGLVOPGSLRLSCATSGFTSDPYMEVWRQSPGKLEWVAIRNKANDYTT 60
QY 59 FYADSVKGRFTISRDNSKNTVYLENNSLRADDTAIYYCAKGRGGYKYYGMDWGQGTIV 118
DB 61 EYSASVKGKRFIVSRDTSQSIILYLQNNALRAEDTAIYYCARYGSSYWF--DVMGAGTTV 118
QY 119 TVSS 122
DB 119 TVSS 122

RESULT 15
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01787;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).

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RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1, HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "Igg antibodies to phosphorylcholine exhibit more diversity than
their Igm counterparts.";
RL Nature 291:29-34(1981)
CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 114 IG-LIKE.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DBE12F7000 CRC64;

Query Match 65.5%; Score 420.5; DB 1; Length 123;
Best Local Similarity 68.5%; Pred. No. 3.2e-36;
Matches 85; Conservative 13; Mismatches 23; Indels 3; Gaps 2;

QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNFMASWVRQAPGKLEWVAIGRSG--TT 58
DB 1 EVKLVESSGGLVOPGSLRLSCATSGFTSDPYMEVWRQSPGKLEWVAIRNKANDYTT 60
QY 59 FYADSVKGRFTISRDNSKNTVYLENNSLRADDTAIYYCAKGRGGYKYYGMDWGQGTIV 118
DB 61 EYSASVKGKRFIVSRDTSQSIILYLQNNALRAEDTAIYYCA-RDYGSSYWFQVWGAGTTV 119
QY 119 TVSS 122
DB 120 TVSS 123

Search completed: December 30, 2003, 10:55:55
Job time : 7.54102 secs

```



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Query Match      67.4%: Score 433; DB 1; Length 126;
Best Local Similarity 66.7%: Pred. No. 1.7e-37;
Matches 84; Conservative 15; Mismatches 23; Indels 4; Gaps 1

QY 1 EVQLVESGGGLVPGGSLRLCSAASGFFPSNFAAMSVWRQAPGKGLIEWVAIGRSGTTFY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVESGGGVVQPGSLRLCSGSSGPIFSSVYAMTWVRGAPGKGLIEWALLINDDSQHY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSYKGRFTTISRDN SKNTVYLEMNSLRADETAIYYCAKRGCGY---KTYGMADVGGGT 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSYKGRFTTISRDN SKNTVYLEMNSLRADETAIYYCAKRGCGY---KTYGMADVGGGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 TVTVSS 122
   |||||
Db 121 PTVVSS 126

RESULT 9
HV3E_HUMAN
ID_HV3E_HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II1 region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein."
RL Immunohistochemistry 33:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
CC CC
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02049; M3HUBW.
DR HSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003106; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match      67.4%: Score 432.5; DB 1; Length 120;
Best Local Similarity 72.5%: Pred. No. 1.8e-37;
Matches 87; Conservative 10; Mismatches 18; Indels 5; Gaps 2

QY 1 EVQLVESGGDLVPGGSLRLCSAASGFFPSNFAAMSVWRQAPGKGLIEWVAIGRSGTTFY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGVVQPGSLRLCSAASGFFPSNFAAMSVWRQAPGKGLIEWVAIGRSGTTFY 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 ADSYKGRFTTISRDN SKNTVYLEMNSLRADETAIYYCAKRG---RGYKYTYGMADVGGGT 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 ADSYKGRFTTISRDN SKNTVYLEMNSLRADETAIYYCAKRPVSLVDGWLYYGYGSGVGGT 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
HV3B_HUMAN
ID_HV3B_HUMAN STANDARD; PRT; 114 AA.

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AC P01763; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=693273707; PubMed=6410398;
RA Coni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal Igm
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -I MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -I SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02046; M3HWE.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03006; Ig_MHC.
DR InterPro; IPRO03596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Pyritidone carboxylic acid.
KW DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 114 114.
SQ SEQUENCE 114 AA; 12256 MW; D88294FBA18A07B7 CRC64;

Query Match 67.1%; Score 431; DB 1; Length 114;
Beat Local Similarity 68.9%; Pred.No. 2.4e-37;
Matches 84; Conservative 18; Mismatches 12; Indels 8; Gaps 2

QY 1 EVGVESGGDLVVGCGSLRUSCAASGFPSFAMSWVAOPGKGLWVAIGRGSTFY 60
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1 QOVLYDSGGGLVEGGSRLRSCASAGFFSANDMNVQAQPGKGLWLSFIQSGSTIYY 60
   :|::||::||::||::||::||::||::||::||::||::||::||::||

QY 61 ADSVKGRFTTISRDNISKNTVLNNKSLRLADPAIYYCARGRGRGYKYQGMDVGCSTTV 120
   :|::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 ADSVKGRFTTISRDNISKNTVLNNKSLRLADPAIYYCAR-----GW-----LHWGSGTLTV 112
   :|::||::||::||::||::||::||::||::||::||::||::||::||

QY 121 SS 122
   ||
Db 113 SS 114

RESULT 11
HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human Igm immunoglobulins.";
Biochemistry 13:2482-2498(1974).

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Query Match 68.1%; Score 437; DB 1; Length 116;
 Best Local Similarity 70.5%; Pred. No. 6,1e-38;
 Matches 86; Conservative 9; Mismatches 21; Indels 6; Gaps 1;

QY 1 EVOLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAGKGLLEWVAIGRSGTTFY 60
 DB 1 EVOLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAGKGLLEWVAIKZBGSZBY 60
 QY 61 ADSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGKGYKGYGMDVWGQTTVTY 120
 DB 61 VDSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGKGYKGYGMDVWGQTTVTY 114
 QY 121 SS 122
 DB 115 ST 116

RESULT 7

HV3A_HUMAN STANDARD; PRT; 122 AA.
 AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region TRO.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE (WEI)LOMA PROTEIN TRO.
 RX MEDLINE=76023781; PubMed=809331;
 RA Kretzschmar H., Altevogt P., Rudan E., Kortt A., Starescuk K.,
 RA Hilschmann N.;
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup II;
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- SIMILARITY: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02045; A1HUTR.
 DR HSSP; P01772; 2F84.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 108
 FT MOD_RES 1 1 IG-LIKE.
 FT NON_TER 122 122 PYROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 67.4%; Score 433; DB 1; Length 122;
 Best Local Similarity 60.7%; Pred. No. 1,6e-37;
 Matches 74; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVOLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAGKGLLEWVAIGRSGTTFY 60
 DB 1 EVOLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAGKGLLEWVAIKZBGSZBY 60
 QY 61 ADSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGKGYKGYGMDVWGQTTVTY 120
 DB 61 ADSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGKGYKGYGMDVWGQTTVTY 120
 QY 121 SS 122
 DB 121 SS 122

RESULT 8

HV3K_HUMAN STANDARD; PRT; 126 AA.
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region KOL.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RA "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=81072295; PubMed=741755;
 RA Marguier M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact
 RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
 RT and 1.0-A resolution.";
 RL J. Mol. Biol. 141:369-391(1980).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02055; G1HDKL.
 DR PDB; 2FG2; 12-JUL-89.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; 3D-structure; Pyroliidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT DISULFID 105 110
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT TURN 18 25
 FT HELIX 29 31
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 45 51
 FT TURN 53 54
 FT STRAND 58 60
 FT STRAND 62 64
 FT HELIX 65 67
 FT STRAND 68 73
 FT TURN 74 77
 FT STRAND 78 83
 FT STRAND 88 90
 FT HELIX 92 99
 FT STRAND 106 106
 FT TURN 107 108
 FT STRAND 109 109
 FT STRAND 113 116
 FT STRAND 120 124
 FT NON_TER 126 126
 FT SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match	Best Local Similarity	Matches	Score	DB 1;	Length	DB 2;	Gaps
86; Conservative	69.9%;	14;	69.9%;	Pred. No. 1.6e-38;	122;	2;	Gaps 2;
1 EVLVESGCDLVQPGSGRLSCAASGFTFSPFAMSWRQADPGKGLGVAAIGSGSTTFY	60	1	EVLVESGCDLVQPGSGRLSCAASGFTFSPFAMSWRQADPGKGLGVAAIGSGSTTFY	60			
1 QVELLESGGVVZPERSRLSCAASGFTFSPFAMSWRQADPGKGLGVAAISYBGBKXY	60	1	QVELLESGGVVZPERSRLSCAASGFTFSPFAMSWRQADPGKGLGVAAISYBGBKXY	60			
61 ADVSVGRFTISRDNKNTVLEMSLRADPAIYYCARGGGY-KYYGMVWGQGTIVT	119	61	ADSVGRFTISRDNKNTVLEMSLRADPAIYYCARGGGY-KYYGMVWGQGTIVT	119			
61 ABSVVGRTFTISRDNKNTVLEMSLRADPAIYYCARGGGY-KYYGMVWGQGTIVT	119	61	ABSVVGRTFTISRDNKNTVLEMSLRADPAIYYCARGGGY-KYYGMVWGQGTIVT	119			
120 VSS 122							
120 VSS 122							
120 VSS 122							

DR	GO	GO:0005576;	C:extracellular;	NAS.
DR	GO	GO:0003823;	F:antigen binding activity;	NAS.
DR	GO	GO:0006955;	P:immune response;	NAS.
DR	InterPro	IPR007110;	IG-like.	
DR	InterPro	IPR003006;	IG_MHC.	
DR	InterPro	IPR003596;	IG_V.	
DR	Pfam	PF00047;	IG_1.	
DR	SMART	SM00406;	IGV_1.	
DR	PROSITE	PS50835;	IG LIKE; 1.	
KW	Immunoglobulin V region.			
FT	DOMAIN	1	111	
FT	NON_TER	115	115	IG-LIKE.
SO	SEQUENCE	115 AA;	12379 MW;	208876A7DPF52DQF4 CRC64;
Query Match				
Beat Local Similarity		68.5%;	Score 439.5;	DB 1; Length 115;
Matches		86;	Conservative 17;	Mismatches 12; Indels 7; Gaps 2
OY	1 EVLVESGGDVLVQGGSLRLSCAASGFFPSNFMASWVRQAPGKGLVVAITGCRGRTTY 60			
DB	1 EVQVETGGGIIQPGGSLRLSCAASGFTVSHSMWSWVQAPGKALZWVSAI-YRGITTY 59			
OY	61 ADSVKGRTTIRSDNSKNVTVLENNSLRAEDPAIYTCARGRGKYKYGVGDVWGCGTTTV 120			
DB	60 ADSVKGRTTIRSDNSRBTIVLQMSLRADPAIYTCAR-----DLAARLFGKGTTV 113			
OY	121 SS 122			
DB	114 SS 115			
RESULT 6				
H3T3	HUMAN			
ID	H3T3	HUMAN	STANDARD;	PRT; 116 AA.
AC	P01781;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Ig heavy chain V-II region GAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=75059123;	PubMed=4803843;		
RA	Watanabe S., Barnikol H.U., Horn J., Bertam J., Hilschmann N.;			
RT	"The primary structure of a monoclonal IgM-immunoglobulin			
RT	(macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-			
RT	type)", subgroup H II. Architecture of the complete IgM-molecule.";			
RL	Hoppe-seyler's Z. Physiol. Chem. 354:1505-1509(1973).			
RN	[2]			
RP	REVISION TO 28-33.			
RA	Hilschmann N.;			
RL	Submitted (JUN-1975) to the PIR data bank.			
CC	-I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S			
CC	MACROGLOBULIN.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR	A02054;	MAHUGL.	
DR	HSSP	P01772;	2FB4.	
DR	GO	GO:0005576;	C:extracellular;	NAS.
DR	GO	GO:0003823;	F:antigen binding activity;	NAS.
DR	GO	GO:0006955;	P:immune response;	NAS.
DR	InterPro	IPR007110;	IG-like.	
DR	InterPro	IPR003006;	IG_MHC.	
DR	InterPro	IPR003596;	IG_V.	
DR	Pfam	PF00047;	IG_1.	
DR	SMART	SM00406;	IGV_1.	
DR	PROSITE	PS50835;	IG LIKE; 1.	
KW	Immunoglobulin V region.			
FT	DOMAIN	1	112	
FT	NON_TER	116	116	IG-LIKE.
SO	SEQUENCE	116 AA;	12730 MW;	26G7CA9AAAAA1282 CRC64;

Seq	Sequence	136 AA;	15071 MW;	2276A9BDBDF7016 CRC64;
Query Match		72.7%;	Score 467;	DB 1; Length 136;
Best Local Similarity		73.8%;	Pred. No. 6.2e-41;	
Matches	90;	Conservative	11;	Mismatches 19; Indels 2; Gaps 1;
QY	1 EVOLVEGGDILVQGGSLRLSCAASGFTPSNPAWSYRQAPGKLEWVAALIGRSGTFF 60			
DB	17 DVQLVEGGGLVDPGGRKSLSCAASGFTFSSFGHWRQAPDKCLEWVAALISGSSLTLY 76			
QY	61 ADVKGRFTTISRDNKNTVYLENNSLRAEDTAIYYCAKRGGRGKYKGMDVGQITVTV 120			
DB	77 ADYKGRFTTISRDPKNTLFLQMTSLSSDPTAMYYCA--WGNYPYAMDMVGQGSVTY 134			
QY	121 SS 122			
DB	135 SS 136			
RESULT 2				
ID	HV3C_HUMAN	STANDARD;	PRT;	117 AA.
AC	P01764;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	1g heavy chain V-III region VH26 precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81101090; PubMed=6450418;			
RA	Matthysens G., Rabbits T.H.;			
RT	"Structure and multiplicity of genes for the human immunoglobulin			
RL	heavy chain variable region.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J00236; AAA53516.1; -			
DR	EMBL; M35415; AAA58735.1; -			
DR	PIR; A02047; H3HU26.			
DR	PDB; 1HOU; 23-DEC-99.			
DR	Genew; HGNC:5545; IGHV0.			
DR	GO; GO:0005523; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	InterPro; IPR003596; Ig_V.			
DR	PIfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Signal; 3D-structure.			
FT	SIGNAL 1			
FT	CHAIN 19			
FT	CHAIN 20			
FT	DOMAIN 20			
FT	NON_TER 117			
FT	SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;			
Query Match		70.6%;	Score 453;	DB 1; Length 117;
Best Local Similarity		85.7%;	Pred. No. 1.4e-39;	
Matches	84;	Conservative	9;	Mismatches 5; Indels 0; Gaps 0;

Oy	1	EVOLVESGGDLVPGCSGLRLTSCAASGTFENFPMNSWRQAPGKLEWVAIIGRSSTTFY	60
Dt	20	EVOLLEBGGGLVPGGSLRLTSCAASGTFESYVMSWRQAPGKLEWVAISGSGSSTFY	79
Oy	61	ADSVKGRFTISRDNKNTVYLEMNSLRADETAIYYCAK	98
Dt	80	GDSVKGRTISRDNKNTVLYLQNSLRADETAIYYCAK	117
RESULT 3			
HV3D	HUMAN	STANDARD;	PRT; 115 AA.
AC	P01765;		
Dt	21-JUL-1986	(Rel. 01, Created)	
Dt	21-JUL-1986	(Rel. 01, Last sequence update)	
Dt	15-SEP-2003	(Rel. 42, Last annotation update)	
Dt	IG heavy chain V-II region	TIL.	
Dt	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CC	NCBI_TaxId=9606;		
CC	[1]		
CC	SEQUENCE.		
CC	MEDLINE=78005528; PubMed=409716;		
CC	Wang A.-C., Wang I.Y., Fudenberg H.H.;		
CC	"Immunoglobulin structure and genetics. Identity between variable		
CC	regions of a mu and a gamma2 chain.";		
CC	J. Biol. Chem. 252:7192-7199 (1977).		
CC	-1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS		
CC	OF IGH AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL		
CC	GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO		
CC	IDENTICAL.		
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.		
CC	PIR: A02048; H3HUTL.		
CC	HSSP: P01772; 2PB4.		
CC	GO: GO:0005572; C:extracellular; NAS.		
CC	GO: GO:0003823; F:antigen binding activity; NAS.		
CC	GO: GO:0006955; P:immune response; NAS.		
CC	InterPro: IPR007110; IG-1like.		
CC	InterPro: IPR003006; IG_MHC.		
CC	InterPro: IPR003596; IG_V.		
CC	Pfam: PF00047; Ig_1.		
CC	SMART; SM00406; IGV_1.		
CC	PROSITE; PS50835; IG-LIKE; 1.		
CC	Immunoglobulin V region.		
CC	DOMAIN 1 108		
CC	NON_TER 115 115		
CC	SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;		
Query Match 69.4%; Score 445.5; DB 1; Length 115;			
Best Local Similarity 73.0%; Pred. No. 8.1e-39;			
Matches 89; Conservative 9; Mismatches 17; Indels 7; Gaps 2;			
Oy	1	EVOLVESGGDLVPGCSGLRLTSCAASGTFENFPMNSWRQAPGKLEWVAIIGRSSTTFY	60
Dt	1	EVOLLEBGGGLVPGGSLRLTSCAASGTFESYVMSWRQAPGKLEWVAISGSGSSTFY	60
Oy	61	ADSVKGRFTISRDNKNTVYLEMNSLRADETAIYYCAKRGGRGYRYGMDVWGOSTTIV	120
Dt	61	ABSVMGRFTISRDNKNTVYLEMNSLRADETAIYYCAK---GKVSAYFYBVMGSGTIVT	113
Oy	121	SS 122	
Dt	114	SS 115	
RESULT 4			
HV3G	HUMAN	STANDARD;	PRT; 122 AA.
AC	P01768;		
Dt	21-JUL-1986	(Rel. 01, Created)	
Dt	21-JUL-1986	(Rel. 01, Last sequence update)	
Dt	15-SEP-2003	(Rel. 42, Last annotation update)	

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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:43:09 ; Search time 6.54102 Seconds
(without alignments)

877,119 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642
Sequence: 1 EVQLVESGGDLVPGGSLRL.....GKYRYGMVDWGQITTVSS 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	72.7	136	1	HV16_MOUSE
2	453	70.6	117	1	HV3C_HUMAN
3	445.5	69.4	115	1	HV3D_HUMAN
4	443	69.0	122	1	HV3G_HUMAN
5	439.5	68.5	115	1	HV3F_HUMAN
6	437	68.1	116	1	HV3I_HUMAN
7	433	67.4	122	1	HV3K_HUMAN
8	433	67.4	126	1	HV3L_HUMAN
9	432.5	67.1	120	1	HV3B_HUMAN
10	431	67.1	114	1	HV3H_HUMAN
11	428	66.7	122	1	HV3M_HUMAN
12	427.5	66.6	121	1	HV3J_HUMAN
13	422	65.7	119	1	HV3N_MOUSE
14	422	65.7	122	1	HV2I_MOUSE
15	420.5	65.5	123	1	HV18_MOUSE
16	420.5	65.5	123	1	HV25_MOUSE
17	419.5	65.3	123	1	HV19_MOUSE
18	419.5	65.3	123	1	HV23_MOUSE
19	419	65.0	122	1	HV20_MOUSE
20	417.5	65.0	120	1	HV3U_HUMAN
21	417	65.0	120	1	HV3V_HUMAN
22	416.5	64.9	123	1	HV22_MOUSE
23	410	63.9	111	1	HV35_MOUSE
24	409.5	63.8	116	1	HV05_CARAU
25	409.5	63.8	123	1	HV24_MOUSE
26	408.5	63.6	144	1	HV26_MOUSE
27	406	63.2	114	1	HV01_CANFA
28	405.5	63.2	115	1	HV33_MOUSE
29	405.5	63.2	119	1	HV31_MOUSE
30	405	63.1	119	1	HV40_MOUSE
31	403.5	62.9	119	1	HV37_MOUSE
32	403.5	62.9	113	1	HV30_MOUSE
33	403.5	62.9	142	1	HV01_RAT

34	398.5	62.1	113	1	HV27_MOUSE	P01796	mus	musculu
35	398.5	62.1	117	1	HV42_MOUSE	P01812	mus	musculu
36	397.5	61.9	118	1	HV39_MOUSE	P01809	mus	musculu
37	396.5	61.8	115	1	HV33_MOUSE	P01802	mus	musculu
38	396	61.7	119	1	HV3M_HUMAN	P01774	homo	sapien
39	395.5	61.6	113	1	HV31_MOUSE	P01800	mus	musculu
40	394.5	61.4	116	1	HV3Q_HUMAN	P01778	homo	sapien
41	394	61.4	117	1	HV3O_HUMAN	P01776	homo	sapien
42	393.5	61.3	119	1	HV3L_HUMAN	P01773	homo	sapien
43	392.5	61.1	113	1	HV28_MOUSE	P01797	mus	musculu
44	389	60.6	119	1	HV29_MOUSE	P01775	homo	sapien
45	388.5	60.5	113	1	HV29_MOUSE	P01798	mus	musculu

ALIGNMENTS

RESULT 1
HV16_MOUSE
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NDb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Mlstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).

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CC EMBL: J05522; AAD15290.1; -
DR PIR; B90809; GIM521.
DR PDB; 1ICG; 03-JUN-95.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
DR NON TER
FT SIGNAL 1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90
FT CONFLICT 115 115
FT CONFLICT 120 120
FT NON_TER 136 136
HYAD -> DYAD (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).

A>Title: Somatic diversification in the heavy chain variable region genes expressed by H
 A/Reference number: A36876; MUID:94119917; PMID:8290556
 A/Accession: J37780
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-147 <RES>
 A/Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/28-111/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 521; DB 2; Length 147;
 Best Local Similarity 82.3%; Pred. No. 1.4e-39;
 Matches 102; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 60
 |||||
 DB 14 EVOLVESGGGLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 73
 |||||
 QY 61 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 118
 |||||
 DB 74 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 133
 |||||
 QY 119 TVSS 122
 |||||
 DB 134 TVSS 137

RESULT 3

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31666
 R/Custringer: A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
 Submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31666
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-138 <CUI>
 A/Cross-references: EMBL:214202; NID:g30963; PIDN:CAA78571.1; PID:g30964
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 514.5; DB 2; Length 138;
 Best Local Similarity 81.1%; Pred. No. 4.9e-39;
 Matches 99; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 60
 |||||
 DB 20 EVOLVESGGGLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 79
 |||||
 QY 61 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 120
 |||||
 DB 80 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 136
 |||||
 QY 121 SS 122
 |||||
 DB 137 SS 138

RESULT 4

Ig heavy chain - human

C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31107
 R/Asphoret, P.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
 A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31107
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-119 <RAA>
 A/Cross-references: EMBL:X62955
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 510.5; DB 2; Length 119;
 Best Local Similarity 82.0%; Pred. No. 9.7e-39;
 Matches 100; Conservative 8; Mismatches 11; Indels 3; Gaps 2;

QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 60
 |||||
 DB 1 EVOLVESGGGLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 60
 |||||
 QY 61 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 120
 |||||
 DB 61 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 117
 |||||
 QY 121 SS 122
 |||||
 DB 118 SS 119

RESULT 5

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human

C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S48798
 R/Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 Submitted to the EMBL Data Library, October 1994
 A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A/Reference number: S48797
 A/Accession: S48798
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-120 <MAH>
 A/Cross-references: EMBL:Z46382; NID:g562324; PIDN:CAA86521.1; PID:g1340167
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 509; DB 2; Length 120;
 Best Local Similarity 80.8%; Pred. No. 1.3e-38;
 Matches 101; Conservative 9; Mismatches 7; Indels 8; Gaps 3;

QY 1 EVOLVESGDLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 60
 |||||
 DB 1 EVOLVESGGGLVOPGSLRLSCAASGFTFSNPAWVRQAPGKLEWVAIGRSGTTFY 60
 |||||
 QY 61 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 117
 |||||
 DB 61 ADSVKGRTTISRDNKNTLYLEKNSLRADTAIYYCAKRGKGYKYYGMDVWGQGTTV 115
 |||||
 QY 118 TVSS 122
 |||||
 DB 116 TVSS 120

RESULT 6

Ig heavy chain V region (30p1) - human

C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
 C/Accession: C36005
 R/Schroeder Jr., H.M.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A/Reference number: A36005; MUID:90349571; PMID:2117273

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OM protein - protein search, using BW model

Run on: December 30, 2003, 10:47:09 ; Search time 11.6946 Seconds
(without alignments)
1003.251 Million cell updates/sec

Title: US-09-674-752-53

Sequence: 1 EVQLVESGGDLVPGGSLRL.....GKYKGMVDVWGQTTVTS 122

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	547.5	85.3	160	2 S05271	Ig heavy chain pre
2	521	81.2	147	2 I37780	Ig variable region
3	514.5	80.1	138	2 S31666	Ig heavy chain V r
4	510.5	79.5	119	2 S31107	Ig heavy chain - h
5	509	79.3	120	2 S48798	Ig heavy chain V r
6	507.5	79.0	119	2 C36005	Ig heavy chain V r
7	500.5	78.0	119	2 S31108	Ig heavy chain - h
8	500.5	78.0	127	2 S38489	Ig heavy chain - h
9	499.5	77.8	140	2 S31588	Ig heavy chain V r
10	499	77.7	122	2 B36005	Ig heavy chain V r
11	498.5	77.6	119	2 D36005	Ig heavy chain V r
12	497.5	77.5	123	2 S26794	Ig heavy chain V r
13	494.5	77.0	140	2 S31686	Ig heavy chain V r
14	493.5	76.9	123	2 S31114	Ig heavy chain - h
15	491.5	76.6	120	2 S23624	Ig heavy chain V r
16	490	76.3	123	2 S49590	Ig heavy chain V r
17	488.5	76.1	121	2 I55673	Ig heavy chain - h
18	487	75.9	128	2 S48797	Ig heavy chain V r
19	485.5	75.6	134	2 S31699	Ig heavy chain V r
20	484.5	75.5	140	2 A30532	Ig heavy chain pre
21	484	75.4	122	2 PC2398	anti-tetanus toxin
22	482	75.1	123	2 PH1647	Ig heavy chain V r
23	480.5	74.8	123	2 S38493	Ig heavy chain - h
24	479.5	74.7	121	2 S31113	Ig heavy chain - h
25	479.5	74.7	125	2 S30531	Ig heavy chain V r
26	478	74.5	124	2 S20782	Ig heavy chain V r
27	476.5	74.2	109	2 PH1649	Ig heavy chain V r
28	474	73.8	120	2 S44111	Ig heavy chain V-D
29	473	73.7	135	2 I37778	Ig variable region

30	470.5	73.3	134	2 S31679	Ig heavy chain V r
31	470	73.2	128	2 S31595	Ig heavy chain V r
32	469.5	73.1	117	2 S78486	Ig heavy chain V r
33	469	73.1	140	2 S70442	Ig heavy chain pre
34	469	73.1	141	2 S31669	Ig heavy chain V r
35	467	72.7	108	2 PH1648	Ig heavy chain V r
36	467	72.7	128	2 S26790	Ig heavy chain V r
37	467	72.7	136	1 G1MS21	Ig heavy chain pre
38	466.5	72.7	121	2 S19666	Ig heavy chain V r
39	465	72.4	139	2 S38808	Ig heavy chain - m
40	464.5	72.4	127	2 S19878	Ig heavy chain V r
41	464	72.3	139	2 S31674	Ig heavy chain V r
42	462.5	72.0	121	2 S31106	Ig heavy chain (eu
43	462.5	72.0	121	2 S31106	Ig heavy chain - h
44	462	72.0	145	2 S11239	Ig heavy chain V r
45	461.5	71.9	119	2 F36005	Ig heavy chain V r

ALIGNMENTS

RESULT 1

Ig heavy chain precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996

C/Accession: S05271, S04602

R/Kishimoto, T.
Submitted to the EMBL Data Library, March 1989

A/Reference number: S05270

A/Accession: S05271

A/Molecule type: mRNA

A/Residues: 1-160 <KIS1>

A/Cross-references: EMBL:X14584

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A/Reference number: S04601; MUID:89296497; PMID:2500644

A/Accession: S04602

A/Molecule type: mRNA

A/Residues: 1-144 <KIS2>

A/Cross-references: EMBL:X14584

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/1-19/Domain: signal sequence #status predicted <Sig>

F/20-160/Product: Ig heavy chain (fragment) #status predicted <Mat>

F/34-117/Domain: immunoglobulin homology <Imm>

Query Match 85.3%; Score 547.5; DB 2; Length 160;

Best Local Similarity 84.0%; Pred. No. 6.5e-42;

Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFRPMQVRQAPGKLEWVAALIGRSSTYY 60

Db 20 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFRPMQVRQAPGKLEWVAALIGRSSTYY 79

QY 61 AOSVKGRTISRDNSTVLENNSLRAEDTAIVYCAK---RGRGKYKGMVDVWGQTT 117

Db 80 AOSVKGRTISRDNSTVLENNSLRAEDTAIVYCAKAVRQVSTYYTGDMVGQTT 139

QY 118 VTVSS 122

Db 140 VTVSS 144

RESULT 2

Ig variable region (VDJ) (clone T20-11) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C/Accession: I37780; S25474

R/Demaision, C.; Chaetegner, P.; These, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

QY 61 AOKFQGRVTTTADSTSTAYMELSTLTSEDTAVYCYELD-----WFIYMGQ 107
DB 80 SQNFORVITTDKSTSTAYMELSTLTSEDTAVYCYELRQANPDRARVGFDPWGG 139
QY 108 TMTVSS 114
DB 140 TMTVSS 146

RESULT 15

US-08-652-816A-7

; Sequence 7, Application US/08652816A

; Patent No. 5872215

; GENERAL INFORMATION:

; APPLICANT: Osbourn, JK

; APPLICANT: Allen, DJ

; TITLE OF INVENTION: Specific binding members, materials and

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,816A

; FILING DATE: 23-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9125579.4

; FILING DATE: 02-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9125579.8

; FILING DATE: 02-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206372.6

; FILING DATE: 23-SEP-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9525004.9

; FILING DATE: 07-DEC-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9610824.6

; FILING DATE: 23-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/02240

; FILING DATE: 02-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/244,597

; FILING DATE: 01-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: David W. Clough

; REGISTRATION NUMBER: 36,107

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 123 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-652-816A-7

; Query Match

; Best Local Similarity

Matches 95; Conservative 8; Mismatches 11; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPGQLEWGGDIIPIIGTGY 60

DB 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPGQLEWGGDIIPIIGTGY 60

QY 61 AOKFQGRVTTTADSTSTAYMELSTLTSEDTAVYCYELD-----WFIYMGQ 111

DB 61 AOKFQGRVTTTADSTSTAYMELSTLTSEDTAVYCYELD-----WFIYMGQ 120

QY 112 VSS 114

DB 121 VSS 123

Search completed: December 30, 2003, 11:05:36

Job time: 11.6593 secs

78.8%; Score 470.5; DB 2; Length 123;

77.2%; Pred. No. 2.1e-41;

```
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howell, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: BOR
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
PCT-US93-10555-12

Query Match          79.5%; Score 474.5; DB 5; Length 120;
Best Local Similarity 79.2%; Pred. No. 8e-42;
Matches 95; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

OY 2 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 61
DB 1 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 60
OY 62 OKFGQRTVITADESTAYMELSTLTSEDTAVYYC-----ELDMFYWGQTMVTYSS 114
DB 61 OKFGQRTVITADESTAYMELSTLTSEDTAVYYC-----ELDMFYWGQTMVTYSS 120

RESULT 13
PCT-US93-10555-13
Sequence 13, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Judas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howell, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
```

```
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: KAS
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
PCT-US93-10555-13

Query Match          79.5%; Score 474.5; DB 5; Length 120;
Best Local Similarity 78.3%; Pred. No. 8e-42;
Matches 94; Conservative 7; Mismatches 12; Indels 7; Gaps 1;

OY 2 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 61
DB 1 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 60
OY 62 OKFGQRTVITADESTAYMELSTLTSEDTAVYYCELDW-----FYWGQTMVTYSS 114
DB 61 OKFGQRTVITADESTAYMELSTLTSEDTAVYYCAKEGYDYGPRPDPFGQGLTVYSS 120

RESULT 14
US-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-10

Query Match          79.0%; Score 471.5; DB 2; Length 476;
Best Local Similarity 72.4%; Pred. No. 8.4e-41;
Matches 92; Conservative 11; Mismatches 11; Indels 13; Gaps 1;

OY 1 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 60
DB 20 QMVOVSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTPTV 79
```

TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: BOR
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
US-08-428-197-12
Query Match 79.5%; Score 474.5; DB 2; Length 120;
Best Local Similarity 79.2%; Pred. No. 8e-42;
Matches 95; Conservative 7; Mismatches 11; Indels 7; Gaps 1;
QY 2 VOLVSGAEVKKKPGSSVKVSCKASGTFSSHAISWVROAPGGGLEMMGDIIPILGTGNYA 61
DB 1 VOLVSGAEVKKKPGSSVKVSCKASGTFSSHAISWVROAPGGGLEMMGDIIPILGTGNYA 60
QY 62 OKFGQRTITADESTAYMELSTLTSEDYAVYCELDWFIYWGGMVTVSS 114
DB 61 OKFGQRTITADESTAYMELSTLTSEDYAVYCELDWFIYWGGMVTVSS 120
RESULT 11
US-08-428-197-13
Sequence 13, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California

COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: KAS
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
US-08-428-197-13
Query Match 79.5%; Score 474.5; DB 2; Length 120;
Best Local Similarity 78.3%; Pred. No. 8e-42;
Matches 94; Conservative 7; Mismatches 12; Indels 7; Gaps 1;
QY 2 VOLVSGAEVKKKPGSSVKVSCKASGTFSSHAISWVROAPGGGLEMMGDIIPILGTGNYA 61
DB 1 VOLVSGAEVKKKPGSSVKVSCKASGTFSSHAISWVROAPGGGLEMMGDIIPILGTGNYA 60
QY 62 OKFGQRTITADESTAYMELSTLTSEDYAVYCELDWFIYWGGMVTVSS 114
DB 61 OKFGQRTITADESTAYMELSTLTSEDYAVYCELDWFIYWGGMVTVSS 120
RESULT 12
PCT-US93-10555-12
Sequence 12, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993

Db 61 AOKFQGRLLTTADESTAYMELSLRSEDYAVYVCAGSHITYELYYMDVWGQTMVT 120
QY 112 VSS 114
121 VSS 123

RESULT 8
US-08-232-081B-41
Sequence 41, Application US/08232081B
Patent No. 5886152

GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: peptide

Query Match 79.8%; Score 476.5; DB 2; Length 121;
Best Local Similarity 77.7%; Pred. No. 5.1e-42;
Matches 94; Conservative 8; Mismatches 12; Indels 7; Gaps 1;

QY 1 QVQVVGSGAEVKKPSSVYKSCVAGSGTSSHAISWVROAPGQGLEMGDIIPIIGTGY 60
Db 1 EYVLVSGAEVKKPSSVYKSCVAGSGTSSHAISWVROAPGQGLEMGDIIPIIGTGY 60
QY 61 AOKFQGRVITTADESTAYMELSLTSEDTAVYYC-----FTYWGQTMVTS 113
Db 61 AOKFQGRVITTADESTAYMELSLRSDTAVYCAKEGYGDPFDFWGQTLVTS 120
QY 114 S 114
Db 121 S 121

RESULT 9
US-08-983-607-50
Sequence 50, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Klineky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes

IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fuses
LIBRARY: fusion phage construct
CLONE: 2-71
FEATURE:
NAME/KEY: heavy chain

US-08-983-607-50
Query Match 79.5%; Score 474.5; DB 3; Length 119;
Best Local Similarity 83.9%; Pred. No. 8e-42;
Matches 94; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 8 GAEVKKPSSVYKSCVAGSGTSSHAISWVROAPGQGLEMGDIIPIIGTGYAOKFQGR 67
Db 8 GLEVKKPSSVYKSCVAGSGTSSHAISWVROAPGQGLEMGDIIPIIGTGYAOKFQGR 67
QY 68 VITTADESTAYMELSLTSEDTAVYYC-----ELDFYIWGQTMVTS 114
Db 68 VITTADESTAYMELSLRSEDYAVYVCAGGGRYDAFDIWGQTLVTS 119

RESULT 10
US-08-428-197-12
Sequence 12, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF